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## DialogIP

**In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer**

**Patent Assignee:** HENKEL KGAA

**Inventors:** CONRADT M; HOFMANN K; PETERSOHN D

## Patent Family

Patent Number	Kind	Date	Application Number	Kind	Date	Week	Type
WO 200253774	A2	20020711	WO 2001EP15179	A	20011220	200263	B
DE 10100127	A1	20021002	DE 1000127	A	20010103	200273	

**Priority Applications (Number Kind Date):** DE 1000127 A ( 20010103)

## Patent Details

Patent	Kind	Language	Page	Main IPC	Filing Notes
WO 200253774	A2	G		C12Q-001/68	
Designated States (National): AU BG BR BY CA CN CZ DZ HU ID IL IN JP KR MX NO NZ PL RO RU SG SI SK UA US UZ VN YU ZA					
Designated States (Regional): AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR					
DE 10100127	A1			C12Q-001/68	

**Abstract:**

WO 200253774 A2

**NOVELTY** In vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors (A), from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression, is new.

**DETAILED DESCRIPTION INDEPENDENT CLAIMS** are also included for:

- (1) identifying (M2) genes important for skin homeostasis which includes comparing the SAGE results with similar results from other tissues to identify those genes having markedly different expression in skin compared with other tissues;
- (2) determining (M3) homeostasis of skin by comparing the pattern of (A) in a test sample with the pattern derived from SAGE analysis;
- (3) test kit, or biochip, for (M3);
- (4) determining (M4) activity of pharmaceutical or cosmetic compounds for maintenance or promotion of skin homeostasis and for treating skin disorders;
- (5) test kit for (M4); and
- (6) screening (M5) to identifying compounds useful for maintenance or promotion of skin homeostasis and for treating

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skin disorders.

**ACTIVITY** Dermatological; Vulnerary; Antipsoriatic; Antiseborrheic; Immunosuppressive; Antiinflammatory; Cytostatic.

No test details given.

**MECHANISM OF ACTION** None given.

**USE** (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintain or promote skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin.

pp; 1345 DwgNo 0/0

**Technology Focus:**

**TECHNOLOGY FOCUS - BIOLOGY** - Preferred Materials: (A) are proteins, mRNA or their fragments.

**Preferred Method:** In (M3), the (A) being detected/quantified are reproduced in tables in the specification, together with their relative expression frequencies and expression quotients. A sample is assessed as healthy if most (A) present are those expressed in skin at least twice the level in other tissues, but as unhealthy if most (A) are normally expressed at higher levels in tissues other than skin. Especially the samples are tested for (A) that have even higher levels of differential expression, particularly up to 100-fold higher level in skin. The test sample is whole skin or epidermis and (A) are isolated by microdialysis. (A) that are proteins are detected e.g. by electrophoresis, affinity chromatography or by using a protein chip, and those that are mRNA are detected e.g. by Northern blotting, reverse-transcription polymerase chain reaction and subtractive hybridization. Samples are tested for up to 500, preferably 10-50, different (A).

**Preferred Biochip:** This comprises a carrier on which are immobilized probes that bind specifically to (A). The probes are nucleic acids or antibodies.

**Preferred Process:** In (M4), the status of gene expression in the skin is tested before and after treatment with active compounds and the results compared. (M5) is essentially the same.

**BIOTECHNOLOGY** - Preferred materials: Where (A) is mRNA, the probes on the biochip are RNA, peptide-nucleic acid or particularly DNA of 10-1000, preferably 200-400 bases.

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Dialog® File Number 351 Accession Number 14769934

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⑮ **BUNDESREPUBLIK  
DEUTSCHLAND**



**DEUTSCHES  
PATENT- UND  
MARKENAMT**

⑫ **Offenlegungsschrift**  
⑩ **DE 101 00 127 A 1**

⑤① Int. Cl.<sup>7</sup>:  
**C 12 Q 1/68**

⑦① Aktenzeichen: 101 00 127.4  
⑦② Anmeldetag: 3. 1. 2001  
⑦③ Offenlegungstag: 2. 10. 2002

**DE 101 00 127 A 1**

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⑤⑤ Entgegenhaltungen:

US 58 07 581 A

Combining serial analysis of gene expression and array technologies to identify genes differentially expressed in breast cancer, NACHT, M. u.a., Cancer Research (1999) 59, 5464-5470; Datenbank MEDLINE bei STN; AN 2001070517 zu: miniSAGE: gene expression profiling using serial analysis of gene expression from 1 microg total RNA. YE, S.Q. u.a., ANALYTICAL BIOCHEMISTRY, (2000 Dec 1) 287 (1) 144-52 [recherchiert am 12.10.2001];

Expression analysis with oligonucleotide micro-arrays reveals that MYC regulates genes involved in growth, cell cycle, signaling, and adhesion. COLLIER, H.A. u.a., Proc. Natl. Acad. Sci. USA (March 28 2000) 97, 3260-3265;

**Die folgenden Angaben sind den vom Anmelder eingereichten Unterlagen entnommen**

Prüfungsantrag gem. § 44 PatG ist gestellt

⑤④ Verfahren zur Bestimmung der Homeostase der Haut

⑤⑦ Die vorliegende Erfindung betrifft ein Verfahren zur Bestimmung der Homeostase der Haut bei Menschen in vitro, Test-Kits und Biochips zur Bestimmung der Homeostase der Haut sowie die Verwendung von Proteinen, mRNA-Molekülen oder Fragmenten von Proteinen oder mRNA-Molekülen als Marker für die Homeostase der Haut; ferner ein Testverfahren zum Nachweis der Wirksamkeit von kosmetischen oder pharmazeutischen Wirkstoffen zur Aufrechterhaltung oder Förderung der Homeostase der Haut bzw. zur Behandlung pathologischer Zustände der Haut sowie ein Screening-Verfahren zur Identifikation von kosmetischen oder pharmazeutischen Wirkstoffen zur Aufrechterhaltung oder Förderung der Homeostase der Haut bzw. zur Behandlung pathologischer Zustände der Haut und ein Verfahren zur Herstellung einer kosmetischen oder pharmazeutischen Zubereitung zur Aufrechterhaltung oder Förderung der Homeostase der Haut bzw. zur Behandlung pathologischer Zustände der Haut.

**DE 101 00 127 A 1**

[0001] Die vorliegende Erfindung betrifft ein Verfahren zur Bestimmung der Homeostase der Haut bei Menschen in vitro, Test-Kits und Biochips zur Bestimmung der Homeostase der Haut sowie die Verwendung von Proteinen, mRNA-Molekülen oder Fragmenten von Proteinen oder mRNA-Molekülen als Marker für die Homeostase der Haut; ferner ein Testverfahren zum Nachweis der Wirksamkeit von kosmetischen oder pharmazeutischen Wirkstoffen zur Aufrechterhaltung oder Förderung der Homeostase der Haut bzw. zur Behandlung pathologischer Zustände der Haut, sowie ein Screening-Verfahren zur Identifikation von kosmetischen oder pharmazeutischen Wirkstoffen zur Aufrechterhaltung oder Förderung der Homeostase der Haut bzw. zur Behandlung pathologischer Zustände der Haut und ein Verfahren zur Herstellung einer kosmetischen oder pharmazeutischen Zubereitung zur Aufrechterhaltung oder Förderung der Homeostase der Haut bzw. zur Behandlung pathologischer Zustände der Haut.

[0002] Die Entwicklung eukaryotischen Lebens beginnt, abgesehen von der vegetativen Vermehrung, mit der Fusion zweier Gameten. Es entsteht eine Zygote, die der Ursprung einer jeden Zelle eines Eukaryoten ist. Die räumlich und zeitlich geordnete Differenzierung der Tochterzellen einer Zygote ist entscheidend für die Ontogenese eines vielzelligen Organismus. Sie führt zu verschiedensten Zelltypen, die sich in ihrer Morphologie und in ihrer Funktion unterscheiden. Vergleicht man beim Menschen z. B. eine Nervenzelle mit einer Zelle der Epidermis, so sind die Zellen sehr unterschiedlich, obwohl beide den gleichen Ursprung und das gleiche Genom haben. Die Differenzierung von Zellen geht mit Veränderung von Genexpressionsmustern einher. Im differenzierten Zustand exprimieren Zellen die für sie typischen Gene. Welche Gene dabei eine Rolle für die Morphologien und Funktionen z. B. der Hautzellen spielen ist bis heute weitgehend unklar. Die geordnete Regulation der Genexpression in der Haut ist für die Aufrechterhaltung der Homeostase des Organs von entscheidender Bedeutung. Jede lebende Zelle ist in der Lage auf Signale ihrer Umwelt zu reagieren. Die Reaktionen der Zellen werden durch eine geordnete Regulation der Genexpression realisiert, sodaß der Metabolismus von Zellen nicht statisch sondern sehr dynamisch ist.

[0003] Die Expression der Gene in differenzierten Zellen der Haut ist nicht statisch sondern sehr dynamisch. Extrazelluläre Stimuli wirken über zum Teil komplexe Signaltransduktionskaskaden auf die Transkription lebender Zellen. Die Regulation der Transkription als Antwort auf extrazelluläre Signale wird als Stimulus-Transkriptions-Kopplung bezeichnet. Die Beeinflussung dieses empfindlichen Regulationsmechanismus kann zur Störung der Homeostase der Haut und möglicherweise zur Entstehung und Manifestation pathogener Zustände der Haut führen.

[0004] Das menschliche Genom umfasst nach jüngsten Schätzungen ca. 140 000 Gene. Von diesem immensen Informationsangebot verwendet jede Zelle jedoch lediglich einen kleinen, für sie spezifischen Teil für die Synthese von Proteinen, der sich im Genexpressionsmuster widerspiegelt. Welche Gene insbesondere in der Haut eine Rolle spielen ist bisher weitgehend unklar.

[0005] Die Haut ist das größte Organ des menschlichen Körpers. Sie ist ein sehr komplex aufgebautes Organ, welches aus einer Vielzahl verschiedener Zelltypen besteht und die Grenzfläche des Körpers zur Umwelt bildet. Diese Tatsache verdeutlicht, dass die Zellen der Haut in besonderem Maße exogenen Signalen der Umwelt, physikalischer und chemischer Natur ausgesetzt. Für das Verständnis von Hautreaktionen auf exogene Stimuli ist die Analyse der Genexpression in der Haut von entscheidender Bedeutung.

[0006] Ein entscheidendes Merkmal der Haut ist, dass mit zunehmendem Alter, unter dem Einfluss hautschädigender Stimuli oder bei pathologischen Zuständen der Haut die Zellen ihre Fähigkeit verlieren die Homeostase des Organs aufrecht zu erhalten. Welche molekularen Mechanismen dieser Entwicklung zugrunde liegen ist bislang weitgehend unklar. Die Identifikation neuer hautspezifischer Marker ermöglicht, den komplexen Zustand der Homöostase, die Entstehung und Manifestation hautpathogener Zustände zu begreifen. Nur mit diesem Wissen können neue Konzepte für Produkte zur Hautbehandlung entwickelt werden.

[0007] Jeder Zelltyp der Haut exprimiert ca. 15 000 verschiedene Gene und synthetisiert daraus entsprechend viele Proteine. Welche Gene davon für die Homeostase der Haut eine Rolle spielen oder an pathogenen Prozessen beteiligt sind ist bisher jedoch weitgehend unklar.

[0008] Die Haut besteht aus mehreren verschiedenen Zelltypen (Fibroblasten, Keratinozyten in verschiedenen Differenzierungszuständen, Melanozyten, Merkelzellen, Langerhanszellen, Haarfollikelzellen, Schweißdrüsenzellen etc.), so dass die Komplexität in der Haut exprimierter Gene sehr groß ist. Es ist bisher nicht möglich gewesen, diese immense Komplexität zu beschreiben. Ebenso wenig war es bisher möglich aus dieser Komplexität die Gene zu identifizieren, die exklusiv bzw. besonders stark in der Haut exprimiert werden.

[0009] In lebenden Zellen kommen mRNA-Moleküle in Konzentrationen zwischen einigen wenigen und mehreren hundert Kopien vor. Die schwach exprimierten Gene sind bisherigen Analysen nicht oder nur sehr schwer zugänglich gewesen. Diese Moleküle können aber durchaus eine entscheidende Rolle für die Homeostase der Haut spielen oder an der Entstehung bzw. Manifestation pathogener Prozesse in der Haut beteiligt sein.

[0010] Die Gesamtheit aller mRNA-Moleküle, die von einer Zelle oder einem Gewebe zu einem bestimmten Zeitpunkt synthetisiert werden, bezeichnet man als "Transkriptom". Bis heute ist es nicht möglich gewesen das komplette Transkriptom, also die Gesamtheit aller transkribierten Gene, der humanen Haut zu beschreiben.

[0011] Die Analyse der Genexpression ist zwar mit der Quantifizierung spezifischer mRNA-Moleküle möglich (z. B. Northern-Blot, RNase-Schutzexperimente). Mit diesen Techniken können jedoch nur eine relativ begrenzte Anzahl an Genen gemessen werden.

[0012] Es besteht daher ein Bedarf an der Identifikation möglichst vieler, vorzugsweise aller, in menschlicher Haut aktiven Gene.

[0013] Aufgabe der vorliegenden Erfindung ist es daher, einen möglichst großen Teil der in menschlicher Haut exprimierten Gene zu identifizieren; ferner, die für die Homeostase der Haut bedeutsamen Gene zu identifizieren. Außerdem sollen mittels der identifizierten Gene, Verfahren zur Bestimmung der Homeostase der Haut bereitgestellt werden.

[0014] Diese erste Aufgabe wird erfindungsgemäß gelöst durch ein Verfahren (1) zur Identifizierung der in Haut exprimierten Gene bei Menschen in vitro, das dadurch gekennzeichnet ist, daß man

- a) ein Gemisch von in menschlicher Haut exprimierten, d. h. transkribierten genetisch codierten Faktoren, also von mRNA-Molekülen oder Fragmenten von mRNA-Molekülen aus menschlicher Haut gewinnt und  
 b) das in a) gewonnenen Gemisch einer Seriellen Analyse der Genexpression (SAGE) unterwirft, und dadurch die in menschlicher Haut exprimierten Gene identifiziert und ihre Expression quantifiziert.

[0015] Die zweite Aufgabe wird erfindungsgemäß gelöst durch ein Verfahren (2) zur Identifizierung der für die Homeostase der Haut bedeutsamen Gene bei Menschen in vitro, das dadurch gekennzeichnet ist, daß man

- a) ein Gemisch von in menschlicher Haut exprimierten, d. h. transkribierten genetisch codierten Faktoren, also von mRNA-Molekülen oder Fragmenten von mRNA-Molekülen aus menschlicher Haut gewinnt,  
 b) das in a) gewonnenen Gemisch einer Seriellen Analyse der Genexpression (SAGE) unterwirft, und dadurch die in menschlicher Haut exprimierten Gene identifiziert und ihre Expression quantifiziert und  
 c) die Analyseergebnisse aus b) mit Expressionsmustern anderer Gewebe vergleicht und so die Gene identifiziert, die in Haut und anderen Geweben unterschiedlich stark (differentiell) exprimiert werden.

[0016] Expressionsmuster anderer Gewebe sind beispielsweise in den Datenbanken des Cancer Genome Anatomy Project (CGAP) im Internet unter folgender Adresse zugänglich: <http://cgap.nci.nih.gov/>

[0017] Zur Erfassung des Transkriptoms der Haut wurde die Technik der "Seriellen Analyse der Genexpression" (SAGE™) eingesetzt. Diese Technik erlaubt gleichzeitig die Identifikation und Quantifizierung aller in der Haut exprimierten Gene. Der Vergleich des Transkriptoms der Haut, mit dem Transkriptom anderer Gewebe lässt die Unterscheidung zwischen relevanten und nicht relevanten Genen für die Homeostase der Haut zu.

[0018] Für die SAGE™-Analyse wurde humane Haut von gesunden weiblichen Spendern verwendet. Die Durchführung der SAGE™-Analyse erfolgte wie in der EP-A-0 761 822 und bei Velculescu, V. E. et al., 1995 Science 270, 484-487, beschrieben und führte zur Identifikation der in Haut aktiven Gene.

[0019] Diese Gene sind dazu geeignet die Homeostase der Haut zu bestimmen oder pathologische Prozesse oder Zustände zu detektieren.

[0020] Die Tabelle 6 enthält eine detaillierte Auflistung der mit Hilfe des erfindungsgemäßen Verfahrens (1) ermittelten, in menschlicher Haut aktiven Gene unter Angabe

- einer laufenden Ordnungsnummer in Spalte 1,  
 der verwendeten Tag-Sequenz in Spalte 2,  
 der ermittelten relativen Expressionsfrequenz in Haut in Spalte 3,  
 der Signifikanz in Spalte 4,  
 der UniGene-Accession-Number in Spalte 5 und  
 einer Kurzbeschreibung des Gens bzw. Genproduktes in Spalte 6.

[0021] Die Tabellen 1 bis 5 enthalten eine detaillierte Auflistung der mit Hilfe des erfindungsgemäßen Verfahrens (2) ermittelten, in Haut und in anderen Geweben differentiell exprimierten Gene unter Angabe

- einer laufenden Ordnungsnummer in Spalte 1,  
 der verwendeten Tag-Sequenz in Spalte 2,  
 der ermittelten relativen Expressionsfrequenz im CGAP (Cancer Genome Anatomy Project) in Spalte 3,  
 der ermittelten relativen Expressionsfrequenz in Haut in Spalte 4,  
 des Quotienten der Frequenzen (aus Spalte 3 und Spalte 4) in Spalte 5,  
 der Signifikanz in Spalte 6,  
 der UniGene-Accession-Number in Spalte 7 und  
 einer Kurzbeschreibung des Gens bzw. Genproduktes in Spalte 8.

[0022] Der Quotient in Spalte 5 gibt die Stärke der differentiellen Expression an, d. h., um welchen Faktor das jeweilige Gen in Haut stärker exprimiert wird, als in anderen Geweben.

[0023] Unter ihrer UniGene-Accession-Number sind die jeweiligen Gene bzw. Genprodukte in der Datenbank des National Center for Biotechnology Information (NCBI) offenbart. Diese Datenbank ist im Internet unter folgender Adresse zugänglich: <http://www.ncbi.nlm.nih.gov/>.

[0024] Die Gene bzw. Genprodukte sind außerdem unter den Internet-Adressen  
<http://www.ncbi.nlm.nih.gov/UniGene/Hs.Home.html> oder  
<http://www.ncbi.nlm.nih.gov/genomic/guide> direkt zugänglich.

[0025] Die Daten des Cancer Genome Anatomy Project sind im Internet unter folgender Adresse zugänglich: <http://cgap.nci.nih.gov/>

[0026] In Tabelle 1 sind alle Gene aufgelistet, die mindestens 2-fach und weniger als 5-fach differentiell exprimiert sind.

[0027] In Tabelle 2 sind alle Gene aufgelistet, die mindestens 5-fach und weniger als 10-fach differentiell exprimiert sind.

[0028] In Tabelle 3 sind alle Gene aufgelistet, die mindestens 10-fach und weniger als 20-fach differentiell exprimiert sind.

[0029] In Tabelle 4 sind alle Gene aufgelistet, die mindestens 20-fach und weniger als 100-fach differentiell exprimiert sind.

[0030] In Tabelle 5 sind alle Gene aufgelistet, die mindestens 100-fach differentiell exprimiert sind.

[0031] Die dritte der vorliegenden Erfindung zugrundeliegende Aufgabe wird erfindungsgemäß gelöst durch ein Ver-

fahren (3) zur Bestimmung der Homeostase der Haut bei Menschen, insbesondere bei Frauen, in vitro, das dadurch gekennzeichnet ist, daß man

- a) ein Gemisch von Proteinen, mRNA-Molekülen oder Fragmenten von Proteinen oder mRNA-Molekülen aus menschlicher Haut gewinnt,
- b) das gewonnene Gemisch auf das Vorhandensein und gegebenenfalls die Menge von mindestens einem der Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen untersucht, die mittels Serieller Analyse der Genexpression (SAGE) als in Haut und anderen Geweben unterschiedlich stark (differentiell) exprimiert identifiziert werden,
- c) die Untersuchungsergebnisse aus b) mit den mittels Serieller Analyse der Genexpression (SAGE) identifizierten Expressionsmustern vergleicht und
- d) das in b) untersuchte Gemisch gesunder bzw. in Homeostase befindlicher Haut zuordnet, wenn es überwiegend Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen enthält, die in Haut stärker exprimiert werden als in anderen Geweben, oder das in b) untersuchte Gemisch kranker bzw. in gestörter Homeostase befindlicher Haut zuordnet, wenn es überwiegend Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen enthält, die in anderen Geweben stärker exprimiert werden als in Haut.

[0032] Es kann in Schritt b) des Verfahrens zur Bestimmung der Homeostase der Haut ausreichend sein, das gewonnene Gemisch auf das Vorhandensein von mindestens einem der Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen zu untersuchen, die mittels Serieller Analyse der Genexpression (SAGE) als in Haut und anderen Geweben differentiell exprimiert identifiziert werden, wenn diese ausschließlich in Haut oder ausschließlich in anderen Geweben exprimiert werden. In allen anderen Fällen muß in Schritt b) auch die Menge der differentiell exprimierten Moleküle untersucht werden, d. h., die Expression muß quantifiziert werden.

[0033] In Schritt d) des Verfahrens zur Bestimmung der Homeostase der Haut wird das in b) untersuchte Gemisch gesunder bzw. in Homeostase befindlicher Haut zugeordnet, wenn es überwiegend Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen enthält, die in Haut stärker exprimiert werden als in anderen Geweben, d. h., daß das Gemisch entweder mehr unterschiedliche typischerweise in Haut exprimierte Verbindungen enthält, als solche, die typischerweise in anderen Geweben exprimiert werden (qualitative Differenzierung), oder mehr Kopien von typischerweise in Haut exprimierten Verbindungen enthält, als typischerweise in anderen Geweben vorhanden sind (quantitative Differenzierung). Für die Zuordnung zu kranker bzw. in gestörter Homeostase befindlicher Haut wird in komplementärer Weise verfahren.

[0034] Eine bevorzugte Ausführungsform des erfindungsgemäßen Verfahrens zur Bestimmung der Homeostase der Haut ist dadurch gekennzeichnet, daß man in Schritt b) das gewonnene Gemisch auf das Vorhandensein und gegebenenfalls die Menge von mindestens einem der Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen untersucht, die in den Tabellen 1 bis 5 in Spalte 7 durch ihre UniGene-Accession-Number definiert werden, in Schritt c) die Untersuchungsergebnisse aus b) mit den in den Tabellen 1 bis 5 in den Spalten 3 und 4 angegebenen relativen Expressionsfrequenzen sowie den in Spalte 5 angegebenen Expressionsquotienten vergleicht und in Schritt d) das in b) untersuchte Gemisch gesunder bzw. in Homeostase befindlicher Haut zuordnet, wenn es überwiegend Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen enthält, die in Haut mindestens doppelt so stark exprimiert werden wie in anderen Geweben, oder das in b) untersuchte Gemisch kranker bzw. in gestörter Homeostase befindlicher Haut zuordnet, wenn es überwiegend Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen enthält, die in anderen Geweben mindestens doppelt so stark exprimiert werden wie in Haut.

[0035] Eine weitere bevorzugte Ausführungsform des erfindungsgemäßen Verfahrens zur Bestimmung der Homeostase der Haut ist dadurch gekennzeichnet, daß man in Schritt b) das gewonnene Gemisch auf das Vorhandensein und gegebenenfalls die Menge von mindestens einem der Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen untersucht, die in den Tabellen 2 bis 5 in Spalte 7 durch ihre UniGene-Accession-Number definiert werden, in Schritt c) die Untersuchungsergebnisse aus b) mit den in den Tabellen 2 bis 5 in den Spalten 3 und 4 angegebenen relativen Expressionsfrequenzen sowie den in Spalte 5 angegebenen Expressionsquotienten vergleicht und in Schritt d) das in b) untersuchte Gemisch gesunder bzw. in Homeostase befindlicher Haut zuordnet, wenn es überwiegend Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen enthält, die in Haut mindestens 5-fach so stark exprimiert werden wie in anderen Geweben, oder das in b) untersuchte Gemisch kranker bzw. in gestörter Homeostase befindlicher Haut zuordnet, wenn es überwiegend Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen enthält, die in anderen Geweben mindestens 5-fach so stark exprimiert werden wie in Haut.

[0036] Eine weitere bevorzugte Ausführungsform des erfindungsgemäßen Verfahrens zur Bestimmung der Homeostase der Haut ist dadurch gekennzeichnet, daß man in Schritt b) das gewonnene Gemisch auf das Vorhandensein und gegebenenfalls die Menge von mindestens einem der Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen untersucht, die in den Tabellen 3 bis 5 in Spalte 7 durch ihre UniGene-Accession-Number definiert werden, in Schritt c) die Untersuchungsergebnisse aus b) mit den in den Tabellen 3 bis 5 in den Spalten 3 und 4 angegebenen relativen Expressionsfrequenzen sowie den in Spalte 5 angegebenen Expressionsquotienten vergleicht und in Schritt d) das in b) untersuchte Gemisch gesunder bzw. in Homeostase befindlicher Haut zuordnet, wenn es überwiegend Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen enthält, die in Haut mindestens 10-fach so stark exprimiert werden wie in anderen Geweben, oder das in b) untersuchte Gemisch kranker bzw. in gestörter Homeostase befindlicher Haut zuordnet, wenn es überwiegend Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen enthält, die in anderen Geweben mindestens 10-fach so stark exprimiert werden wie in Haut.

[0037] Eine weitere bevorzugte Ausführungsform des erfindungsgemäßen Verfahrens zur Bestimmung der Homeo-



stase der Haut ist dadurch gekennzeichnet, daß man

in Schritt b) das gewonnene Gemisch auf das Vorhandensein und gegebenenfalls die Menge von mindestens einem der Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen untersucht, die in den Tabellen 4 und 5 in Spalte 7 durch ihre UniGene-Accession-Number definiert werden,

in Schritt c) die Untersuchungsergebnisse aus b) mit den in den Tabellen 4 und 5 in den Spalten 3 und 4 angegebenen relativen Expressionsfrequenzen sowie den in Spalte 5 angegebenen Expressionsquotienten vergleicht und

in Schritt d) das in b) untersuchte Gemisch gesunder bzw. in Homeostase befindlicher Haut zuordnet, wenn es überwiegend Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen enthält, die in Haut mindestens 20-fach so stark exprimiert werden wie in anderen Geweben, oder das in b) untersuchte Gemisch kranker bzw. in gestörter Homeostase befindlicher Haut zuordnet, wenn es überwiegend Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen enthält, die in anderen Geweben mindestens 20-fach so stark exprimiert werden wie in Haut.

**[0038]** Eine weitere bevorzugte Ausführungsform des erfindungsgemäßen Verfahrens zur Bestimmung der Homeostase der Haut ist dadurch gekennzeichnet, daß man

in Schritt b) das gewonnene Gemisch auf das Vorhandensein und gegebenenfalls die Menge von mindestens einem der Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen untersucht, die in Tabelle 5 in Spalte 7 durch ihre UniGene-Accession-Number definiert werden,

in Schritt c) die Untersuchungsergebnisse aus b) mit den in Tabelle 5 in den Spalten 3 und 4 angegebenen relativen Expressionsfrequenzen sowie den in Spalte 5 angegebenen Expressionsquotienten vergleicht und

in Schritt d) das in b) untersuchte Gemisch gesunder bzw. in Homeostase befindlicher Haut zuordnet, wenn es überwiegend Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen enthält, die in Haut mindestens 100-fach so stark exprimiert werden wie in anderen Geweben, oder das in b) untersuchte Gemisch kranker bzw. in gestörter Homeostase befindlicher Haut zuordnet, wenn es überwiegend Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen enthält, die in anderen Geweben mindestens 100-fach so stark exprimiert werden wie in Haut.

**[0039]** Man kann den Zustand der Haut auch dadurch beschreiben, daß mehrere Marker (Expressionprodukte der für die Homeostase der Haut bedeutsamen Gene) quantifiziert werden, die dann untereinander in einem bestimmten Verhältnis aktiv sein müssen, um in Homeostase befindliche Haut zu repräsentieren. Alle Abweichungen hiervon deuten darauf hin, daß die untersuchte Haut sich nicht in Homeostase befindet.

**[0040]** Ein weiterer Gegenstand der vorliegenden Erfindung ist daher ein Verfahren (4) zur Bestimmung der Homeostase der Haut bei Menschen, insbesondere bei Frauen, in vitro, das dadurch gekennzeichnet ist, daß man

a) ein Gemisch von Proteinen, mRNA-Molekülen oder Fragmenten von Proteinen oder mRNA-Molekülen aus menschlicher Haut gewinnt,

b) in dem gewonnenen Gemisch mindestens zwei der Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen quantifiziert, die mittels Verfahren (2) als für die Homeostase der Haut bedeutsam identifiziert werden,

c) die Expressionsverhältnisse der mindestens zwei Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen zueinander bestimmt,

d) die Expressionsverhältnisse aus c) mit den Expressionsverhältnissen vergleicht, die für die in b) quantifizierten Moleküle typischerweise in homeostatischer Haut vorliegen, insbesondere mit den Expressionsverhältnissen, die sich aus Tabelle 6, Spalte 3 bzw. aus den Tabellen 1 bis 5, Spalte 4 ergeben, und

e) das in a) gewonnene Gemisch gesunder bzw. in Homeostase befindlicher Haut zuordnet, wenn die Expressionsverhältnisse der untersuchten Haut den Expressionsverhältnissen in Homeostase befindlicher Haut entsprechen, oder das in a) gewonnene Gemisch kranker bzw. in gestörter Homeostase befindlicher Haut zuordnet, wenn die Expressionsverhältnisse der untersuchten Haut von den Expressionsverhältnissen in Homeostase befindlicher Haut abweichen.

**[0041]** Vorzugsweise gewinnt man in Schritt a) der erfindungsgemäßen Verfahren zur Bestimmung der Homeostase der Haut das Gemisch aus einer Hautprobe, insbesondere aus einer Vollhautprobe oder aus einer Epidermisprobe. Hierbei eröffnet die Vollhautprobe umfassendere Vergleichsmöglichkeiten mit den gleichfalls aus Vollhaut gewonnenen SAGE-Libraries. Die Epidermisprobe ist hingegen leichter zu gewinnen, beispielsweise durch Aufbringen eines Klebebandes auf die Haut und Abreißen desselben, wie in der WO 00/10579 beschrieben, auf die hiermit in vollem Umfang Bezug genommen wird.

**[0042]** In einer weiteren Ausführungsform der erfindungsgemäßen Verfahren zur Bestimmung der Homeostase der Haut gewinnt man in Schritt a) das Gemisch mittels Mikrodialyse. Die Technik der Mikrodialyse wird beispielsweise in "Microdialysis: A method for measurement of local tissue metabolism", Nielsen PS, Winge K, Petersen LM: Ugeskr Laeger 1999 Mar 22 161: 12 1735-8; sowie in "Cutaneous microdialysis for human in vivo dermal absorption studies", Anderson, C. et al.: Drugs Pharm. Sci., 1998, 91, 231-244; und auch im Internet unter <http://www.microdialysis.se/technique.htm> beschrieben, worauf hiermit in vollem Umfang Bezug genommen wird.

**[0043]** Bei der Anwendung der Mikrodialyse führt man typischerweise eine Sonde in die Haut ein und beginnt mit einer geeigneten Trägelösung die Sonde langsam zu spülen. Nach dem Abklingen der akuten Reaktionen nach dem Einstich liefert die Mikrodialyse Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen, die im extrazellulären Raum vorkommen und die, beispielsweise durch Fraktionierung der Trägerflüssigkeit, dann in vitro isoliert und analysiert werden können. Die Mikrodialyse ist weniger invasiv, als die Entnahme einer Vollhautprobe; sie ist aber nachteiligerweise auf die Gewinnung im extrazellulären Raum vorkommender Verbindungen beschränkt.

**[0044]** Eine weitere bevorzugte Ausführungsform der erfindungsgemäßen Verfahren zur Bestimmung der Homeostase der Haut ist dadurch gekennzeichnet, daß man in Schritt b) in Verfahren (3) die Untersuchung auf das Vorhandensein und

gegebenenfalls die Menge von mindestens einem der Proteine oder Proteinfragmente; bzw. in Verfahren (4) die Quantifizierung mindestens zweier Proteine oder Proteinfragmente, mittels einer Methode durchführt, die ausgewählt ist unter

- Ein- oder zweidimensionaler Gelelektrophorese
- Affinitätschromatographie
- Protein-Protein-Komplexierung in Lösung
- Massenspektrometrie, insbesondere Matrix Assistierter Laser Desorptions Ionisation (MALDI) und insbesondere
- Einsatz von Proteinchips,

oder mittels geeigneter Kombinationen dieser Methoden.

[0045] Diese erfindungsgemäß einsetzbaren Methoden sind in dem Übersichtsartikel von Akhilesh Pandey und Matthias Mann: "Proteomics to study genes and genomes", Nature, Volume 405, Number 6788, 837-846 (2000), und den dort angegebenen Referenzen beschrieben, worauf hiermit in vollem Umfang Bezug genommen wird.

[0046] Die 2D-Gelelektrophorese, wird beispielsweise in L. D. Adams, Two-dimensional Gel Electrophoresis using the Isodalt System oder in L. D. Adams & S. R. Gallagher, Two-dimensional Gel Electrophoresis using the O'Farrell System; beide in Current Protocols in Molecular Biology (1997, Eds. F. M. Ausubel et al.), Unit 10.3.1-10.4.13; oder in 2-D Electrophoresis-Manual; T. Berkelman, T. Sensiedt; Amersham Pharmacia Biotech, 1998 (Bestell-Nr. 80-6429-60), beschrieben.

[0047] Die massenspektrometrische Charakterisierung der Proteine oder Proteinfragmente erfolgt in der Fachwelt bekannter Weise, beispielsweise wie in den folgenden Literaturstellen beschrieben:

[0048] Methods in Molecular Biology, 1999; Vol 112: 2-D Proteome Analysis Protocols; Editor: A. J. Link; Humana Press; Totowa; New Jersey. Darin insbesondere: Courchesne, P. L. und Patterson, S. D.; S. 487-512.

[0049] Carr, S. A. und Annan, R. S.; 1997; in: Current Protocols in Molecular Biology; Editor: Ausubel, F. M. et al.; John Wiley and Sons, Inc. 10.2.1-10.21.27.

[0050] Eine weitere bevorzugte Ausführungsform der erfindungsgemäßen Verfahren zur Bestimmung der Homeostase der Haut ist dadurch gekennzeichnet, daß man in Schritt b) in Verfahren (3) die Untersuchung auf das Vorhandensein und gegebenenfalls die Menge von mindestens einem der mRNA-Moleküle oder mRNA-Molekülfragmente; bzw. in Verfahren (4) die Quantifizierung mindestens zweier mRNA-Moleküle oder mRNA-Molekülfragmente mittels einer Methode durchführt, die ausgewählt ist unter

- i. Northern Blots,
- ii. Reverse Transkriptase Polymerasekettenreaktion (RT-PCR),
- iii. RNase-Schutzexperimente,
- iv. Dot-Blots,
- v. cDNA-Sequenzierung,
- vi. Klon-Hybridisierung,
- vii. Differential Display,
- viii. Subtraktive Hybridisierung,
- ix. cDNA-Fragment-Fingerprinting,
- x. Total Gene Expression Analysis (TOGA)
- xi. Sérielle Analyse der Genexpression (SAGE) und insbesondere
- xii. Einsatz von Nukleinsäurechips.

oder mittels geeigneter Kombinationen dieser Methoden.

[0051] Diese erfindungsgemäß einsetzbaren Methoden sind in den Übersichtsartikeln von Akhilesh Pandey und Matthias Mann: "Proteomics to study genes and genomes", Nature, Volume 405, Number 6788, 837-846 (2000), und "Genomics, gene expression and DNA arrays", Nature, Volume 405, Number 6788, 827-836 (2000), und den dort angegebenen Referenzen beschrieben, worauf hiermit in vollem Umfang Bezug genommen wird.

[0052] Das TOGA-Verfahren ist in "J. Gregor Sutcliffe et al. TOGA: An automated parsing technology for analyzing expression of nearly all genes, Proceedings of the National Academy of Sciences of the United States of America (PNAS), Vol. 97, No. 5, pp. 1976-1981 (2000)" beschrieben, worauf hiermit vollumfänglich Bezug genommen wird.

[0053] Es können jedoch erfindungsgemäß auch andere dem Fachmann bekannte Methoden zur Untersuchung auf das Vorhandensein und gegebenenfalls die Menge von mindestens einem der Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen eingesetzt werden.

[0054] Eine weitere bevorzugte Ausführungsform der erfindungsgemäßen Verfahren zur Bestimmung der Homeostase der Haut ist dadurch gekennzeichnet, daß man in Schritt b) auf das Vorhandensein und gegebenenfalls die Menge von 1 bis etwa 5000, bevorzugt 1 bis etwa 1000, insbesondere etwa 10 bis etwa 500, vorzugsweise etwa 10 bis etwa 250, besonders bevorzugt etwa 10 bis etwa 100 und ganz besonders bevorzugt etwa 10 bis etwa 50 der Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen untersucht, die in den Tabellen 1 bis 5 in Spalte 7 durch ihre UniGene-Accession-Number definiert werden.

[0055] Ein weiterer Gegenstand der vorliegenden Erfindung ist ein Test-Kit zur Bestimmung der Homeostase der Haut bei Menschen in vitro, umfassend Mittel zur Durchführung der erfindungsgemäßen Verfahren zur Bestimmung der Homeostase der Haut.

[0056] Ein weiterer Gegenstand der vorliegenden Erfindung ist ein Biochip zur Bestimmung der Homeostase der Haut bei Menschen in vitro, umfassend

- i. einen festen, d. h. starren oder flexiblen Träger und
- ii. auf diesem immobilisierte Sonden, die zur spezifischen Bindung an mindestens eines der Proteine, mRNA-Mo-

leküle oder Fragmente von Proteinen oder mRNA-Molekülen befähigt sind, die in den Tabellen 1 bis 5 in Spalte 7 durch ihre UniGene-Accession-Number definiert werden.

- [0057] Bei einem BioChip handelt es sich um ein miniaturisiertes Funktionselement mit auf einer Oberfläche immobilisierten Molekülen, insbesondere Biomolekülen, die als spezifische Interaktionspartner dienen können. 5
- [0058] Häufig weist die Struktur dieser Funktionselemente Reihen und Spalten auf; man spricht dann von Chip-"Arrays". Da tausende von biologischen bzw. biochemischen Funktionselementen auf einem Chip angeordnet sein können, müssen diese in der Regel mit mikrotechnischen Methoden angefertigt werden. Als biologische und biochemische Funktionselemente kommen insbesondere in Frage: DNA, RNA, PNA, (bei Nukleinsäuren und ihren chemischen Derivaten können z. B. Einzelstränge, Triplex-Strukturen oder Kombinationen hiervon vorliegen), Saccharide, Peptide, Proteine 10 (z. B. Antikörper, Antigene, Rezeptoren) und Derivate der kombinatorischen Chemie (z. B. organische Moleküle). Im allgemeinen haben BioChips eine 2D-Basisfläche für das Beschichten mit biologisch oder biochemisch funktionellen Materialien. Die Basisflächen können beispielsweise auch von Wänden einer oder mehrerer Kapillaren oder von Kanälen gebildet sein.
- [0059] Zum Stand der Technik kann z. B. auf folgende Publikationen hingewiesen werden: Nature Genetics, Vol. 21, supplement (Gesamt), Jan. 1999 (BioChips); Nature Biotechnology, Vol. 16, S. 981-983, Okt. 1998 (BioChips); Trends in Biotechnology, Vol. 16, S. 301-306, Jul. 1998 (BioChips) sowie die bereits genannten Übersichtsartikel von Akhilesh Pandey und Matthias Mann: "Proteomics to study genes and genomes", Nature, Volume 405, Number 6788, 837-846 (2000), und "Genomics, gene expression and DNA arrays", Nature, Volume 405, Number 6788, 827-836 (2000), und die dort angegebenen Referenzen, worauf hiermit in vollem Umfang Bezug genommen wird. 15
- [0060] Eine übersichtliche Darstellung der praktischen Anwendungsverfahren der DNA-Chiptechnologie liefern die Bücher "DNA Microarrays: A Practical Approach" (Editor: Mark Schena, 1999, Oxford University Press) und "Microarray Biochip Technology" (Editor: Mark Schena, 2000, Eaton Publishing), auf die hiermit in vollem Umfang Bezug genommen wird. 20
- [0061] Die im Rahmen der vorliegenden Erfindung besonders bevorzugte DNA-Chiptechnologie beruht auf der Fähigkeit von Nukleinsäuren komplementäre Basenpaarungen einzugehen. Dieses als Hybridisierung bezeichnete technische Prinzip wird bereits seit Jahren bei der Southern-Blot- und Northern-Blot-Analyse eingesetzt. Im Vergleich zu diesen herkömmlichen Methoden, bei denen lediglich einige wenige Gene analysiert werden, gestattet es die DNA-Chiptechnologie einige hundert bis zu mehreren zehntausend Genen parallel zu untersuchen. 25
- [0062] Ein DNA-Chip besteht im wesentlichen aus einem Trägermaterial (z. B. Glas oder Kunststoff), auf dem einzelsträngige, genspezifische Sonden in hoher Dichte an einer definierten Stelle (Spot) immobilisiert werden. Als problematisch wird dabei die Technik der Sonden-Applikation und die Chemie der Sonden-Immobilisierung eingeschätzt. 30
- [0063] Nach dem derzeitigen Stand der Technik sind mehrere Wege der Sondenimmobilisierung realisiert:
- [0064] E. M. Southern (E. M. Southern et al. (1992), Nucleic Acid Research 20, 1679-1684 und E. M. Southern et al. (1997), Nucleic Acid Research 25, 1155-1161) beschreibt die Herstellung von Oligonukleotidanordnungen durch direkte Synthese an einer Glasoberfläche, die mit 3-Glycidoxypolytrimethoxysilan und anschließend mit einem Glycol derivatisiert wurde. 35
- [0065] Ein ähnliches Verfahren realisiert die in situ Synthese von Oligonukleotiden mittels einer photosensitiven, kombinatorischen Chemie, die mit photolithographischen Techniken verglichen werden kann (Pease, A. C. et al. (1994), Proc. Natl Acad Sci USA 91, 5022-5026). 40
- [0066] Neben diesen auf der in situ-Synthese von Oligonukleotiden beruhenden Techniken können ebenso bereits vorhandene DNA-Moleküle an Oberflächen von Trägermaterial gebunden werden.
- [0067] P. O. Brown (DeRisi et al. (1997), Science 278, 680-686) beschreibt die Immobilisierung von DNA an mit Polylysin beschichteten Glasoberflächen.
- [0068] Die Veröffentlichung von L. M. Smith (Guo, Z. et al. (1994), Nucleic Acid Research 22, 5456-5465) legt ein ähnliches Verfahren offen: Oligonukleotide, die eine 5'terminale Aminogruppe tragen, können an eine Glasoberfläche gebunden werden, die mit 3-Aminopropyltrimethoxysilan und anschließend mit 1,4-Phenyldiisothiocyanat behandelt wurde. 45
- [0069] Die Applikation der DNA-Sonden auf einem Träger kann mit einem sogenannten "Pin-Spotter" erfolgen. Dazu tauchen dünne Metallnadeln mit z. B. einem Durchmesser von 250 µm, in Sondenlösungen ein und überführen anschließend das anhängende Probenmaterial mit definierten Volumina auf das Trägermaterial des DNA-Chips. 50
- [0070] Bevorzugterweise erfolgt die Sondenapplikation jedoch mittels eines piezogesteuerten Nanodispensers, der ähnlich einem Tintenstrahldrucker, Sondenlösungen mit einem Volumen von 100 Picolitern kontaktfrei auf die Oberfläche des Trägermaterials aufbringt.
- [0071] Die Immobilisierung der Sonden erfolgt z. B. wie in der EP-A-0 965 647 beschrieben: Die Generierung von DNA-Sonden erfolgt hierbei mittels PCR unter Verwendung eines sequenzspezifischen Primerpaares, wobei ein Primer am 5'-Ende modifiziert ist und einen Linker mit einer freien Aminogruppe trägt. Damit ist sichergestellt, dass ein definierter Strang der PCR-Produkte an einer Glasoberfläche gebunden werden kann, welche mit 3-Aminopropyltrimethoxysilan und anschließend mit 1,4-Phenyldiisothiocyanat behandelt wurde. Die genspezifischen PCR-Produkte sollen idealerweise eine definierte Nukleinsäuresequenz in einer Länge von 200-400 bp haben und nicht redundante Sequenzen beinhalten. Nach der Immobilisierung der PCR-Produkte über den derivatisierten Primer wird der Gegenstrang des PCR-Produkts durch eine Inkubation bei 96°C für 10 Min entfernt. 55
- [0072] In einer für DNA-Chips typischen Anwendung wird mRNA aus zwei zu vergleichenden Zellpopulationen isoliert. Die isolierten mRNAs werden mittels reverser Transkription unter Verwendung von z. B. fluoreszenzmarkierten Nukleotiden in cDNA umgewandelt. Dabei werden die zu vergleichenden Proben mit z. B. rot bzw. grün fluoreszierenden Nukleotiden markiert. Die cDNAs werden dann mit den auf dem DNA-Chip immobilisierten Sonden hybridisiert und anschließend die gebundenen Fluoreszenzen quantifiziert. 60
- [0073] Der erfindungsgemäße Biochip umfasst bevorzugt 1 bis etwa 5000, bevorzugtermaßen 1 bis etwa 1000, insbe-

sondere etwa 10 bis etwa 500, vorzugsweise etwa 10 bis etwa 250, besonders bevorzugt etwa 10 bis etwa 100 und ganz besonders bevorzugt etwa 10 bis etwa 50 voneinander verschiedene Sonden. Die voneinander verschiedenen Sonden können jeweils in mehrfacher Kopie auf dem Chip vorhanden sein.

[0074] Der erfindungsgemäße Biochip umfasst bevorzugt Nukleinsäuresonden, insbesondere RNA- oder PNA-Sonden, besonders bevorzugt DNA-Sonden. Die Nukleinsäuresonden weisen bevorzugt eine Länge von etwa 10 bis etwa 1000, insbesondere etwa 10 bis etwa 800, vorzugsweise etwa 100 bis etwa 600, besonders bevorzugt etwa 200 bis etwa 400 Nukleotiden auf.

[0075] In einer weiteren bevorzugten Form umfasst der erfindungsgemäße Biochip Peptid- oder Proteinsonden, insbesondere Antikörper.

[0076] Ein weiterer Gegenstand der vorliegenden Erfindung ist die Verwendung der Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen, die in den Tabellen 1 bis 5 in Spalte 7 durch ihre UniGene-Accession-Number definiert werden, als Marker für die Homeostase der Haut bei Menschen.

[0077] Ein weiterer Gegenstand der vorliegenden Erfindung ist ein Testverfahren zum Nachweis der Wirksamkeit von kosmetischen oder pharmazeutischen Wirkstoffen zur Aufrechterhaltung oder Förderung der Homeostase der Haut bzw. zur Behandlung pathologischer Zustände der Haut, wie Neurodermitis, Sonnenbrand, Psoriasis, Sklerodermie, Ichthyosis, atopische Dermatitis, Akne, Seborrhoe, Lupus erythematodes, Rosacea, Melanoma, Basalioma, Hautkarzinom, Hautsarkom in vitro, dadurch gekennzeichnet, daß man

- a) den Hautstatus durch ein erfindungsgemäßes Verfahren zur Bestimmung der Homeostase der Haut, oder mittels eines erfindungsgemäßen Test-Kits zur Bestimmung der Homeostase der Haut, oder mittels eines erfindungsgemäßen Biochips bestimmt,
- b) einen Wirkstoff zur Aufrechterhaltung oder Förderung der Homeostase der Haut bzw. zur Behandlung pathologischer Zustände der Haut einmal oder mehrmals auf die Haut aufbringt,
- c) erneut den Hautstatus durch ein erfindungsgemäßes Verfahren zur Bestimmung der Homeostase der Haut, oder mittels eines erfindungsgemäßen Test-Kits zur Bestimmung der Homeostase der Haut, oder mittels eines erfindungsgemäßen Biochips bestimmt, und
- d) die Wirksamkeit des Wirkstoffs durch den Vergleich der Ergebnisse aus a) und c) bestimmt.

[0078] Zur Beschleunigung des Testverfahrens ist es auch möglich, verschiedene Wirkstoffe oder Placebos parallel auf verschiedene Hautareale aufzubringen; beispielsweise einen Wirkstoff auf den linken Unterarm und ein Placebo auf den rechten Unterarm, oder umgekehrt.

[0079] Ein weiterer Gegenstand der vorliegenden Erfindung ist ein Test-Kit zum Nachweis der Wirksamkeit von kosmetischen oder pharmazeutischen Wirkstoffen zur Aufrechterhaltung oder Förderung der Homeostase der Haut bzw. zur Behandlung pathologischer Zustände der Haut in vitro, umfassend Mittel zur Durchführung des erfindungsgemäßen Testverfahrens.

[0080] Ein weiterer Gegenstand der vorliegenden Erfindung ist die Verwendung der Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen, die in den Tabellen 1 bis 5 in Spalte 7 durch ihre UniGene-Accession-Number definiert werden zum Nachweis der Wirksamkeit von kosmetischen oder pharmazeutischen Wirkstoffen zur Aufrechterhaltung oder Förderung der Homeostase der Haut bzw. zur Behandlung pathologischer Zustände der Haut, wie Neurodermitis, Sonnenbrand, Psoriasis, Sklerodermie, Ichthyosis, atopische Dermatitis, Akne, Seborrhoe, Lupus erythematodes, Rosacea, Melanoma, Basalioma, Hautkarzinom, Hautsarkom.

[0081] Ein weiterer Gegenstand der vorliegenden Erfindung ist ein Screening-Verfahren zur Identifikation von kosmetischen oder pharmazeutischen Wirkstoffen zur Aufrechterhaltung oder Förderung der Homeostase der Haut bzw. zur Behandlung pathologischer Zustände der Haut, wie Neurodermitis, Sonnenbrand, Psoriasis, Sklerodermie, Ichthyosis, atopische Dermatitis, Akne, Seborrhoe, Lupus erythematodes, Rosacea, Melanoma, Basalioma, Hautkarzinom, Hautsarkom in vitro, dadurch gekennzeichnet, daß man

- a) den Hautstatus durch ein erfindungsgemäßes Verfahren zur Bestimmung der Homeostase der Haut, oder mittels eines erfindungsgemäßen Test-Kits zur Bestimmung der Homeostase der Haut, oder mittels eines erfindungsgemäßen Biochips bestimmt,
- b) einen potentiellen Wirkstoff zur Aufrechterhaltung oder Förderung der Homeostase der Haut bzw. zur Behandlung pathologischer Zustände der Haut einmal oder mehrmals auf die Haut aufbringt,
- c) erneut den Hautstatus durch ein erfindungsgemäßes Verfahren zur Bestimmung der Homeostase der Haut, oder mittels eines erfindungsgemäßen Test-Kits zur Bestimmung der Homeostase der Haut, oder mittels eines erfindungsgemäßen Biochips bestimmt, und
- d) wirksame Wirkstoffe durch den Vergleich der Ergebnisse aus a) und c) bestimmt.

[0082] Ein weiterer Gegenstand der vorliegenden Erfindung ist die Verwendung der Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen, die in den Tabellen 1 bis 5 in Spalte 7 durch ihre UniGene-Accession-Number definiert werden, zur Identifikation von kosmetischen oder pharmazeutischen Wirkstoffen zur Aufrechterhaltung oder Förderung der Homeostase der Haut bzw. zur Behandlung pathologischer Zustände der Haut, wie Neurodermitis, Sonnenbrand, Psoriasis, Sklerodermie, Ichthyosis, atopische Dermatitis, Akne, Seborrhoe, Lupus erythematodes, Rosacea, Melanoma, Basalioma, Hautkarzinom, Hautsarkom.

[0083] Ein weiterer Gegenstand der vorliegenden Erfindung ist ein Verfahren zur Herstellung einer kosmetischen oder pharmazeutischen Zubereitung zur Aufrechterhaltung oder Förderung der Homeostase der Haut bzw. zur Behandlung pathologischer Zustände der Haut, wie Neurodermitis, Sonnenbrand, Psoriasis, Sklerodermie, Ichthyosis, atopische Dermatitis, Akne, Seborrhoe, Lupus erythematodes, Rosacea, Melanoma, Basalioma, Hautkarzinom, Hautsarkom, dadurch gekennzeichnet, daß man

- a) wirksame Wirkstoffe mit Hilfe des erfindungsgemäßen Screening-Verfahrens, oder der Verwendung zur Identifikation von kosmetischen oder pharmazeutischen Wirkstoffen zur Aufrechterhaltung oder Förderung der Homöostase der Haut bzw. zur Behandlung pathologischer Zustände der Haut bestimmt und
- b) als wirksam befundene Wirkstoffe mit kosmetisch und pharmakologisch geeigneten und verträglichen Trägern vermischt.

## Tabellen

Tabelle 6

Nr.	Tag_Sequence	rel. Expr.	signific.	UniGene	Beschreibung
		In Haut		Acc.-Nr.	
1	ATCCGCGAGGC	45,00	63,99	Hs.180142	CLSP Calmodulin-like skin protei
2	GAGATAAATGA	23,00	31,88	Hs.3185	lymphocyte antigen 6 complex, locus D
3	TAAACCTGCTG	110,00	150,08	Hs.99923	lectin, galactoside-binding, soluble, 7 (galectin 7)
4	GATGTGCACGA	216,00	289,47	Hs.117729	keratin 14 (epidermolysis bullosa simplex, Dowling-M
5	ACATTTCAAAG	161,00	248,57	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)
6	TTTGTAGAGGA	37,00	47,97	Hs.279671	katanin p60 (ATPase-containing) subunit A 1
7	ACCTCCACTGG	139,00	214,56	Hs.112457	ESTs
8	AATCTTGTTTC	93,00	115,24	Hs.32343	ESTs
9	GAAAACAAAGT	467,00	100,00	Hs.99936	keratin 10 (epidermolytic hyperkeratosis; keratosis
10	GCCCCTGCTGA	148,00	181,69	Hs.195850	keratin 5 (epidermolysis bullosa simplex, Dowling-Me
11	CACACGGGCGA	26,00	32,16	Hs.194679	WNT1 inducible signaling pathway protein 2
12	GACAATAAATG	9,00	10,38	Hs.137556	Homo sapiens mRNA; cDNA DKFZp434A132 (from clone DKF
13	ACTACCATAAC	7,00	8,06	Hs.57929	slit (Drosophila) homolog 3
14	CATTGTAAATA	7,00	8,06	Hs.55279	protease inhibitor 5 (maspin)
15	ACCGGCGCCCG	29,00	32,51	Hs.65424	tetranectin (plasminogen-binding protein)
16	CCACCACGCTT	16,00	17,84	Hs.285275	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY
17	CCCCGGCCACC	42,00	44,79	Hs.279604	(Manual assignment) desmin, muscle intermediate fila
18	TGAAATAAAAG	12,00	12,90	Hs.48516	ESTs
19	ACTGAGTAGGT	4,00	4,39	Hs.38095	ATP-binding cassette, sub-family A (ABC1), member 8
20	ATCCTTGCTGA	26,00	26,12	Hs.2621	cystatin A (stefin A)
21	CAGCCTGGGTG	5,00	5,10	Hs.171941	ESTs
22	GATATGTTATA	5,00	5,10	Hs.117938	collagen, type XVII, alpha 1
23	TGGCTTCATCA	4,00	4,10	Hs.646	carboxypeptidase A3 (mast cell)
24	CCTGTAACACC	3,00	3,09	Hs.74304	periplakin
25	CCCCGGAGGTC	3,00	3,09	Hs.47913	coagulation factor X
26	AGATCAGTTGA	3,00	3,09	Hs.191805	ESTs
27	CCCTCAGCACC	9,00	8,78	Hs.87268	annexin A8
28	CTTTATTCCAG	49,00	45,24	Hs.172928	collagen, type I, alpha 1
29	TCCACTGGCCT	23,00	21,32	Hs.57548	ESTs
30	CACGCAGTGGC	5,00	4,85	Hs.245545	EST

31	TACATTATATA	3,00	2,85	Hs.198862	fibulin 2
32	ATGGATACGGG	10,00	9,05	Hs.250722	(Manual assignment) unclear, probably reverse tag o
33	CCGGGGGAGCC	43,00	36,36	Hs.172928	collagen, type I, alpha 1
34	CAGTTTTTTC	2,00	1,84	Hs.99597	ESTs
35	GTGGATTCAAG	2,00	1,84	Hs.93847	NADPH oxidase 4
36	TGTCTGTGTGT	2,00	1,84	Hs.93739	ESTs
37	TCTACACGTGC	2,00	1,84	Hs.53155	properdin P factor, complement
38	GAAATGGCAGT	2,00	1,84	Hs.30853	ESTs
39	ACGAAACCTCG	2,00	1,84	Hs.285785	Homo sapiens cDNA FLJ20115 fis, clone COL05594
40	GGCAATGCAGT	2,00	1,84	Hs.275505	ESTs
41	CCTTTTCAGCA	2,00	1,84	Hs.25930	ESTs
42	CCTCTTTAACA	2,00	1,84	Hs.25750	ESTs
43	TATCTAGCTGC	2,00	1,84	Hs.241545	hypothetical protein
44	GCTGTAATCCT	2,00	1,84	Hs.241382	tumor necrosis factor (ligand) super-family, member 1
45	GGGCAGCCGCC	2,00	1,84	Hs.23598	CREB binding protein (Rubinstein-Taybi syndrome)
46	CGCTTGTTTAA	2,00	1,84	Hs.180398	LIM domain-containing preferred translocation partne
47	GCACACACCTG	2,00	1,84	Hs.171143	EST, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE
48	CTGGAGTCGGC	2,00	1,84	Hs.166371	Interleukin-1 Superfamily z
49	GAGGTCAGTTG	2,00	1,84	Hs.151696	DKFZP727G051 protein
50	CCAGGCAAGAC	2,00	1,84	Hs.134194	distal-less homeo box 3
51	GAAATCAAAAA	13,00	11,30	Hs.117005	sialic acid binding Ig-like lectin 5
52	AATCTAGTTCT	22,00	33,72	Hs.251440	Human profilaggrin gene exons 1-3, 5' end
53	AAGCTAATAAA	9,00	7,89	Hs.88474	prostaglandin-endoperoxide synthase 1 (prostaglandin
54	TGTGCGGCTTC	5,00	4,43	Hs.162196	hypothetical protein FLJ20321
55	CAGGTTTCATA	66,00	54,72	Hs.24395	small inducible cytokine subfamily B (Cys-X-Cys), me
56	CTGTCGTCATC	7,00	5,98	Hs.183860	hypothetical protein FLJ20277
57	ATAGCACGTGC	3,00	2,66	Hs.277329	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC
58	GTGAGAACTCG	3,00	2,66	Hs.250639	ESTs
59	ACTTATTATGC	29,00	23,46	Hs.76152	decorin
60	CTTGCACTCCT	5,00	4,25	Hs.27018	Ris
61	CATCTGTACTC	14,00	11,49	Hs.180255	major histocompatibility complex, class II, DR beta
62	GTGGAGGGGCAC	18,00	14,16	Hs.83393	cystatin E/M
63	AGGCAGGAAAA	5,00	4,09	Hs.133081	ESTs, Weakly similar to hypothetical protein [H.sapi
64	AATTGAAAAGG	10,00	7,94	Hs.78344	myosin, heavy polypeptide 11, smooth muscle
65	CTTTAAAATGA	3,00	2,50	Hs.8217	stromal antigen 2
66	TGTGCCAGTTT	3,00	2,50	Hs.53358	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX

67	AGTAGCTGGGA	3,00	2,50	Hs.224534	EST, Weakly similar to alternatively spliced product
68	CCTCTGTCTCC	3,00	2,50	Hs.161031	Homo sapi ns mRNA; cDNA DKFZp434K0322 (from clone DK
69	AACATTTAGGA	3,00	2,50	Hs.138380	KIAA0624 protein
70	CAATAAAATTT	3,00	2,50	Hs.137569	tumor protein 63 kDa with strong homology to p53
71	GCCGCTCAAGG	3,00	2,50	Hs.126064	ESTs
72	CCTGGTCAAGA	2,00	1,68	Hs.95972	silver (mouse homolog) like
73	CCACCGCAGGA	2,00	1,68	Hs.85112	insulin-like growth factor 1 (somatomedia C)
74	ACACTTCTCAA	2,00	1,68	Hs.75652	glutathione S-transferase M5
75	CCTCTCTGGTC	2,00	1,68	Hs.56874	heat shock 27kD protein family, member 7 (cardiovasc
76	GCATATCTGTG	2,00	1,68	Hs.5459	KIAA1436 protein
77	AGCTGTGATGG	2,00	1,68	Hs.249983	ESTs
78	GCTAACTTAAA	2,00	1,68	Hs.20787	ESTs
79	CCTTGAAATCA	2,00	1,68	Hs.183161	ESTs
80	CTTTATCAATA	2,00	1,68	Hs.166017	microphthalmia-associated transcription factor
81	ACAGCCCTGAT	2,00	1,68	Hs.163593	ribosomal protein L18a
82	GATACTCAGAA	2,00	1,68	Hs.144726	ESTs
83	GCCTGGGAGAC	2,00	1,68	Hs.118346	ESTs
84	TGGGTGGTGGT	13,00	10,06	Hs.82712	fragile X mental retardation, autosomal homolog 1
85	AGCTACCACAG	9,00	6,87	Hs.169886	tenascin XB
86	ACAGCGGCAAT	69,00	49,04	Hs.74316	desmoplakin (DPI, DPII)
87	GTAAATCCCA	3,00	2,36	Hs.278623	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
88	CACTTGTAATC	3,00	2,36	Hs.268488	KIAA1185 protein
89	CTTGTAAGTTCC	3,00	2,36	Hs.155983	KIAA0677 gene product
90	GGGTTTTCTGG	3,00	2,36	Hs.153703	ESTs, Moderately similar to DHSA_HUMAN SUCCINATE DEH
91	CAGCAGAACTG	3,00	2,36	Hs.117582	CGI-43 protein
92	CCACAGGAGAA	81,00	56,23	Hs.169902	solute carrier family 2 (facilitated glucose transpo
93	ATAGCCAGGGA	4,00	3,02	Hs.95582	SRY (sex determining region Y)-box 20
94	GTACAAAAGTA	4,00	3,02	Hs.9552	binder of Arl Two
95	TCACAGGGTCC	4,00	3,02	Hs.77886	lamin A/C
96	TTCTGTGTGCC	4,00	3,02	Hs.58715	ESTs
97	TAGCCGGGACG	10,00	7,22	Hs.107740	Kruppel-like factor 2 (lung)
98	ATCACACAGCT	6,00	4,44	Hs.79386	leiomodulin 1 (smooth muscle)
99	ATCTCGAAAGG	8,00	5,84	Hs.10784	hypothetical protein FLJ20037
100	GACCCAAGTGG	2,00	1,54	Hs.89575	CD79B antigen (immunoglobulin-associated beta)
101	CACAGGGAGGA	2,00	1,54	Hs.84753	KIAA0246 protein
102	CAGCTGGCCCA	2,00	1,54	Hs.79732	fibulin 1
103	GAGGGCTTTGC	2,00	1,54	Hs.78183	aldo-keto reductase family 1, member C3 (3-alpha hyd
104	GTGAGCCAAGA	2,00	1,54	Hs.75410	heat shock 70kD protein 5 (glucose-

					regulated protein
	105	TACCCCAAAAA	2,00	1,54	Hs.6449 hypothetical protein FLJ20542
5	106	CAGGATGCTTG	2,00	1,54	Hs.56729 lymphocyte-specific protein 1
	107	AGTGTGTTGCA	2,00	1,54	Hs.56105 ESTs, Weakly similar to WDNM_RAT WDNM1 PROTEIN PRECU
	108	AGGACCTGAAG	2,00	1,54	Hs.32352 hypothetical protein DKFZp434K1210
10	109	ATTCTGGTCAT	2,00	1,54	Hs.18878 ESTs, Weakly similar to dJ876B10.4 [H.sapiens]
	110	CCTTTTGGGAG	2,00	1,54	Hs.186600 ESTs
	111	CGGTCATACA	2,00	1,54	Hs.169487 Kreisler (mouse) maf-related leucine zipper homolog
15	112	ATGGTGCCACC	2,00	1,54	Hs.161554 hypothetical protein FLJ20159
	113	TAATGTAAATG	2,00	1,54	Hs.153924 death-associated protein kinase 1
	114	AGGGCCCTCTG	2,00	1,54	Hs.129014 hypothetical protein FLJ20207
20	115	GTGGCACGCGT	2,00	1,54	Hs.118243 deoxyribonuclease II, lysosomal
	116	AGCTTGAGTTC	2,00	1,54	Hs.117582 CGI-43 protein
	117	GTGGGGCCAAG	7,00	5,08	Hs.24194 folate receptor 2 (fetal)
	118	GTGAAGCCTCA	5,00	3,67	Hs.271823 ESTs
25	119	ACCAGACAGAC	3,00	2,23	Hs.7882 ESTs
	120	GTGAAACTCTT	3,00	2,23	Hs.29759 RNA POLYMERASE I AND TRANSCRIPT RELEASE FACTOR
	121	ATTTCCATTAA	3,00	2,23	Hs.284126 hairless (mouse) homolog
30	122	GTGGTAAGCAC	3,00	2,23	Hs.271827 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY
	123	GTTTTGCCAC	3,00	2,23	Hs.151407 cartilage intermediate layer protein, nucleotide pyr
35	124	GCCCACACAGC	8,00	5,71	Hs.1690 heparin-binding growth factor binding protein
	125	TTTCCTCTCAA	38,00	25,30	Hs.184510 stratifin
	126	CGGGAGCGCTA	13,00	8,84	Hs.148590 ESTs, Weakly similar to AF208846_1 BM-004 [H.sapiens]
40	127	TTGCATATCAG	10,00	6,84	Hs.82237 ataxia-telangiectasia group D-associated protein
	128	AGGCCTCGGCA	5,00	3,55	Hs.286202 Homo sapiens cDNA FLJ11346 fis, clone PLACE1010900
45	129	GTGGCGAATGA	12,00	18,26	Hs.69752 desmocollin 1
	130	TGTGAAGCCTT	12,00	18,26	Hs.5476 serine protease inhibitor, Kazal type, 5
	131	TCAGACTTTTG	9,00	6,10	Hs.5889 ESTs, Weakly similar to AC004876_5 similar to predic
50	132	ATTTCTTCAAG	9,00	6,10	Hs.31386 ESTs, Highly similar to JE0174 frizzled protein-2 -
	133	GAATTATACTT	10,00	6,73	Hs.104800 hypothetical protein FLJ10134
55	134	TCTGGGGAACA	3,00	2,12	Hs.184390 similar to aspartate beta hydroxylase (ASPH)
	135	GCAAAAACCCG	3,00	2,12	Hs.184109 ribosomal protein L37a
	136	AATGTTGTGCA	4,00	2,78	Hs.91546 cytochrome P450 retinoid metabolizing protein
60	137	ACAATGTTGTA	2,00	1,43	Hs.7678 cellular retinoic acid-binding protein 1
	138	CGAGAGTGTGA	2,00	1,43	Hs.58210 ESTs
	139	GTATAAAAAA	2,00	1,43	Hs.27337 hypothetical protein FLJ20623

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140	AGGTCGAGGCT	2,00	1,43	Hs.270125	ESTs
141	CCCGGCCAGT	2,00	1,43	Hs.243324	EST, Weakly similar to ALUA_HUMAN !!!! ALU CLASS A W
142	TTGACCCAGCC	2,00	1,43	Hs.193745	ESTs
143	TATTTTATTTG	2,00	1,43	Hs.189999	purinergic receptor (family A group 5)
144	GCATCATAGGT	2,00	1,43	Hs.184108	ribosomal protein L21 (gene or pseudo-gene)
145	TACCGCTCCCT	2,00	1,43	Hs.172803	Homo sapiens mRNA; cDNA DKFZp434G2416 (from clone DK
146	CTCCTGTGGTC	2,00	1,43	Hs.169851	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAMILY SB2
147	GGTGTCTCCTC	2,00	1,43	Hs.146038	ESTs
148	CAATCTTGTGA	2,00	1,43	Hs.104353	ESTs
149	CCTACAAAAA	1,00	0,69	Hs.98288	ESTs
150	TGTGCCAGCC	1,00	0,69	Hs.97905	ovo (Drosophila) homolog-like 1
151	GATGGGGACAG	1,00	0,69	Hs.92195	ESTs
152	TAAAAATATTG	1,00	0,69	Hs.89695	insulin receptor
153	TTTAAGTTAGG	1,00	0,69	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatosis 1)
154	GTATATGTATT	1,00	0,69	Hs.7917	DKFZP564K247 protein
155	CTAAAGTGTCA	1,00	0,69	Hs.7910	RING1 and YY1 binding protein
156	AATTTGGCTTT	1,00	0,69	Hs.7734	Homo sapiens cDNA FLJ20684 fis, clone KAIA3469
157	CCGTGGCACCA	1,00	0,69	Hs.77208	ESTs
158	AGCACCTTGT	1,00	0,69	Hs.75871	protein kinase C binding protein 1
159	CCTTTGAGAGC	1,00	0,69	Hs.71791	hypothetical protein
160	TAAATGTAAAT	1,00	0,69	Hs.64096	KIAA0427 gene product
161	TACAGACATAC	1,00	0,69	Hs.63984	cadherin 13, H-cadherin (heart)
162	GTAGCATTTGC	1,00	0,69	Hs.63302	myotubularin related protein 3
163	AAGTAGGTTTT	1,00	0,69	Hs.50216	zinc finger protein (ZFD25)
164	ATCACTCCCCA	1,00	0,69	Hs.37058	calcitonin/calcitonin-related polypeptide, alpha
165	TAGGCAGACCT	1,00	0,69	Hs.35488	ESTs, Moderately similar to ALU6_HUMAN ALU SUBFAMILY
166	GCCTGGCCAGG	1,00	0,69	Hs.3343	phosphoglycerate dehydrogenase
167	GTCATCTTGTT	1,00	0,69	Hs.32366	ESTs, Moderately similar to TWIST_HUMAN TWIST RELATED
168	CTCAACAACCA	1,00	0,69	Hs.30036	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
169	TTATATTAATA	1,00	0,69	Hs.29205	alpha integrin binding protein 63
170	GATTAAACCTT	1,00	0,69	Hs.287357	ESTs, Moderately similar to meningioma- expressed ant
171	GATGGAGGTTA	1,00	0,69	Hs.285224	ESTs, Weakly similar to unnamed pro- tein product [H.s
172	TACAGGCGTGG	1,00	0,69	Hs.283329	ESTs
173	TGTGTGTGTAT	1,00	0,69	Hs.278676	Homo sapiens mRNA; cDNA DKFZp434J1630 (from clone DK
174	GGTGCCTGTAA	1,00	0,69	Hs.278425	ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C
175	AAGTTGTGGCC	1,00	0,69	Hs.278242	tubulin, alpha, ubiquitous

176	ACAGGAGCGTT	1,00	0,69	Hs.275896	EST
177	ATGCCTACTCT	1,00	0,69	Hs.274834	EST
178	AGCACAAATCTT	1,00	0,69	Hs.274128	Homo sapiens cDNA FLJ10131 fis, clone HEMBA1003041
179	GTTCTGTTTGG	1,00	0,69	Hs.271040	ESTs
180	TTGTGATTATA	1,00	0,69	Hs.26320	TRABID protein
181	TATGCAGATCA	1,00	0,69	Hs.254948	ESTs
182	GTTGAGGACAT	1,00	0,69	Hs.250520	ESTs
183	GCCAGTGGCTG	1,00	0,69	Hs.249720	ESTs
184	GCAGATCTTTC	1,00	0,69	Hs.248623	EST
185	TTGAAACTTCT	1,00	0,69	Hs.242481	ESTs
186	CAAAAAGTTGA	1,00	0,69	Hs.241425	DKFZP586O1422 protein
187	CTCCATTCTCA	1,00	0,69	Hs.23803	Homo sapiens mRNA; cDNA DKFZp434M2217 (from clone DK
188	GCCACAGCTGG	1,00	0,69	Hs.23565	ESTs
189	GGGAAAGAAGG	1,00	0,69	Hs.233193	EST
190	CAAAAGAATAA	1,00	0,69	Hs.233013	EST
191	TAACAGTAATA	1,00	0,69	Hs.231913	ESTs
192	TGCCTAGGAAA	1,00	0,69	Hs.226356	Homo sapiens mRNA; cDNA DKFZp586F1922 (from clone DK
193	CCCTAGGAGAC	1,00	0,69	Hs.217484	ESTs
194	GGGTTGTTGTA	1,00	0,69	Hs.211258	ESTs
195	AACCCCCAAAC	1,00	0,69	Hs.207181	ESTs
196	CTTTTTCTTT	1,00	0,69	Hs.204917	EST
197	TGGGAATTGTG	1,00	0,69	Hs.203750	EST
198	CATTCCAGCCT	1,00	0,69	Hs.201306	ESTs
199	GCTGGAGTGCA	1,00	0,69	Hs.195484	Homo sapiens mRNA full length insert cDNA clone EURO
200	GAAGGCCAGCT	1,00	0,69	Hs.194624	ESTs
201	ACGTATTTGAG	1,00	0,69	Hs.193488	Homo sapiens mRNA; cDNA DKFZp434O1521 (from clone DK
202	TAATTTAAACC	1,00	0,69	Hs.18800	hypothetical protein FLJ20281
203	CTAAATGTGAA	1,00	0,69	Hs.181163	high-mobility group (nonhistone chromosomal) protein
204	CCTGGCTCTAA	1,00	0,69	Hs.178705	Homo sapiens cDNA FLJ11333 fis, clone PLACE1010616
205	CTGTCCTTGTT	1,00	0,69	Hs.176333	ESTs
206	CAATATTTGAG	1,00	0,69	Hs.174030	a disintegrin and metalloproteinase domain 28
207	CAATGGATGGC	1,00	0,69	Hs.170673	ESTs, Weakly similar to AF126780_1 retinal short-cha
208	GTCCTTGACCA	1,00	0,69	Hs.170524	ESTs
209	GCAATGACCTG	1,00	0,69	Hs.1702	interleukin 9 receptor
210	TCCTAATTCAG	1,00	0,69	Hs.170162	KIAA1357 protein
211	TTAATGATCTT	1,00	0,69	Hs.165240	ESTs
212	TTAAGTGTCT	1,00	0,69	Hs.159239	toll-like receptor 4
213	TGAAGCGTTTA	1,00	0,69	Hs.155693	protein tyrosine phosphatase, non-receptor type 21
214	GTGGAGCTTAA	1,00	0,69	Hs.152385	ESTs
215	GAGACTGGGCG	1,00	0,69	Hs.142854	ESTs

216	GTGGTACTCGC	1,00	0,69	Hs.141840	ESTs, Weakly similar to S59501 inter-feron receptor J
217	TGCAGTGCTTG	1,00	0,69	Hs.141660	chloride channel 2
218	AGCTTATTGGC	1,00	0,69	Hs.137732	KIAA1098 protein
219	ACTTCTGCTTA	1,00	0,69	Hs.13740	ESTs
220	GATAGAAATTT	1,00	0,69	Hs.131987	ESTs
221	TTTGACTAATT	1,00	0,69	Hs.131761	ESTs
222	TCAAAATGACA	1,00	0,69	Hs.131272	ESTs
223	CCAGCTAGTTT	1,00	0,69	Hs.128692	ESTs
224	TAGAGGAGTTG	1,00	0,69	Hs.125815	ESTs
225	GGGAAACACCA	1,00	0,69	Hs.123471	EST
226	GAAATGAGTGT	1,00	0,69	Hs.1200	arachidonate 12-lipoxygenase
227	ATCTTGGTACT	1,00	0,69	Hs.118162	fibronectin 1
228	CATATCATCTC	1,00	0,69	Hs.118130	ESTs
229	ATGTGACTTTT	1,00	0,69	Hs.117582	CGI-43 protein
230	CCACTGTAAGC	1,00	0,69	Hs.117582	CGI-43 protein
231	TATAAGGCTGA	1,00	0,69	Hs.114547	ESTs, Weakly similar to ZN84_HUMAN ZINC FINGER PROTE
232	GCCACTGCCAC	1,00	0,69	Hs.112405	S100 calcium-binding protein A9 (cal-granulin B)
233	TGAGGCCAGGG	1,00	0,69	Hs.110128	hypothetical protein FLJ10060
234	GTTTATTTGAA	1,00	0,69	Hs.109087	ESTs
235	AAAATTGTTAG	1,00	0,69	Hs.10760	hypothetical protein FLJ20129
236	GTGATGGGCTC	9,00	5,88	Hs.25482	envoplakin
237	AGGCTCCTGGC	52,00	31,57	Hs.24395	small inducible cytokine subfamily B (Cys-X-Cys), me
238	AACAGCAAGGA	5,00	3,33	Hs.20665	ESTs
239	CCACGGGATTC	14,00	8,79	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danlos syndrome)
240	GATTTGTTTT	4,00	2,68	Hs.738	early growth response 1
241	TATAGCCCTCA	4,00	2,68	Hs.64311	a disintegrin and metalloproteinase domain 17 (tumor
242	GTGACACGTGC	4,00	2,68	Hs.282996	ESTs
243	AGCTGTCGTAG	3,00	2,02	Hs.86674	ESTs
244	ATTGTTTCAAG	3,00	2,02	Hs.32366	ESTs, Moderately similar to TWST_HUMAN TWIST RELATED
245	AGACCCTGTCT	3,00	2,02	Hs.239283	ESTs
246	TTGGCAAGGCT	3,00	2,02	Hs.184720	ESTs
247	ATCATAGCTCA	6,00	3,87	Hs.97876	ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY
248	CCTACCACCAT	11,00	6,73	Hs.8468	RelA-associated inhibitor
249	CCAGGGCAACA	40,00	23,03	Hs.120980	(Manual assignment) ORF-less transcript in MEN1 regi
250	TACAGTATTTT	2,00	1,33	Hs.82921	solute carrier family 35 (CMP-sialic acid transporte
251	TGCCAGGTGCA	2,00	1,33	Hs.75442	albumin
252	TTTTTTATTCC	2,00	1,33	Hs.327	interleukin 10 receptor, alpha
253	AATATTTTAT	2,00	1,33	Hs.31386	ESTs, Highly similar to JE0174 frizzled protein-2 -
254	GAGAACCACCT	2,00	1,33	Hs.30250	v-maf musculoaponeurotic fibrosarcoma

					(avian) oncogene
5	255	GACACACCGAA	2,00	1,33	Hs.274243 receptor tyrosine kinase-like orphan receptor 1
	256	GGCTTGTCTAT	2,00	1,33	Hs.23294 ESTs, Weakly similar to weak similarity to HSP90 [C.
10	257	GGCAATATAGT	2,00	1,33	Hs.194429 ESTs, Weakly similar to unknown protein [H.sapiens]
	258	AGGATAACTTC	2,00	1,33	Hs.184482 DKFZP586D0624 protein
	259	GATCAATCAGT	2,00	1,33	Hs.16530 small inducible cytokine subfamily A (Cys-Cys), memb
15	260	TTGAATATTAA	2,00	1,33	Hs.161554 hypothetical protein FLJ20159
	261	TCCTCACTTCA	2,00	1,33	Hs.158455 ESTs
	262	GTTGCAGCATT	2,00	1,33	Hs.147189 HYA22 protein
	263	GTGTCTGTCTC	2,00	1,33	Hs.137432 ESTs
20	264	GGCCTCTCCGA	2,00	1,33	Hs.132834 hematopoietic protein 1
	265	ACAGAATGCCT	17,00	9,96	Hs.79732 fibulin 1
	266	GGGGCTGCCCA	15,00	8,82	Hs.195727 tumor endothelial marker 1 precursor
	267	AAAATCGCTTG	5,00	3,14	Hs.226581 COX15 (yeast) homolog, cytochrome c oxidase assembly
25	268	GTATAAACGTC	3,00	1,93	Hs.237356 stromal cell-derived factor 1
	269	CACTTTACCAG	3,00	1,93	Hs.170019 runt-related transcription factor 3
	270	TTAATTACAGT	3,00	1,93	Hs.159640 serum/glucocorticoid regulated kinase
30	271	TCAGCGACCCT	4,00	2,49	Hs.169946 GATA-binding protein 3
	272	ATGGCACATTC	4,00	2,49	Hs.14328 Homo sapiens mRNA; cDNA DKFZp762O124 (from clone DKF
	273	AGGCTCAGGTC	9,00	13,62	Hs.78344 myosin, heavy polypeptide 11, smooth muscle
35	274	AACAGGGGCCA	5,00	3,05	Hs.262958 ESTs, Weakly similar to alternatively spliced product
	275	CTGAAATCTAT	5,00	3,05	Hs.253467 ESTs
	276	GAGAAATCCCG	5,00	3,05	Hs.150298 ESTs
40	277	TCAAAAGACCT	12,00	6,80	Hs.25647 v-fos FBJ murine osteosarcoma viral oncogene homolog
	278	GAAAACAAACA	2,00	1,25	Hs.83004 interleukin 14
	279	TGCATCTGTAC	2,00	1,25	Hs.58589 glycogenin 2
45	280	ATGAAACTCCA	2,00	1,25	Hs.277951 EST
	281	TTTATTCCTCT	2,00	1,25	Hs.26290 ESTs
	282	GGGAGACCTGT	2,00	1,25	Hs.256115 EST, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE
50	283	CACTATGTAAA	2,00	1,25	Hs.24143 Wiskott-Aldrich syndrome protein interacting protein
	284	TACAGCGGCAG	2,00	1,25	Hs.205616 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
55	285	AGTGCCTTGGG	2,00	1,25	Hs.178604 ESTs
	286	CGATGCTGACG	2,00	1,25	Hs.161554 hypothetical protein FLJ20159
	287	GTGGTGTAATC	3,00	1,84	Hs.261734 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY
60	288	TATCCCAGAAT	3,00	1,84	Hs.175819 EST
	289	TCTAAAAGGC	3,00	1,84	Hs.16622 zinc finger protein 185 (LIM domain)
	290	TCGAAACGCTG	3,00	1,84	Hs.136528 ESTs, Moderately similar to

					ALU1_HUMAN ALU SUBFAMILY
291	ACATTCTTTT	22,00	11,94	Hs.82226	glycoprotein (transmembrane) nmb
292	CTGTTTGTTCA	8,00	4,59	Hs.211582	myosin, light polypeptide kinase
293	CAGTACTGTAT	4,00	2,41	Hs.9295	elastin (supravalvular aortic stenosis, Williams-Beu
294	GGTGAAACCCC	4,00	2,41	Hs.284878	EST
295	GCCAAACCCCA	4,00	2,41	Hs.194264	ESTs
296	GCCGACGCCAG	4,00	2,41	Hs.165565	ESTs
297	GAAGAGGACAA	5,00	2,97	Hs.120451	ESTs
298	TAAATAAGAAA	1,00	0,61	Hs.99875	zona pellucida binding protein
299	AAAGATCCCTC	1,00	0,61	Hs.94998	ESTs
300	ATCAAAGGTTA	1,00	0,61	Hs.94795	Homo sapiens mRNA; cDNA DKFZp564O222 (from clone DKF
301	GCAAGGTTGGT	1,00	0,61	Hs.94761	ESTs, Weakly similar to KIAA0561 protein [H.sapiens]
302	GGGACAAAAAA	1,00	0,61	Hs.93788	ESTs
303	ACTACCTCTGA	1,00	0,61	Hs.92254	hypothetical protein FLJ20163
304	GCTGGGCCAG	1,00	0,61	Hs.90964	Homo sapiens cDNA FLJ20812 fis, clone ADSE01316
305	CAAAGAAATAG	1,00	0,61	Hs.88653	ESTs
306	AATACAAGTAT	1,00	0,61	Hs.8707	KIAA1301 protein
307	CTCTGTGGCTC	1,00	0,61	Hs.85112	insulin-like growth factor 1 (somatomedia C)
308	TATTTGAAAGT	1,00	0,61	Hs.82664	ETAA16 protein
309	CCCGCCTCCGT	1,00	0,61	Hs.82071	Cbp/p300-interacting transactivator, with Glu/Asp-ri
310	TCACCGTAGCC	1,00	0,61	Hs.82042	solute carrier family 23 (nucleobase transporters),
311	CCAAAAATTAA	1,00	0,61	Hs.81424	ubiquitin-like 1 (sentrin)
312	ACTCGTATATG	1,00	0,61	Hs.81134	interleukin 1 receptor antagonist
313	TCAAGATGAAG	1,00	0,61	Hs.78948	Rab geranylgeranyltransferase, beta subunit
314	CGTCTATCCAT	1,00	0,61	Hs.76084	lamin B2
315	AAAGTGAAATG	1,00	0,61	Hs.75912	KIAA0257 protein
316	TTCTGGTGCTG	1,00	0,61	Hs.75725	transgelin 2
317	CTGGCGTCGTC	1,00	0,61	Hs.75640	natriuretic peptide precursor A
318	GGCTGGGGAGG	1,00	0,61	Hs.75061	MARCKS-like protein
319	TGCCCCCAAAA	1,00	0,61	Hs.74649	cytochrome c oxidase subunit VIc
320	TTTATTGAACA	1,00	0,61	Hs.74649	cytochrome c oxidase subunit VIc
321	CTTTCCTCATT	1,00	0,61	Hs.7381	voltage-dependent anion channel 3
322	TTGGA CTGAGG	1,00	0,61	Hs.6518	ganglioside expression factor 2
323	AGCATTA AAAA	1,00	0,61	Hs.61638	myosin X
324	CTGCTTT AAAA	1,00	0,61	Hs.56023	brain-derived neurotrophic factor
325	TGCTT AAAAAT	1,00	0,61	Hs.5534	ESTs
326	ATGAACCCCT	1,00	0,61	Hs.5011	RNA binding motif protein 9
327	TGAAACTTCCC	1,00	0,61	Hs.4994	transducer of ERBB2, 2
328	CAAACAAAAAA	1,00	0,61	Hs.43728	hypothetical protein
329	GAGGTA ACTAC	1,00	0,61	Hs.43712	ESTs
330	CATTAAAAAAT	1,00	0,61	Hs.36908	activating transcription factor 1
331	CAATGGTGAAA	1,00	0,61	Hs.35093	lymphoid blast crisis oncogene

332	CTAATGAATGT	1,00	0,61	Hs.29809	Homo sapiens mRNA; cDNA DKFZp434C185 (from clone DKF
333	AGGGCTTTTAC	1,00	0,61	Hs.29797	ribosomal protein L10
334	TAACCGTGGA	1,00	0,61	Hs.29647	uncharacterized hematopoietic stem/progenitor cells
335	TCTCCACACC	1,00	0,61	Hs.2961	S100 calcium-binding protein A3
336	CCTGGATCTCC	1,00	0,61	Hs.28501	ESTs
337	GGCCTGGCACT	1,00	0,61	Hs.283388	ESTs
338	ACTTTGTTTT	1,00	0,61	Hs.28219	protein phosphatase 2 (formerly 2A), regulatory subu
339	GTGACGCCTGT	1,00	0,61	Hs.279361	EST
340	CCATAAGTCCT	1,00	0,61	Hs.279009	seven in absentia (Drosophila) homolog 1
341	AGCCCCCGCGC	1,00	0,61	Hs.272320	Homo sapiens mRNA; cDNA DKFZp434L1226 (from clone DK
342	TATCATCATTC	1,00	0,61	Hs.270877	ESTs
343	TTCCCTGAGCA	1,00	0,61	Hs.26198	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
344	TAGTCTAAGGC	1,00	0,61	Hs.261782	ESTs
345	ATAGTAGTAAT	1,00	0,61	Hs.258863	EST
346	GATTTTAAATG	1,00	0,61	Hs.25333	interleukin 1 receptor, type II
347	CCTGGCTAACA	1,00	0,61	Hs.252124	ESTs
348	CTGTACAGACC	1,00	0,61	Hs.251653	tubulin, beta, 2
349	GGCACCAGAGC	1,00	0,61	Hs.249614	EST
350	GCGAACTCCGT	1,00	0,61	Hs.248844	ESTs
351	CGCGTCCGTGT	1,00	0,61	Hs.243929	ESTs
352	GTTTTGGTTTA	1,00	0,61	Hs.241336	Homo sapiens mRNA; cDNA DKFZp564G0422 (from clone DK
353	CTTTTTGCCAC	1,00	0,61	Hs.240165	ESTs
354	GTGGGGGGGCGC	1,00	0,61	Hs.240031	EST, Weakly similar to ALU2_HUMAN ALU SUBFAMILY SB S
355	TCTTTCCAAC	1,00	0,61	Hs.22394	hypothetical protein FLJ10893
356	TAGTAGGGCTC	1,00	0,61	Hs.21914	ESTs
357	AGGACATAACA	1,00	0,61	Hs.213793	ESTs
358	TTGTTTTAAGA	1,00	0,61	Hs.211519	hypothetical protein LOC56757
359	GTGGCACATCT	1,00	0,61	Hs.208925	ESTs, Weakly similar to alternatively spliced produc
360	CACATTGAGGC	1,00	0,61	Hs.207122	EST
361	AGGCTAGCACT	1,00	0,61	Hs.206259	Homo sapiens mRNA for KIAA1190 protein, partial cds
362	CCCCTGCCCTC	1,00	0,61	Hs.203317	EST
363	TTGTCTCTTGA	1,00	0,61	Hs.20104	ESTs
364	TGGGTACACTG	1,00	0,61	Hs.200030	ESTs, Weakly similar to ALUB_HUMAN !!!! ALU CLASS B
365	GGCAGTGGTAA	1,00	0,61	Hs.197075	ESTs
366	CATAAATGTTA	1,00	0,61	Hs.19479	ESTs
367	AGATTACCCAC	1,00	0,61	Hs.192155	ESTs
368	ACTGGCTCAGG	1,00	0,61	Hs.190719	ESTs
369	CTTGTAAGTCTC	1,00	0,61	Hs.189073	ESTs
370	AGCCCAGCTGG	1,00	0,61	Hs.18857	ESTs

371	GAGGGCAATCT	1,00	0,61	Hs.186753	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
372	CTGAAACAGGA	1,00	0,61	Hs.183601	regulator of G-protein signalling 16
373	GCCCTACCTGC	1,00	0,61	Hs.182740	ribosomal protein S11
374	GCCAACGGCGT	1,00	0,61	Hs.181002	MLL septin-like fusion (NOTE: non- standard symbol an
375	GTAAAGATGAA	1,00	0,61	Hs.175941	B-cell receptor-associated protein BAP29
376	GGGGTAATTTT	1,00	0,61	Hs.173497	Sec23 (S. cerevisiae) homolog B
377	AGGACAATGAA	1,00	0,61	Hs.173135	dual-specificity tyrosine-(Y)- phosphorylation regula
378	TTTGCACTTTT	1,00	0,61	Hs.167114	ESTs, Highly similar to AF070470_1 SPARC-related pro
379	CTGAAGTGCAG	1,00	0,61	Hs.166609	ESTs
380	CCCATTCAGTC	1,00	0,61	Hs.161554	hypothetical protein FLJ20159
381	TAATGTTCTCA	1,00	0,61	Hs.160271	G protein-coupled receptor 48
382	GTTTCTGCAGA	1,00	0,61	Hs.159642	glucosaminyl (N-acetyl) transferase 1, core 2 (beta-
383	GCAGATTCTCA	1,00	0,61	Hs.157716	ESTs
384	GGAATGAGGGG	1,00	0,61	Hs.156452	ESTs
385	GAGAGGAATA	1,00	0,61	Hs.153523	ESTs
386	TTCGACAGGCT	1,00	0,61	Hs.152925	KIAA1268 protein
387	CTCCAGCCTGG	1,00	0,61	Hs.145331	ESTs, Weakly similar to ALUF_HUMAN !!!! ALU CLASS F
388	AGTCTGTATTT	1,00	0,61	Hs.144906	ESTs
389	GAGTATTATTT	1,00	0,61	Hs.143738	ESTs, Weakly similar to EPS8_HUMAN EPIDERMAL GROWTH
390	TACTGTACTCC	1,00	0,61	Hs.143198	hypothetical protein similar to tumor suppressor p33
391	AAAATAAAATG	1,00	0,61	Hs.142908	E2F-like protein
392	CCCAGGAGTTT	1,00	0,61	Hs.13785	ESTs
393	AAAATACAGTG	1,00	0,61	Hs.136433	ESTs
394	CATTTGGCCGG	1,00	0,61	Hs.136031	ESTs
395	CAGGACCTGAA	1,00	0,61	Hs.135971	ESTs
396	TCATTAACAAA	1,00	0,61	Hs.135260	ESTs
397	CAGTAGGATAA	1,00	0,61	Hs.134541	ESTs
398	GCCTCACCTGG	1,00	0,61	Hs.128514	ESTs
399	TCTGTATCAAA	1,00	0,61	Hs.128408	ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY
400	TGATTTGTGAA	1,00	0,61	Hs.12282	ESTs
401	AGGATATTGGA	1,00	0,61	Hs.117721	ESTs
402	GTGGTACACAG	1,00	0,61	Hs.117582	CGI-43 protein
403	TTGGCCAGATT	1,00	0,61	Hs.117582	CGI-43 protein
404	ATTCTTGACAA	1,00	0,61	Hs.117527	ESTs
405	CCTTCTTGGGG	1,00	0,61	Hs.117474	ESTs
406	TACTGGAAGGC	1,00	0,61	Hs.116874	ESTs, Weakly similar to putative p150 [H.sapiens]
407	GTGGTGGTTGG	1,00	0,61	Hs.114408	toll-like receptor 5
408	AGTAATGAAAA	1,00	0,61	Hs.11217	KIAA0877 protein
409	TTAGTTTTGCT	1,00	0,61	Hs.108885	collagen, type VI, alpha 1
410	GCTAATATATT	1,00	0,61	Hs.107883	ESTs

411	TCTTGACTCCC	1,00	0,61	Hs.107265	ESTs
412	TGTACTTAATT	1,00	0,61	Hs.107082	ESTs, Moderately similar to alternatively spliced pr
413	CTCAGCAGGAG	1,00	0,61	Hs.105489	ESTs, Weakly similar to AF109127_1 stromal cell-deri
414	GGTACAATCCG	1,00	0,61	Hs.104557	hypothetical protein FLJ10697
415	ACTCCAGACCT	1,00	0,61	Hs.104350	ESTs
416	GAGAAACTCCG	9,00	5,04	Hs.184367	GTPase activating protein-like
417	CCCAGAGACCC	19,00	10,13	Hs.21223	calponin 1, basic, smooth muscle
418	GCAAGAAAGTG	23,00	12,05	Hs.155376	hemoglobin, beta
419	AAACAATAAAA	8,00	12,08	Hs.229971	EST
420	CGTGGGACACT	8,00	12,08	Hs.110196	NICE-1 protein
421	CTGTTCTCTTG	4,00	2,33	Hs.46824	ESTs
422	TAGTTGGAAAA	33,00	16,82	Hs.1119	nuclear receptor subfamily 4, group A, member 1
423	GTGAAAGCCTG	6,00	3,35	Hs.258926	EST
424	TTGGTTTGCTG	3,00	1,76	Hs.284326	Human clone 23960 mRNA sequence
425	CCTGTAATTCA	3,00	1,76	Hs.277331	EST, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC S
426	AAACCCCGTCT	3,00	1,76	Hs.273464	ESTs, Weakly similar to ALU2_HUMAN ALU SUBFAMILY SB
427	ATCGCACTACT	3,00	1,76	Hs.161721	ESTs
428	TTGAGGGGGTG	17,00	8,86	Hs.76549	(Manual assignment) MEMOREC unassignable (probably r
429	TTTGGTTTTCC	115,00	56,20	Hs.179573	collagen, type I, alpha 2
430	ACAAAACCCCG	7,00	3,82	Hs.259505	EST
431	GTGCTCAATAG	2,00	1,18	Hs.8687	ESTs
432	CAACCAGTAAA	2,00	1,18	Hs.79914	lumican
433	AGTTTATGCCC	2,00	1,18	Hs.76591	KIAA0887 protein
434	TTCACATTGTC	2,00	1,18	Hs.285804	ESTs
435	CCTGGCCTAGA	2,00	1,18	Hs.285472	ESTs
436	AAACTGGGAGG	2,00	1,18	Hs.231722	ESTs
437	GCCCGCCTTCT	2,00	1,18	Hs.201292	ESTs
438	TGCAGGTTTGT	2,00	1,18	Hs.183800	Ran GTPase activating protein 1
439	CTCAACTTGTA	2,00	1,18	Hs.117582	CGI-43 protein
440	TTTGCTTTTGT	10,00	5,27	Hs.234642	aquaporin 3
441	TAAATGAAAAA	3,00	1,69	Hs.82120	nuclear receptor subfamily 4, group A, member 2
442	GCCCCCTTCCT	3,00	1,69	Hs.212680	tumor necrosis factor receptor superfamily, member 1
443	CCTGTAATTGC	3,00	1,69	Hs.181464	ESTs
444	TCACCCTCCAG	3,00	1,69	Hs.15251	hypothetical protein
445	AAGCTCTGTGT	5,00	2,67	Hs.19813	ESTs
446	ATGGTGGGCGC	4,00	2,19	Hs.266417	EST
447	CCTGTAGTTCT	4,00	2,19	Hs.231918	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC
448	CATCTGTAATC	4,00	2,19	Hs.153290	ESTs, Weakly similar to prostate-specific transgluta
449	TCTATAATCCC	6,00	3,14	Hs.96866	ESTs
450	ATGGCACGTGC	7,00	3,61	Hs.179999	stromal cell protein



451	CTGGTGCCTG	2,00	1,11	Hs.96752	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX
452	ATAAAAAGAAA	2,00	1,11	Hs.83942	cathepsin K (pseudosclerosis)
453	CACTTGTAGTC	2,00	1,11	Hs.7845	Homo sapiens cDNA FLJ20820 fis, clone ADSE00490
454	ATTTGGAGAGG	2,00	1,11	Hs.55777	Fukuyama type congenital muscular dystrophy
455	CAGCAGCTTGT	2,00	1,11	Hs.55405	ESTs, Weakly similar to Rab7 [H.sapiens]
456	GTATTTTCATA	2,00	1,11	Hs.42140	hypothetical protein FLJ10103
457	CTTGTTGCAAT	2,00	1,11	Hs.29640	suppression of tumorigenicity 15 (rever- sion-inducing)
458	CAGGGTGGGTG	2,00	1,11	Hs.278222	ESTs, Highly similar to endothelial nitric oxide syn
459	AGCCACTACGC	2,00	1,11	Hs.249956	EST
460	TGGCATAATCA	2,00	1,11	Hs.237063	ESTs
461	CCTTCCTCTCC	2,00	1,11	Hs.199752	ESTs
462	CCCTGAATGAA	2,00	1,11	Hs.19545	frizzled (Drosophila) homolog 4
463	GATTAGCACCA	2,00	1,11	Hs.180946	ribosomal protein L5
464	GCCGTGAAAAA	2,00	1,11	Hs.164257	ESTs
465	AGAAAGAAGGA	2,00	1,11	Hs.1501	syndecan 2 (heparan sulfate proteogly- can 1, cell sur
466	GCTTCCTCCTC	5,00	2,60	Hs.85289	CD34 antigen
467	TTTCTTCCCTT	5,00	2,60	Hs.283009	tuftelin 1
468	TGCCTGTAGTC	111,00	49,37	Hs.285275	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY
469	CCCTCAATCCC	6,00	3,07	Hs.83077	interleukin 18 (interferon-gamma- inducing factor)
470	ACAACCTTTAT	6,00	3,07	Hs.283213	EST
471	GCAAACCTAAA	3,00	1,62	Hs.80686	prefoldin 5
472	GAGTGCAACCC	3,00	1,62	Hs.54680	ESTs
473	TTGAATAGTGA	4,00	2,12	Hs.38516	ESTs
474	AGCCGGATGCT	4,00	2,12	Hs.284232	KIAA0720 protein
475	GCAAAACACTG	4,00	2,12	Hs.198552	Homo sapiens mRNA; cDNA DKFZp566B193 (from clone DKF
476	CATTTGGGAAG	4,00	2,12	Hs.111334	ferritin, light polypeptide
477	CAAGAGATGCT	1,00	0,54	Hs.99741	ESTs, Weakly similar to cell division control relate
478	AGTTTATTTCA	1,00	0,54	Hs.99016	Human DNA sequence from clone 310J6 on chromosome 6q
479	GAGGATCTGCG	1,00	0,54	Hs.90998	KIAA0128 protein; septin 2
480	ACTCTGGCTCA	1,00	0,54	Hs.88974	cytochrome b-245, beta polypeptide (chronic granulom
481	GGGGTTAGGGG	1,00	0,54	Hs.85050	phospholamban
482	TAATATATCTG	1,00	0,54	Hs.8203	endomembrane protein emp70 precursor isolog
483	TAAGTCTATAT	1,00	0,54	Hs.78864	Fc fragment of IgG, low affinity IIa, re- ceptor for (
484	CACAAAAGGAT	1,00	0,54	Hs.77603	ESTs
485	GAGAAACCCTT	1,00	0,54	Hs.7739	ESTs

486	GAAAACAGTAA	1,00	0,54	Hs.76111	dystroglycan 1 (dystrophin-associated glycoprotein 1)
487	GGCAATTTACT	1,00	0,54	Hs.75813	polycystic kidney disease 1 (autosomal dominant)
488	TTTTGTGCTAG	1,00	0,54	Hs.74649	cytochrome c oxidase subunit VIc
489	TTCCCGTGGCT	1,00	0,54	Hs.70983	PTPL1-associated RhoGAP 1
490	GGCCCAGGCCT	1,00	0,54	Hs.575	aldehyde dehydrogenase 3
491	CGGCCACGTAT	1,00	0,54	Hs.55993	ESTs
492	TATAGCTGCAT	1,00	0,54	Hs.55964	ESTs, Weakly similar to C4HU complement C4A precursor
493	CTTGTGTTTAT	1,00	0,54	Hs.50748	chromosome 21 open reading frame 18
494	CACAAAAATGC	1,00	0,54	Hs.49944	ESTs
495	CTGTAATTTTA	1,00	0,54	Hs.48480	ESTs
496	CAATTCTTTCT	1,00	0,54	Hs.48403	hypothetical protein FLJ10847
497	ATTCTGCAGAG	1,00	0,54	Hs.47232	ESTs
498	TTTATATCATT	1,00	0,54	Hs.47099	ESTs
499	ACTCCATAAAA	1,00	0,54	Hs.4273	Human DNA sequence from clone RP1-104A17 on chromoso
500	TTTTATTATA	1,00	0,54	Hs.42656	ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY
501	GACTCGACCAG	1,00	0,54	Hs.31922	ESTs
502	GGTGTGTTTTA	1,00	0,54	Hs.31566	ESTs
503	ATAAATTTATG	1,00	0,54	Hs.30715	ESTs
504	GGAGGCCGAGA	1,00	0,54	Hs.285565	ESTs
505	ATATTCAGCTG	1,00	0,54	Hs.285379	ESTs
506	GAACTTGTCTG	1,00	0,54	Hs.279934	Homo sapiens mRNA; cDNA DKFZp434I0835 (from clone DK
507	CCCGTATATGT	1,00	0,54	Hs.279844	hypothetical protein FLJ10033
508	GTGGACCTGAG	1,00	0,54	Hs.279059	ESTs
509	AGCCTGGAAGG	1,00	0,54	Hs.278549	ESTs
510	TGGTTTTTGAG	1,00	0,54	Hs.275865	ribosomal protein S18
511	GCTTGTTCAAA	1,00	0,54	Hs.274969	ESTs
512	TCCACCAGCCA	1,00	0,54	Hs.27457	ESTs
513	GCACTCCAACC	1,00	0,54	Hs.273682	EST
514	CCCATAATCCT	1,00	0,54	Hs.270797	ESTs
515	AGTCACAGCTT	1,00	0,54	Hs.267448	hypothetical protein FLJ20039
516	TAGAAAAAACC	1,00	0,54	Hs.262476	S-adenosylmethionine decarboxylase 1
517	TAAAGATGGCA	1,00	0,54	Hs.25357	Homo sapiens clone 24488 mRNA sequence
518	GGCTATGCCCT	1,00	0,54	Hs.243855	ESTs
519	AGACATTGACA	1,00	0,54	Hs.239934	CGI-96 protein
520	TATGCTTTAAA	1,00	0,54	Hs.237225	ribosomal protein S5 pseudogene 1
521	TATTGCTAAAT	1,00	0,54	Hs.23590	solute carrier family 16 (monocarboxylic acid transp
522	CCAAGGCACTG	1,00	0,54	Hs.234863	ESTs
523	AACTTTCCAAA	1,00	0,54	Hs.23457	ESTs
524	TCTACAAGGG	1,00	0,54	Hs.233476	ESTs
525	CCACTATGCCT	1,00	0,54	Hs.231229	ESTs
526	GGGCGCCTGGC	1,00	0,54	Hs.224242	EST
527	GGGGGGAAAAA	1,00	0,54	Hs.223590	EST, Weakly similar to RL3_HUMAN

					60S RIBOSOMAL PROTE
528	TTGTTTATGTA	1,00	0,54	Hs.21958	Homo sapiens cDNA FLJ10532 fis, clone NT2RP2001044
529	TTGAGATAAGA	1,00	0,54	Hs.21887	ESTs
530	GCTATATCCAA	1,00	0,54	Hs.218008	ESTs
531	TTTGGTTTTCT	1,00	0,54	Hs.21431	suppressor of fused
532	GATTGTCCTTG	1,00	0,54	Hs.211517	ESTs
533	GGTTATCAAAG	1,00	0,54	Hs.208334	ESTs
534	GTCTCGCTGAC	1,00	0,54	Hs.207911	ESTs
535	AGCCATCGCGC	1,00	0,54	Hs.207749	EST
536	ACCACCCGTGT	1,00	0,54	Hs.202033	EST
537	ACACTCTTCCT	1,00	0,54	Hs.20103	ESTs
538	GGAGATGTTTG	1,00	0,54	Hs.199545	ESTs
539	CTCAACCTTAA	1,00	0,54	Hs.199243	KIAA0231 protein
540	GCAAGACTCCC	1,00	0,54	Hs.198011	ESTs
541	CAATACTATTC	1,00	0,54	Hs.197642	hypothetical protein FLJ10388
542	GTTGTGCTCAG	1,00	0,54	Hs.191228	hypothetical protein FLJ20284
543	GGGCTAGCACT	1,00	0,54	Hs.190722	ESTs
544	ACATTACGCC	1,00	0,54	Hs.184141	glutaryl-Coenzyme A dehydrogenase
545	TATATTTAGTT	1,00	0,54	Hs.183037	protein kinase, cAMP-dependent, regulatory, type I,
546	CCAGCTAGCGA	1,00	0,54	Hs.179756	LW-1
547	TGAGGATACAG	1,00	0,54	Hs.177820	Homo sapiens mRNA; cDNA DKFZp564L102 (from clone DKF
548	TGCCTACAGTC	1,00	0,54	Hs.176207	EST
549	CTCATATGCAA	1,00	0,54	Hs.173540	ATPase, Class V, type 10D
550	AAGGAGGTGGA	1,00	0,54	Hs.172730	ESTs
551	CAAGCCCTGCC	1,00	0,54	Hs.172035	hypothetical protein similar to mouse HN1 (Hematolo
552	GCGCTGGGAGG	1,00	0,54	Hs.171763	CD22 antigen
553	TCCTTGGCGTG	1,00	0,54	Hs.168640	Ank, mouse, homolog of
554	TTGCCATATGC	1,00	0,54	Hs.164024	ESTs, Weakly similar to unnamed protein product [H.s
555	GCTCCCTTCAC	1,00	0,54	Hs.162222	EST
556	CTGTGCAAGGA	1,00	0,54	Hs.161554	hypothetical protein FLJ20159
557	TGTGCTTGTGT	1,00	0,54	Hs.161554	hypothetical protein FLJ20159
558	CTTTTCCCCC	1,00	0,54	Hs.156007	Down syndrome critical region gene 1-like 1
559	TCTTTTCTTT	1,00	0,54	Hs.155606	paired mesoderm homeo box 1
560	AAAAGCTGTTT	1,00	0,54	Hs.15550	ESTs
561	GTCCCCCCCCC	1,00	0,54	Hs.152454	ESTs
562	CCTGGCGGGAT	1,00	0,54	Hs.149347	ESTs, Highly similar to KIAA1043 protein [H.sapiens]
563	GATTGGTATGA	1,00	0,54	Hs.147049	cut (Drosophila)-like 1 (CCAAT displacement protein)
564	GTGAAGACTAC	1,00	0,54	Hs.14665	ESTs
565	TAAATGGGTTG	1,00	0,54	Hs.1395	early growth response 2 (Krox-20 (Drosophila) homolo
566	TGTAAACTTTG	1,00	0,54	Hs.13849	ESTs
567	GACACGTTGCC	1,00	0,54	Hs.136574	arachidonate 12-lipoxygenase, 12R type

568	TGTGAATTTTA	1,00	0,54	Hs.132834	hematopoietic protein 1
569	TAAACACTTG	1,00	0,54	Hs.130636	ESTs
570	TGGCAATTTTC	1,00	0,54	Hs.129636	ESTs
571	TCTGTAGCACA	1,00	0,54	Hs.128766	hypothetical protein FLJ10600
572	TCAGCAGTTAA	1,00	0,54	Hs.128571	ESTs
573	AATGAGGTGCT	1,00	0,54	Hs.128400	ESTs
574	TTCAGAACTCT	1,00	0,54	Hs.125914	ESTs
575	GAATAAGATAT	1,00	0,54	Hs.12479	associated molecule with the SH3 domain of STAM
576	TGTCCCAGCCA	1,00	0,54	Hs.1211	acid phosphatase 5, tartrate resistant
577	CCCATCTCAGA	1,00	0,54	Hs.120769	Homo sapiens cDNA FLJ20463 fis, clone KAT06143
578	AGAAGCTCCAG	1,00	0,54	Hs.120021	DKFZP434I092 protein
579	AGTCTTCAAAA	1,00	0,54	Hs.117582	CGI-43 protein
580	GAGTTTTTATT	1,00	0,54	Hs.117582	CGI-43 protein
581	TTTTGCAATAA	1,00	0,54	Hs.11614	ESTs
582	AGCTCTATGAG	1,00	0,54	Hs.115831	ESTs
583	AATAGGTCCCA	1,00	0,54	Hs.113029	ribosomal protein S25
584	TAGTCTACTGT	1,00	0,54	Hs.112472	ESTs
585	ATCCTTACATC	1,00	0,54	Hs.111720	ESTs
586	AACTTTTATAT	1,00	0,54	Hs.108787	phosphatidylinositol glycan, class N
587	CCGTAAAAAAA	1,00	0,54	Hs.107187	divalent cation tolerant protein CUTA
588	TGAAGATGTAA	1,00	0,54	Hs.106217	ESTs
589	GAACCATTTGC	1,00	0,54	Hs.104305	KIAA0926 protein
590	CTGTGGAGCTG	1,00	0,54	Hs.103379	ESTs
591	AGAATTACAGA	1,00	0,54	Hs.101915	ESTs
592	TGTTGCTCCCA	5,00	2,54	Hs.82210	zinc finger protein 220
593	TAGTTTGAAGG	5,00	2,54	Hs.79033	glutaminyl-peptide cyclotransferase (glutaminyl cycl
594	CCCAACGCGCT	47,00	20,67	Hs.272572	hemoglobin, alpha 2
595	CCTATAATCTC	13,00	6,08	Hs.117582	CGI-43 protein
596	TCTCCTGGACT	4,00	2,06	Hs.50915	kallikrein 5
597	ATCTTGCCACT	4,00	2,06	Hs.32945	glutamate receptor, metabotropic 1
598	AGGATAAAAAA	3,00	1,56	Hs.79404	neuron-specific protein
599	GACCACAAATA	3,00	1,56	Hs.76476	cathepsin H
600	AGCATATCTTC	3,00	1,56	Hs.275865	ribosomal protein S18
601	AACACAGGAGG	3,00	1,56	Hs.222874	ESTs, Moderately similar to zinc transporter 4 [H.sa
602	CGGGGACGAGG	3,00	1,56	Hs.124942	protein phosphatase 2A 48 kDa regulatory subunit
603	GCGAAGCCCCG	7,00	3,35	Hs.103804	heterogeneous nuclear ribonucleoprotein U (scaffold
604	GTGGCAGGTAC	9,00	4,21	Hs.190467	EST
605	TCTGTTGTTCA	9,00	4,21	Hs.117582	CGI-43 protein
606	CCTGTATCCCA	4,00	2,00	Hs.270072	ESTs
607	ATGGATGCTTG	2,00	1,05	Hs.89404	msh (Drosophila) homeo box homolog 2
608	GACTTCTGTCC	2,00	1,05	Hs.87539	aldehyde dehydrogenase 8
609	AAAAAGAAACT	2,00	1,05	Hs.73287	KIAA1235 protein
610	TACTGAAAAAA	2,00	1,05	Hs.5111	hypothetical protein FLJ20729
611	CACCTGGAGGC	2,00	1,05	Hs.30864	ESTs

612	GCAAGAGCCCA	2,00	1,05	Hs.26670	Human PAC clone RP3-515N1 from 22q11.2-q22	
613	AACCCGGGGAG	2,00	1,05	Hs.228009	EST	
614	TTGCCAGGGT	2,00	1,05	Hs.225093	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC	5
615	AAGCAGTTACA	2,00	1,05	Hs.22116	CDC14 (cell division cycle 14, S. cerevisiae) homolo	
616	GCAGTCATACA	2,00	1,05	Hs.182626	chromosome 22 open reading frame 5	10
617	GGGGCACACAC	2,00	1,05	Hs.181900	ESTs	
618	AGGGAAGGTGA	2,00	1,05	Hs.126927	ESTs	
619	AGCCGCTGTGC	2,00	1,05	Hs.106771	ESTs	
620	TCAAGCCATCA	35,00	14,85	Hs.738	early growth response 1	15
621	GTGGCGGGCAT	5,00	2,42	Hs.230564	EST	
622	ACCTGGGTGCT	5,00	2,42	Hs.159643	ESTs, Weakly similar to MLD [H.sapiens]	
623	TGTGGCGTATA	8,00	3,69	Hs.211582	myosin, light polypeptide kinase	
624	CGGGCACCTTC	6,00	8,99	Hs.198249	gap junction protein, beta 5 (connexin 31.1)	20
625	CCCTTGAGGAG	6,00	8,99	Hs.1076	(Manual assignment) SPRR1B, cornifin B	
626	AATGTTTTTAA	3,00	1,50	Hs.75335	glycine amidinotransferase (L-arginine:glycine amidi	25
627	CCTCTCCCAT	3,00	1,50	Hs.177533	Homo sapiens mRNA, chromosome 1 specific transcript	
628	TGTTCTGATTT	3,00	1,50	Hs.167835	acyl-Coenzyme A oxidase 1, palmitoyl	30
629	CCTGTAGTGCC	5,00	2,36	Hs.269645	Homo sapiens cell-line E8CASS clone E24L estradiol-i	
630	CCACTGTATTC	6,00	2,77	Hs.235041	EST	
631	AGAAATGTATG	6,00	2,77	Hs.232068	transcription factor 8 (represses interleukin 2 expr	35
632	AGGTCAGAAGA	10,00	4,38	Hs.23437	Homo sapiens mRNA; cDNA DKFZp586G0623 (from clone DK	
633	ATTAAGAAAAT	14,00	5,95	Hs.76549	AHNAK nucleoprotein (desmoyokin)	40
634	AACCCGGGGGG	6,00	2,72	Hs.6214	KIAA0731 protein	
635	CACCACAACAA	6,00	2,72	Hs.174139	chloride channel 3	
636	TTCCCCAGGGT	2,00	0,99	Hs.59545	ring finger protein 15	
637	CACACTATAGG	2,00	0,99	Hs.58924	ESTs, Weakly similar to JC5594 jerky gene protein ho	45
638	GGGAAAGAGGG	2,00	0,99	Hs.35096	KIAA1538 protein	
639	GCTGGGCGCGG	2,00	0,99	Hs.278070	EST	
640	GGGGCAACAGC	2,00	0,99	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	50
641	GTGGCAGGCC	2,00	0,99	Hs.266105	EST	
642	CATATCCCTC	2,00	0,99	Hs.250746	ESTs	
643	CTTAGGAGTCA	2,00	0,99	Hs.23853	ESTs	
644	CAGCACAGTGG	2,00	0,99	Hs.227806	ras GTPase activating protein-like	55
645	ATGCTCAAAGG	2,00	0,99	Hs.226018	Homo sapiens mRNA full length insert cDNA clone EURO	
646	TTCTGTGCATA	2,00	0,99	Hs.16803	hypothetical protein FLJ10231	
647	GCATAATGTTT	2,00	0,99	Hs.11050	F-box only protein 9	60
648	TGGCCAGCTCC	19,00	7,83	Hs.170121	protein tyrosine phosphatase, receptor type, C	

649	TCTGGCCCAGC	3,00	1,45	Hs.183	Duffy blood group
650	ATCCTGAGTTA	12,00	5,06	Hs.73931	major histocompatibility complex, class II, DQ beta
651	ACAAATGAAAA	1,00	0,49	Hs.96657	hypothetical protein
652	TACATTTCAAG	1,00	0,49	Hs.94376	proprotein convertase subtilisin/kexin type 5
653	GCAAAATGCTG	1,00	0,49	Hs.92254	hypothetical protein FLJ20163
654	TTTAAGAAATG	1,00	0,49	Hs.91139	ESTs
655	ACCCACCTGTG	1,00	0,49	Hs.8736	Homo sapiens mRNA; cDNA DKFZp564H203 (from clone DKF
656	GCAGCAGTGTC	1,00	0,49	Hs.86538	ESTs
657	CCATTAAAAAA	1,00	0,49	Hs.85885	ESTs
658	AAAGAGGGACG	1,00	0,49	Hs.84229	splicing factor, arginine/serine-rich 8 (suppressor-
659	ACACTTAAAAA	1,00	0,49	Hs.83381	guanine nucleotide binding protein 11
660	TCACAAAAAAA	1,00	0,49	Hs.7976	KIAA0332 protein
661	ATTTAATATAT	1,00	0,49	Hs.7972	KIAA0871 protein
662	AGTTCAAGGCT	1,00	0,49	Hs.79058	suppressor of Ty (S.cerevisiae) 4 homolog 1
663	GAGTTGCTATT	1,00	0,49	Hs.78575	prosaposin (variant Gaucher disease and variant meta
664	GACTGTCAAAA	1,00	0,49	Hs.69330	ESTs
665	GCGCAACAAC	1,00	0,49	Hs.61950	DKFZp434A0131 protein
666	TAAATCAGAGA	1,00	0,49	Hs.61929	Homo sapiens cDNA FLJ11010 fis, clone PLACE1003145
667	TAAATGAATGA	1,00	0,49	Hs.57967	ESTs
668	AATAGGAAGAT	1,00	0,49	Hs.50745	ESTs
669	CAATTAAAAAT	1,00	0,49	Hs.50123	zinc finger protein 189
670	GTGTATGTGGT	1,00	0,49	Hs.49881	fatty acid binding protein 3, muscle and heart (mamm
671	ACAAACCCACA	1,00	0,49	Hs.49282	hypothetical protein FLJ11088
672	CAAGTGAAAGG	1,00	0,49	Hs.47822	KIAA0380 gene product; RhoA-specific guanine nucleot
673	GAACAGAACGC	1,00	0,49	Hs.47566	ESTs
674	CTAATGGCCCT	1,00	0,49	Hs.3416	adipose differentiation-related protein
675	TAATGTTTTTT	1,00	0,49	Hs.31930	ESTs
676	ATTTGGCCTGT	1,00	0,49	Hs.285519	Homo sapiens OVN6-2 mRNA, partial cds
677	TCTGGGAGGGG	1,00	0,49	Hs.285313	core promoter element binding protein
678	GACTAAATTGT	1,00	0,49	Hs.283643	ESTs
679	TATTTTCACAA	1,00	0,49	Hs.279896	hypothetical protein FLJ20546
680	GAGGTTTTCTG	1,00	0,49	Hs.279639	Homo sapiens mRNA; cDNA DKFZp586M2022 (from clone DK
681	CCTAGAATCCC	1,00	0,49	Hs.278982	PRO1779 protein
682	CAGCCCCTGTC	1,00	0,49	Hs.278234	Homo sapiens mRNA; cDNA DKFZp434H1323 (from clone DK
683	GTGTCGGGCTC	1,00	0,49	Hs.278010	EST
684	CACCTGTAAAC	1,00	0,49	Hs.277311	EST
685	GCGGCGACTGC	1,00	0,49	Hs.271980	mitogen-activated protein kinase 6
686	GGAATGAATGA	1,00	0,49	Hs.270824	ESTs

687	TGGGATATAGT	1,00	0,49	Hs.269888	ESTs
688	GTGGTTGATGC	1,00	0,49	Hs.267083	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ
689	GTGGTAGGTAC	1,00	0,49	Hs.264844	EST, Moderately similar to ALU1_HUMAN ALU SUBFAMILY
690	GCCTGCCTTTA	1,00	0,49	Hs.25371	ESTs, Weakly similar to A37232 mucin, tracheal [H.sa]
691	GATCTCGCTTT	1,00	0,49	Hs.250773	signal sequence receptor, alpha (translo- con-associat
692	CTCCTATTTTT	1,00	0,49	Hs.25010	hypothetical protein P15-2
693	GTGCGCACCTG	1,00	0,49	Hs.243957	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
694	ATAAAATGTCT	1,00	0,49	Hs.24181	ESTs
695	TTTCACCCCGT	1,00	0,49	Hs.23492	ESTs
696	TATGTTTAAAA	1,00	0,49	Hs.234392	platelet-activating factor acetylhydrolase 2 (40kD)
697	GATCACTTGAG	1,00	0,49	Hs.231798	EST
698	TTGAGAAAAAA	1,00	0,49	Hs.22971	ESTs
699	ACCCTGGGAGG	1,00	0,49	Hs.228529	ESTs
700	TGTGGTGGTGC	1,00	0,49	Hs.223618	EST
701	GATTGGCCAGA	1,00	0,49	Hs.21739	Homo sapiens mRNA; cDNA DKFZp586I1518 (from clone DK
702	GCTGAGTTATT	1,00	0,49	Hs.216363	ESTs
703	AGTATTCCTAA	1,00	0,49	Hs.21621	hypothetical protein DKFZp762O076
704	TGTCTGCCATT	1,00	0,49	Hs.21580	ESTs
705	CCCCTGTACTC	1,00	0,49	Hs.213016	ESTs, Highly similar to cytokine receptor related pr
706	CTTTTTAAAGA	1,00	0,49	Hs.212788	EST
707	TACCCGAAAAC	1,00	0,49	Hs.210858	ESTs, Weakly similar to ALUD_HUMAN !!!! ALU CLASS D
708	TGCCTCTAGTC	1,00	0,49	Hs.209413	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
709	CCGCCGCACTC	1,00	0,49	Hs.204049	ESTs
710	CTAAGAGGGGT	1,00	0,49	Hs.196102	ESTs
711	CTGCTGTAGTC	1,00	0,49	Hs.194319	ESTs
712	GGACCCTCATT	1,00	0,49	Hs.191063	ESTs
713	AACTAATTCTC	1,00	0,49	Hs.189513	hypothetical protein FLJ10213
714	GCAGTGCCAAG	1,00	0,49	Hs.183528	ESTs, Weakly similar to Bem46-like protein [D.melano
715	ATTGGAGCGCA	1,00	0,49	Hs.180433	rTS beta protein
716	TGAAAACTCCC	1,00	0,49	Hs.180248	zinc finger protein 124 (HZF-16)
717	CTCCCAGCCAC	1,00	0,49	Hs.177582	surfactant, pulmonary-associated protein A1
718	GTTTTAAAAAA	1,00	0,49	Hs.174756	EST
719	GAATCAAGCTG	1,00	0,49	Hs.17296	ESTs
720	CTGGGCATTTT	1,00	0,49	Hs.172207	non-POU-domain-containing, octamer- binding
721	TTGTTTGTGTA	1,00	0,49	Hs.170162	KIAA1357 protein
722	AGGACTGGCAT	1,00	0,49	Hs.170114	KIAA0061 protein
723	TCGCTTTTAAG	1,00	0,49	Hs.168640	Ank, mouse, homolog of

724	AAGTGAAAAA	1,00	0,49	Hs.168159	apoptosis regulator
725	CAAATTAGAAT	1,00	0,49	Hs.162271	ESTs, Moderately similar to CO3 HUMAN COMPLEMENT C3
726	ATACCACTAAG	1,00	0,49	Hs.153792	5-methyltetrahydrofolate-homocysteine methyltransfer
727	GGTGATGGAGG	1,00	0,49	Hs.149692	ESTs, Highly similar to G43284 zinc finger protein Z
728	TTGGGTTTCTG	1,00	0,49	Hs.147975	ESTs
729	AATAAATGCCC	1,00	0,49	Hs.145522	ESTs
730	CATACACACAT	1,00	0,49	Hs.143460	protein kinase C, nu
731	GTTATACAACA	1,00	0,49	Hs.141183	ESTs
732	CTCACAGGCAC	1,00	0,49	Hs.139784	ESTs
733	TACCCATTACC	1,00	0,49	Hs.136981	ESTs
734	TTTCTTTCCCT	1,00	0,49	Hs.135055	ESTs
735	CATCTGTACTG	1,00	0,49	Hs.132892	Homo sapiens protocadherin 10 (PCDH10) mRNA, partial
736	GAGCTGTTTGT	1,00	0,49	Hs.127476	ESTs
737	ACACGTACTAT	1,00	0,49	Hs.120828	Human DNA sequence from clone RP5- 876B10 on chromoso
738	TTTATATTTCA	1,00	0,49	Hs.11958	oxidative 3 alpha hydroxysteroid dehy- drogenase; reti
739	CACAGTTTTAA	1,00	0,49	Hs.118918	ESTs
740	TGGTTTTACCA	1,00	0,49	Hs.117582	CGI-43 protein
741	GTGCCTGGTAT	1,00	0,49	Hs.116459	hypothetical protein PRO2198
742	TACCTTAGAAC	1,00	0,49	Hs.114963	Homo Sapiens (clone B3B3E13) chro- mosome 4p16.3 DNA f
743	GTGTAGGAGGT	1,00	0,49	Hs.113029	ribosomal protein S25
744	CCCTGGAGACA	1,00	0,49	Hs.111334	ferritin, light polypeptide
745	CCTGTAGCCCA	1,00	0,49	Hs.109370	ESTs
746	TATCCATATTA	1,00	0,49	Hs.107942	DKFZP564M112 protein
747	CTACTAATTGC	1,00	0,49	Hs.101916	Homo sapiens mRNA; cDNA DKFZp564K133 (from clone DKF
748	GGCCTCCAAGA	5,00	2,25	Hs.286220	ESTs
749	GTGGCTGACAC	4,00	1,83	Hs.202234	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAMILY SB2
750	CTGTACTTGTG	8,00	3,37	Hs.75678	FBJ murine osteosarcoma viral onco- gene homolog B
751	ACAAAACCCCA	8,00	3,37	Hs.140208	ESTs
752	AGCCACCACCC	3,00	1,40	Hs.232045	ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY
753	TGCCTGTAGTT	7,00	2,97	Hs.246646	EST
754	GCTAACCCTG	15,00	5,92	Hs.279772	brain specific protein
755	GCAAAACCTG	86,00	31,14	Hs.117582	CGI-43 protein
756	AAACATTAAAA	21,00	8,08	Hs.77443	actin, gamma 2, smooth muscle, enteric
757	GTGGCACTTGC	4,00	1,78	Hs.272322	Homo sapiens mRNA; cDNA DKFZp434L092 (from clone DKF
758	GAAGCTACACC	4,00	1,78	Hs.107253	ESTs
759	TAAGGTAGAGG	2,00	0,94	Hs.99908	nuclear receptor coactivator 4
760	TGGGTCATTTG	2,00	0,94	Hs.98073	ESTs
761	GCTCACTGAAG	2,00	0,94	Hs.9568	zinc finger protein 261



762	CACCTATCAAT	2,00	0,94	Hs.58617	Rho-associated, coiled-coil containing protein kinas
763	CTTCAATCTTA	2,00	0,94	Hs.58419	DKFZP586L2024 protein
764	CAGTCCTCTTG	2,00	0,94	Hs.57553	tousled-like kinase 2
765	TTACCAAAGCA	2,00	0,94	Hs.30246	solute carrier family 19 (thiamine transporter), mem
766	ATGAAACCCTA	2,00	0,94	Hs.282671	EST
767	TCACTCCAGCC	2,00	0,94	Hs.270497	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
768	AAAGGCATCAG	2,00	0,94	Hs.256297	integrin, alpha 11
769	GACATCTGTCC	2,00	0,94	Hs.25566	ESTs
770	TGTCTTTTCTG	2,00	0,94	Hs.250882	bradykinin receptor B2
771	TGACTGTATTA	2,00	0,94	Hs.198241	amine oxidase, copper containing 3 (vascular adhesio
772	GCAAGACCTCA	2,00	0,94	Hs.181592	ESTs
773	AGGAAGGAAAA	2,00	0,94	Hs.180532	heat shock 90kD protein 1, alpha
774	CTGCCGGAGCA	2,00	0,94	Hs.164779	ESTs
775	TATTCCAGAAC	2,00	0,94	Hs.161554	hypothetical protein FLJ20159
776	AGCGAAACTCC	2,00	0,94	Hs.106597	ESTs
777	CTGGGGGTCAG	2,00	0,94	Hs.102664	vesicle-associated membrane protein 4
778	GCTGTAATCCC	15,00	5,82	Hs.184019	Homo sapiens clone 23551 mRNA sequence
779	CACCTGTGGTC	16,00	6,11	Hs.209585	EST
780	CTCTAGAGAAA	3,00	1,35	Hs.97925	hypothetical protein
781	GCAAATCCTGT	3,00	1,35	Hs.79059	transforming growth factor, beta receptor III (betag
782	TATATGCTGGG	3,00	1,35	Hs.2969	v-ski avian sarcoma viral oncogene homolog
783	GGGAGACCCCA	3,00	1,35	Hs.24884	ESTs, Moderately similar to RNA polymerase I associa
784	TGGAAATGAAA	3,00	1,35	Hs.172928	collagen, type I, alpha 1
785	CCTGTAATCTG	3,00	1,35	Hs.159975	ESTs
786	TGTATTGTACA	3,00	1,35	Hs.118562	Link guanine nucleotide exchange factor II
787	ACATAGACCGA	7,00	2,87	Hs.173594	pigment epithelium-derived factor
788	GTTCCACAGAA	12,00	4,66	Hs.179573	collagen, type I, alpha 2
789	GTGGCAGAGAC	4,00	1,74	Hs.75813	polycystic kidney disease 1 (autosomal dominant)
790	AGCCGAGATCG	4,00	1,74	Hs.278053	EST
791	CCTGTAGTTCC	24,00	8,84	Hs.189242	Homo sapiens mRNA; cDNA DKFZp434A202 (from clone DKF
792	GTAAAACCCTG	29,00	10,50	Hs.281680	peroxisomal trans 2-enoyl CoA reductase; putative sh
793	AGTCTGCTGGG	5,00	7,44	Hs.259508	ESTs
794	CTGGGCAGAGA	5,00	7,44	Hs.200735	ESTs, Moderately similar to AF105377_1 heparan sulfa
795	TCACACAAAGG	5,00	2,11	Hs.46783	ESTs
796	CGCCTGTAATT	5,00	2,11	Hs.14333	ESTs
797	ATTGCTCTCTG	8,00	3,18	Hs.245188	tissue inhibitor of metalloproteinase 3 (Sorsby fund

798	CCTGTGGTTCC	10,00	3,88	Hs.286061	ESTs
799	TGTCCACACAT	4,00	1,69	Hs.5897	Homo sapiens mRNA; cDNA DKFZp586P1622 (from clone DK
800	GACGGAGCCTT	4,00	1,69	Hs.37482	COPZ2 for nonclathrin coat protein zeta-COP
801	ACTGGGCAGTG	4,00	1,69	Hs.241257	latent transforming growth factor beta binding prote
802	CGGCACCTTAA	4,00	1,69	Hs.209100	DKFZP434C171 protein
803	CTGAAACAGCT	4,00	1,69	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like 1
804	TGTTACCTGGT	2,00	0,90	Hs.79227	myomesin (M-protein) 2 (165kD)
805	TCTTTGCTCTT	2,00	0,90	Hs.44077	hypothetical protein FLJ10793
806	AAATCACCAAT	2,00	0,90	Hs.4082	lectin, galactoside-binding, soluble, 8 (galectin 8)
807	TGTATTGACTG	2,00	0,90	Hs.29280	ESTs
808	TTCACTTCAAC	2,00	0,90	Hs.250911	Homo sapiens clone 23967 unknown mRNA, partial cds
809	CGTGGGGCTGC	2,00	0,90	Hs.221986	aquaporin 5
810	TCACAGAGTCT	2,00	0,90	Hs.194149	Homo sapiens mRNA; cDNA DKFZp434M011 (from clone DKF
811	TGCCACTGTGC	2,00	0,90	Hs.183165	ESTs, Highly similar to protein kinase [H.sapiens]
812	CTATAAAAGTG	2,00	0,90	Hs.154145	guanine nucleotide binding protein (G protein), alph
813	TTGGCTAGGCT	13,00	4,86	Hs.252259	ribosomal protein S3
814	AGGGAGCAGAG	11,00	4,17	Hs.118223	microfibrillar-associated protein 4
815	TTGGTGTGCTG	7,00	2,78	Hs.240399	EST
816	TGGAAAGTGAA	50,00	17,06	Hs.25647	v-fos FBJ murine osteosarcoma viral oncogene homolog
817	TTGATTGAGTG	3,00	1,31	Hs.9879	ESTs
818	CAGGGATCTGC	3,00	1,31	Hs.7634	ESTs, Moderately similar to semaphorin B [M.musculus
819	ATTGCACCACC	3,00	1,31	Hs.44259	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
820	CTGGTGGCCAC	3,00	1,31	Hs.286028	Human alpha-2 collagen type VI mRNA, 3' end
821	AATCATTGAGG	3,00	1,31	Hs.19150	Homo sapiens mRNA; cDNA DKFZp564A2164 (from clone DK
822	ACCCCTTCCT	3,00	1,31	Hs.181392	major histocompatibility complex, class I, E
823	CCTGGCCAAA	3,00	1,31	Hs.126824	EST
824	TTAACCCCTCC	30,00	10,46	Hs.78224	ribonuclease, RNase A family, 1 (pancreatic)
825	ACAGGCTACGG	118,00	39,00	Hs.75777	transgelin
826	AGATGAGATGA	17,00	6,08	Hs.285313	core promoter element binding protein
827	AAAAAAAAGGC	1,00	0,44	Hs.90077	TG-interacting factor (TALE family homeobox)
828	TACGCTAAAC	1,00	0,44	Hs.87354	ESTs
829	GTAGAAGTGTA	1,00	0,44	Hs.8705	ESTs
830	TGCCCAGCAAT	1,00	0,44	Hs.76297	G protein-coupled receptor kinase 6
831	AGCAGGTTTGC	1,00	0,44	Hs.7434	ESTs

832	AGAGAGAGCCC	1,00	0,44	Hs.724	thyroid hormone receptor, alpha (avian erythroblast)
833	GCACTGATTAA	1,00	0,44	Hs.71741	ESTs, Highly similar to I38945 melanoma ubiquitous m
834	CAGAGACAAGC	1,00	0,44	Hs.71721	ESTs
835	CAGTTGTCTAG	1,00	0,44	Hs.58882	Microfibril-associated glycoprotein-2
836	TGTGTGTGCTA	1,00	0,44	Hs.55533	ESTs
837	GCCTGGACCAG	1,00	0,44	Hs.55407	Homo sapiens mRNA; cDNA DKFZp434K0621 (from clone DK
838	TGTTTAATAAA	1,00	0,44	Hs.50841	ESTs
839	CATTTTCTAAT	1,00	0,44	Hs.48376	Homo sapiens clone HB-2 mRNA sequence
840	AGCTTTCCCAA	1,00	0,44	Hs.45109	ESTs
841	ACTCAGTAGCC	1,00	0,44	Hs.44197	hypothetical protein DKFZp564D0462
842	TCAAATTGAAA	1,00	0,44	Hs.44038	pellino (Drosophila) homolog 2
843	GGCCAGCCCTG	1,00	0,44	Hs.4243	ESTs
844	ACATTTTGTTT	1,00	0,44	Hs.42116	ESTs
845	GGCAAGCAGGC	1,00	0,44	Hs.41688	dual specificity phosphatase 8
846	TGCTTGGTACA	1,00	0,44	Hs.393	prostaglandin I2 (prostaglandin) receptor (IP)
847	TAAGTCTAATT	1,00	0,44	Hs.35804	hect domain and RLD 3
848	TATTTTACTTG	1,00	0,44	Hs.30340	hypothetical protein KIAA1165
849	CTCTCTCCCAG	1,00	0,44	Hs.30172	ESTs
850	AGCAAATTTTC	1,00	0,44	Hs.29423	ESTs, Weakly similar to macrophage lectin 2 [H.sapie
851	CCAAGACCTCT	1,00	0,44	Hs.283619	zinc finger protein 236
852	GACAGGTTCTG	1,00	0,44	Hs.272023	transforming, acidic coiled-coil containing protein
853	CTTCTGGAGAA	1,00	0,44	Hs.267263	hypothetical protein
854	TGGGTTTTGTT	1,00	0,44	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PLACE1007402
855	CACCGCTGCAG	1,00	0,44	Hs.261373	adenosine A2b receptor pseudogene
856	GAAACAGGAAA	1,00	0,44	Hs.257387	EST
857	CCTTCTTGCTA	1,00	0,44	Hs.24743	hypothetical protein FLJ20171
858	ATAATCTGAAG	1,00	0,44	Hs.2441	KIAA0022 gene product
859	CTAAATATAGG	1,00	0,44	Hs.23581	leptin receptor gene-related protein
860	AATGCTATGGT	1,00	0,44	Hs.23450	ESTs
861	GTGAATGAAAC	1,00	0,44	Hs.223437	EST
862	TCCACAAAAAA	1,00	0,44	Hs.21035	KIAA1130 protein
863	AGAATTGCTTA	1,00	0,44	Hs.203188	EST
864	CCTCTAATTCC	1,00	0,44	Hs.192949	ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY
865	TTGGACAAGAA	1,00	0,44	Hs.189902	ESTs
866	GGCTGGGCGCG	1,00	0,44	Hs.188339	ESTs
867	CAACACAAAGC	1,00	0,44	Hs.185013	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY
868	GGCCCGGCCTC	1,00	0,44	Hs.183994	protein phosphatase 1, catalytic subunit, alpha isof
869	GCTAAAAAATT	1,00	0,44	Hs.183760	glucose regulated protein, 58kD
870	TTTTCCTTGTT	1,00	0,44	Hs.182937	peptidylprolyl isomerase A (cyclophilin A)

871	GCCGCCTCTGT	1,00	0,44	Hs.180799	ESTs, Moderately similar to ALU5_HUMAN ALU SUBFAMILY
872	GGCTGGTTCCA	1,00	0,44	Hs.179943	ribosomal protein L11
873	AAGGAAATGAA	1,00	0,44	Hs.174131	ribosomal protein L6
874	AATAGATGATA	1,00	0,44	Hs.174104	ESTs
875	TATAAGTGGAC	1,00	0,44	Hs.17301	ESTs
876	GAAACATAAT	1,00	0,44	Hs.169329	DKFZP564A043 protein
877	CTTTGTAAAAA	1,00	0,44	Hs.16578	ESTs
878	AGCTGTTTAAA	1,00	0,44	Hs.164480	ESTs
879	GGGACAGAGC	1,00	0,44	Hs.161554	hypothetical protein FLJ20159
880	ATAAAGCCAAA	1,00	0,44	Hs.159471	ZAP3 protein
881	CCCCTGCATTC	1,00	0,44	Hs.158302	chromosome 1 open reading frame 1
882	GCTGAGAAGCA	1,00	0,44	Hs.155975	protein tyrosine phosphatase, receptor type, C-assoc
883	GAATACGTTGG	1,00	0,44	Hs.155596	BCL2/adenovirus E1B 19kD-interacting protein 2
884	ATTTCTAACAA	1,00	0,44	Hs.155049	hypothetical protein FLJ11282
885	AGATCTTCTTG	1,00	0,44	Hs.14894	trans-Golgi network protein (46, 48, 51kD isoforms)
886	AAAACTCTAC	1,00	0,44	Hs.146226	ESTs
887	AGGATAAACTC	1,00	0,44	Hs.14427	ESTs
888	CTTGTGAGGCC	1,00	0,44	Hs.142428	KIAA1161 protein
889	GTAACAGTAAT	1,00	0,44	Hs.137396	ESTs
890	TAAACGAAAAT	1,00	0,44	Hs.135465	ESTs
891	AGGGGAATGGG	1,00	0,44	Hs.134933	ESTs
892	GGCCGTGCTGC	1,00	0,44	Hs.131034	ESTs
893	GGAACCTATCC	1,00	0,44	Hs.128807	ESTs
894	CCAGTGCCCTC	1,00	0,44	Hs.128630	ESTs
895	ATTTTGCTTAA	1,00	0,44	Hs.126558	ESTs
896	AGCCAAGAGCC	1,00	0,44	Hs.125877	ESTs
897	GTAGACTGAAA	1,00	0,44	Hs.124165	ESTs
898	TGGTATGCACC	1,00	0,44	Hs.1191	KIAA0073 protein
899	TCTGTTTTGTG	1,00	0,44	Hs.118923	ESTs
900	CCAATCAATGG	1,00	0,44	Hs.116674	pre-mRNA splicing factor
901	TTCCCCAGGCT	1,00	0,44	Hs.116296	ESTs
902	CAACAGCCCCA	1,00	0,44	Hs.11455	ESTs
903	CTCCTGGAATA	1,00	0,44	Hs.11367	hypothetical protein RP1-317E23
904	TGGTGAAGAAC	1,00	0,44	Hs.113052	RNA cyclase homolog
905	CACACCGCCCCG	1,00	0,44	Hs.112015	ESTs, Moderately similar to alpha tubulin [H.sapiens]
906	CCCCCCCCCCA	1,00	0,44	Hs.110953	Homo sapiens mRNA; cDNA DKFZp434A139 (from clone DKF
907	TTTTGTTGCTC	1,00	0,44	Hs.109641	ESTs
908	GTAAAACCCCG	26,00	9,00	Hs.258881	EST, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX S
909	TAATAAAGAAT	4,00	1,65	Hs.80342	keratin 15
910	AAAATAAACCT	4,00	1,65	Hs.74304	periplakin
911	GTGGTAGGTGC	4,00	1,65	Hs.254237	EST
912	GTGAAATTCCA	4,00	1,65	Hs.228168	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S

913	CCTCTAGTCCC	4,00	1,65	Hs.145501	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
914	TGGAAATGACC	106,00	34,28	Hs.172928	collagen, type I, alpha 1
915	AACCCTGGAGG	7,00	2,69	Hs.283927	Homo sapiens cytomegalovirus partial fusion receptor
916	AGGATCACTTG	3,00	1,26	Hs.287355	ESTs
917	CCACTGCATTG	3,00	1,26	Hs.278551	ESTs, Weakly similar to ALU2_HUMAN ALU SUBFAMILY SB
918	AACTGGCTGCT	3,00	1,26	Hs.173381	dihydropyrimidinase-like 2
919	CCTGTAACCCC	28,00	9,54	Hs.176541	ESTs
920	GCACTCCAGCC	32,00	10,69	Hs.274580	Homo sapiens mRNA; cDNA DKFZp434P1019 (from clone DK
921	GTGGTGAGCAC	5,00	1,97	Hs.27311	single-minded (Drosophila) homolog 2
922	ATGGCAGGTGC	16,00	5,61	Hs.236479	EST, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ S
923	CCATTACACTC	8,00	3,00	Hs.8594	KIAA1191 protein
924	GGTGACAGAGT	12,00	4,30	Hs.278314	hypothetical protein
925	GTGGTTTGCTG	9,00	3,31	Hs.157773	ESTs, Moderately similar to OPSB_HUMAN BLUE-SENSITIV
926	TCTGCCTATGC	4,00	1,60	Hs.90291	laminin, beta 2 (laminin S)
927	GCGAAAACCCC	4,00	1,60	Hs.272837	ESTs
928	TACCCCTTGAA	2,00	0,86	Hs.95834	ESTs
929	TAAATGGAAGT	2,00	0,86	Hs.6942	ESTs
930	TGTGTCTGGGA	2,00	0,86	Hs.60548	hypothetical protein PRO1635
931	GCTTCAGTGGG	2,00	0,86	Hs.54828	ESTs
932	CTTTACTGTGT	2,00	0,86	Hs.279853	HSPC018 protein
933	CACTTTGTGTG	2,00	0,86	Hs.24752	spectrin SH3 domain binding protein 1
934	GGTGACAGAAC	2,00	0,86	Hs.234890	EST
935	ACTAAGATTGA	2,00	0,86	Hs.227716	KIAA0934 protein
936	CCAATGTTGTT	2,00	0,86	Hs.22209	ESTs
937	GTGGTGTGAGC	2,00	0,86	Hs.194637	Homo sapiens mRNA; cDNA DKFZp564D113 (from clone DKF
938	TGAAGAATGTG	2,00	0,86	Hs.112557	ESTs, Moderately similar to ZN85_HUMAN ZINC FINGER P
939	GCCAGTGCCTG	2,00	0,86	Hs.106061	RD RNA-binding protein
940	CCACTGCTCTC	12,00	4,26	Hs.23510	Kruppel-like factor 12
941	CTATTGCACTC	6,00	2,29	Hs.160483	erythrocyte membrane protein band 7.2 (stomatin)
942	ATGTACCTGAT	7,00	2,61	Hs.29191	epithelial membrane protein 2
943	GTGGGGGGGAG	7,00	2,61	Hs.10700	hypothetical protein
944	CACCTGTAGTC	37,00	11,92	Hs.267812	sorting nexin 4
945	TCTGCACACAC	3,00	1,22	Hs.78518	natriuretic peptide receptor B/guanylate cyclase B (
946	GACAATTCTGT	3,00	1,22	Hs.186571	hypothetical protein FLJ10700
947	AGGGGAAGGTG	8,00	2,92	Hs.112540	EST
948	CAAGACGGGGG	19,00	6,29	Hs.106185	ral guanine nucleotide dissociation stimu- lator
949	TAATTTGCGTT	4,00	1,56	Hs.79368	epithelial membrane protein 1
950	AGAATCGTTTG	4,00	1,56	Hs.136299	ESTs
951	AACAGTCAAAA	17,00	5,66	Hs.26557	plakophilin 3

5	952	GCAAACTCTG	10,00	3,49	Hs.278746	ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY
	953	GCCAGCCAGTG	10,00	3,49	Hs.149098	smoothelin
	954	GCGAAATCCCA	6,00	2,21	Hs.268728	ESTs
	955	TCTGTGGTCCC	6,00	2,21	Hs.227894	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
10	956	CCTATAATTCC	6,00	2,21	Hs.135491	ESTs
	957	GCAATAAAATA	1,00	0,40	Hs.99621	ESTs
	958	TGGAATCCAGG	1,00	0,40	Hs.98135	ESTs
	959	CTTTTGTACGC	1,00	0,40	Hs.90858	Homo sapiens clone 25023 mRNA sequence
15	960	TTATTGTATTG	1,00	0,40	Hs.89474	ADP-ribosylation factor 6
	961	ATGGAGGTATG	1,00	0,40	Hs.8944	procollagen C-endopeptidase enhancer 2
20	962	TCGTGTTTTCG	1,00	0,40	Hs.87595	translocase of inner mitochondrial membrane 22 (yeas
	963	TTGTGGCCCCA	1,00	0,40	Hs.84630	ESTs
	964	TTTGTGTTT	1,00	0,40	Hs.8355	ESTs
25	965	GTCACGAACAT	1,00	0,40	Hs.82933	protein x 013
	966	GTAAAGGTAAA	1,00	0,40	Hs.79241	B-cell CLL/lymphoma 2
	967	AAGAAGAAAAG	1,00	0,40	Hs.78293	ESTs
	968	TAGCCAGTTAA	1,00	0,40	Hs.74101	spleen tyrosine kinase
30	969	CTGCCCGGGGC	1,00	0,40	Hs.74097	mercaptopyruvate sulfurtransferase
	970	AACGGTGTTTG	1,00	0,40	Hs.71371	ESTs
	971	CATAAACGGGC	1,00	0,40	Hs.69954	laminin, gamma 3
	972	TCCTTAGATTA	1,00	0,40	Hs.69743	GM2 ganglioside activator protein
35	973	CTGGCATAGAA	1,00	0,40	Hs.61272	ESTs
	974	ACTGCCCTGA	1,00	0,40	Hs.59729	semaphorin sem2
	975	TCTGCTGCCTG	1,00	0,40	Hs.58006	ESTs
	976	GAAGATGAATA	1,00	0,40	Hs.54982	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAMILY SB2
40	977	GACCAAAGAAG	1,00	0,40	Hs.48948	ESTs
	978	GAATGAATGCA	1,00	0,40	Hs.48604	DKFZP434B168 protein
	979	GCACAACTAAA	1,00	0,40	Hs.47587	ESTs
45	980	GAATTTTACAC	1,00	0,40	Hs.47522	ESTs
	981	AAGGGGCGGCG	1,00	0,40	Hs.456	leukotriene C4 synthase
	982	AGGGACTTTAT	1,00	0,40	Hs.43148	ESTs
	983	TATTCAGAACC	1,00	0,40	Hs.40289	ESTs
50	984	ACAACCTGGAAT	1,00	0,40	Hs.37372	Homo sapiens DNA binding peptide mRNA, partial cds
	985	TAATAAAATGC	1,00	0,40	Hs.29008	ESTs
	986	TTATGCTTGTA	1,00	0,40	Hs.284153	Fanconi anemia, complementation group A
55	987	TTTTGAAGATA	1,00	0,40	Hs.283322	hypothetical protein
	988	GCAAAATCAGAT	1,00	0,40	Hs.279477	ESTs
	989	GTAAAACCCCT	1,00	0,40	Hs.277896	EST
60	990	GGCCAGGCGTG	1,00	0,40	Hs.276994	EST
	991	AATGTTAGAGC	1,00	0,40	Hs.270331	ESTs
	992	TACCTATAGTC	1,00	0,40	Hs.269838	ESTs
65	993	TGTGAGAAAGT	1,00	0,40	Hs.241493	natural killer-tumor recognition sequence

994	AATTGTGCATT	1,00	0,40	Hs.240443	chondroitin 4-sulfotransferase	
995	GTGGTGCGCAT	1,00	0,40	Hs.236505	EST, Weakly similar to ALU6_HUMAN ALU SUBFAMILY SP S	
996	GTTTATAATTA	1,00	0,40	Hs.231966	ESTs	5
997	CTGGCACCCCTG	1,00	0,40	Hs.212716	EST	
998	AAAAATGGTGG	1,00	0,40	Hs.204930	EST	
999	GAGCAGGCAAA	1,00	0,40	Hs.200333	apolipoprotein B48 receptor	
1000	CCAAAAAAGTG	1,00	0,40	Hs.184242	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase	10
1001	CCAGAGGAATG	1,00	0,40	Hs.180414	heat shock 70kd protein 10 (HSC71)	
1002	CCACAAAAAAA	1,00	0,40	Hs.179091	EST	
1003	GCTTACCTGCT	1,00	0,40	Hs.174031	cytochrome c oxidase subunit VIb	15
1004	TATTAGACACC	1,00	0,40	Hs.17258	ESTs	
1005	GAATGTTGACA	1,00	0,40	Hs.16959	ESTs	
1006	TGAGGGGTGGG	1,00	0,40	Hs.166293	EST	
1007	TATATAAGTAC	1,00	0,40	Hs.166011	catenin (cadherin-associated protein), delta 1	20
1008	TAATAATACAA	1,00	0,40	Hs.16349	KIAA0431 protein	
1009	TGGGAGGCTGA	1,00	0,40	Hs.161554	hypothetical protein FLJ20159	
1010	AGCTCCTTAAG	1,00	0,40	Hs.159509	alpha-2-plasmin inhibitor	25
1011	CTTTTGTGGT	1,00	0,40	Hs.153106	Homo sapiens clone 23728 mRNA se- quence	
1012	CTGTTTTTGAA	1,00	0,40	Hs.152720	M-phase phosphoprotein 6	30
1013	GCAGACTATCC	1,00	0,40	Hs.151696	DKFZP727G051 protein	
1014	GTTCCCTGGTG	1,00	0,40	Hs.146090	ESTs	
1015	CCTACAGTCCC	1,00	0,40	Hs.144874	Homo sapiens mRNA; cDNA DKFZp761C0524 (from clone DK	35
1016	CAATCCTCCTG	1,00	0,40	Hs.138407	ESTs	
1017	AACAAGTAATA	1,00	0,40	Hs.134350	ESTs	
1018	TCCAGTACAGA	1,00	0,40	Hs.12969	hypothetical protein	
1019	GGAGGCTGGGG	1,00	0,40	Hs.127452	ESTs	40
1020	ACTCTGCTCGG	1,00	0,40	Hs.126900	ESTs	
1021	TTCTGTGAGTG	1,00	0,40	Hs.122559	ESTs	
1022	TCCTGTGATTT	1,00	0,40	Hs.12253	ESTs	
1023	AAAGCACAAAGT	1,00	0,40	Hs.111758	keratin 6B	45
1024	TTTTTGAAAAA	1,00	0,40	Hs.109646	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6	
1025	AAGTCCTGGCC	1,00	0,40	Hs.109314	ESTs, Weakly similar to 2202255A AT motif-binding fa	50
1026	TGTTACTGGAT	1,00	0,40	Hs.100861	ESTs, Weakly similar to spastin protein [H.sapiens]	
1027	CCTGTAATCTT	8,00	2,84	Hs.120882	ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY	55
1028	GTGGCGGGCAC	85,00	25,22	Hs.283044	hypothetical protein PRO2859	
1029	CCACTTGCACT	3,00	1,18	Hs.220962	EST, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	
1030	TTCCATACCCC	3,00	1,18	Hs.180398	LIM domain-containing preferred translo- cation partne	60
1031	ATTGCATCACT	5,00	1,85	Hs.209111	EST	
1032	GAGTTAAAAAA	5,00	1,85	Hs.180255	major histocompatibility complex, class	

					II, DR beta
5	1033	GGGCCCTGGCC	4,00	1,53	Hs.25895 ESTs, Weakly similar to PI-3 kinase [H.sapiens]
	1034	CAGATGGAGGC	4,00	1,53	Hs.127273 hypothetical protein FLJ10044
	1035	CCTCTCCACA	2,00	0,82	Hs.99197 ESTs
	1036	GCCAGGGGGTA	2,00	0,82	Hs.96875 ESTs
10	1037	CTCAGTCTTTT	2,00	0,82	Hs.76722 CCAAT/enhancer binding protein (C/EBP), delta
	1038	GATGTATTCTA	2,00	0,82	Hs.75844 ESTs, Highly similar to AF151903_1 CGI-145 protein [
15	1039	CCCTTCTGTAA	2,00	0,82	Hs.75716 plasminogen activator inhibitor, type II (arginine-s
	1040	TGGAAGTGTCA	2,00	0,82	Hs.285802 ESTs
	1041	GGCCTGTAATC	2,00	0,82	Hs.267400 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY
20	1042	AGGTATATATC	2,00	0,82	Hs.24715 Homo sapiens mRNA; cDNA DKFZp434D0215 (from clone DK
	1043	TTCTGAAAGGA	2,00	0,82	Hs.227209 DKFZP586F1019 protein
	1044	AGCCTGTGGTC	2,00	0,82	Hs.154919 KIAA0625 protein
25	1045	TTGCGTGTGTC	2,00	0,82	Hs.1183 dual specificity phosphatase 2
	1046	CATAATTTCTC	2,00	0,82	Hs.104660 eIF-5A2 protein
	1047	TGGGACGTGAG	7,00	2,45	Hs.3796 EphB6
30	1048	GCGAAATCCCG	10,00	3,34	Hs.194251 ESTs, Weakly similar to ALU2_HUMAN ALU SUBFAMILY SB
	1049	ACCAAAAACCA	120,00	34,01	Hs.172928 collagen, type I, alpha 1
	1050	AACCCAGGAGG	126,00	35,53	Hs.161554 hypothetical protein FLJ20159
35	1051	TCTCTGTGTAG	4,00	1,49	Hs.79187 coxsackie virus and adenovirus receptor
	1052	CGCAGTAGGGG	4,00	1,49	Hs.17411 KIAA0699 protein
	1053	CGAGAGGGAGA	4,00	1,49	Hs.158159 FAT tumor suppressor (Drosophila) homolog 2
	1054	GTGGCATCTGC	4,00	1,49	Hs.1244 CD9 antigen (p24)
40	1055	CTAACGGGGCG	7,00	2,42	Hs.102171 immunoglobulin superfamily containing leucine-rich r
	1056	GCAAAACCCCT	6,00	2,10	Hs.75238 chromatin assembly factor 1, subunit B (p60)
45	1057	ACTGCTTTACT	6,00	2,10	Hs.72157 DKFZP564I1922 protein
	1058	CCCCAGGCTGC	3,00	1,15	Hs.9645 ESTs
	1059	TAAAATGTTTA	3,00	1,15	Hs.94109 ESTs
50	1060	CCTACTGCACT	3,00	1,15	Hs.225641 ESTs, Moderately similar to KIAA0680 protein [H.sapi
	1061	GTGGCTCATTC	3,00	1,15	Hs.116577 prostate differentiation factor
	1062	AAGCACAAAAA	12,00	3,87	Hs.9963 TYRO protein tyrosine kinase binding protein
55	1063	GTGGCGGGCGC	94,00	26,43	Hs.129710 malignancy-associated protein
	1064	AGAACCTTAAA	14,00	4,43	Hs.181244 major histocompatibility complex, class I, A
	1065	CCTGAAATCCC	8,00	2,69	Hs.182124 ESTs
60	1066	GCGAAACCCAG	13,00	4,10	Hs.142442 HP1-BP74
	1067	ATGTAGGTGCC	9,00	2,96	Hs.173717 phosphatidic acid phosphatase type 2B
	1068	TTAAATAGCAC	10,00	3,23	Hs.172928 collagen, type I, alpha 1



1069	TTTTATTCCA	4,00	5,89	Hs.93780	ESTs, Weakly similar to ALUB_HUMAN !!!! ALU CLASS B	
1070	AATTACAGCCA	4,00	5,89	Hs.74471	gap junction protein, alpha 1, 43kD (connexin 43)	5
1071	CCTTACCTAAG	4,00	5,89	Hs.240217	dopachrome tautomerase (dopachrome delta-isomerase,	
1072	CTCCCTGAACG	4,00	5,89	Hs.11006	ESTs	10
1073	AACACGAATGA	4,00	1,45	Hs.259855	ESTs	
1074	GTGGCAAGCAC	4,00	1,45	Hs.138860	Rho GTPase activating protein 1	
1075	TTCACCATCCT	4,00	1,45	Hs.101395	ESTs, Weakly similar to tetraspan NET-4 [H.sapiens]	15
1076	AGAGGGAGTGA	2,00	0,78	Hs.85201	C-type (calcium dependent, carbohy- drate-recognition	
1077	AGTCCTTGAAA	2,00	0,78	Hs.81665	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogen	20
1078	CCCAGCCTAAA	2,00	0,78	Hs.47986	Homo sapiens mRNA; cDNA DKFZp586H051 (from clone DKF	
1079	TTTAACTGACA	2,00	0,78	Hs.24880	ESTs	25
1080	CCTTGTAATCC	2,00	0,78	Hs.197054	EST	
1081	GAAGGCTTATC	2,00	0,78	Hs.172674	nuclear factor of activated T-cells, cyto- plasmic 3	
1082	TAGCAAAGATT	2,00	0,78	Hs.166172	aryl hydrocarbon receptor nuclear trans- locator	30
1083	CACATCTGTAA	2,00	0,78	Hs.16533	myosin phosphatase, target subunit 1	
1084	TTCAGTAATAA	2,00	0,78	Hs.13479	hypothetical protein FLJ20847	35
1085	GGTGAAACCCT	2,00	0,78	Hs.117582	CGI-43 protein	
1086	CTTCTGCCTCA	2,00	0,78	Hs.115896	ESTs	
1087	GAGAGGTGATT	2,00	0,78	Hs.114062	protein tyrosine phosphatase-like (proline instead o	40
1088	ATGTATTTTAA	2,00	0,78	Hs.108396	ALR-like protein	
1089	CTATAGGAGAC	5,00	1,75	Hs.8966	integral membrane protein 1	45
1090	TCCGTGTATAA	5,00	1,75	Hs.3321	ESTs, Highly similar to IRX3_MOUSE IROQUOIS-CLASS HO	
1091	GCAAAACCCCA	98,00	26,53	Hs.129708	tumor necrosis factor (ligand) super- family, member 1	50
1092	TTCCATAGCCT	6,00	2,03	Hs.8546	Notch (Drosophila) homolog 3	
1093	CTGTGAAATGC	3,00	1,11	Hs.23618	hypothetical protein FLJ10704	55
1094	AAAGAACATAG	3,00	1,11	Hs.104558	ESTs	
1095	CACCTGTAATC	37,00	10,41	Hs.275819	EST	
1096	GGCAACAAGAG	9,00	2,89	Hs.205739	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ	60
1097	GTGGCGGGTGC	72,00	19,32	Hs.277015	EST	
1098	ACCTTCAAAAA	4,00	1,42	Hs.28444	hypothetical protein FLJ10567	
1099	ACATCTGGCTT	4,00	1,42	Hs.194035	KIAA0737 gene product	
1100	GTACGTATTCT	6,00	2,00	Hs.76325	immunoglobulin J polypeptide, linker protein for imm	
1101	ATCCGCCTGCC	6,00	2,00	Hs.167956	ESTs, Weakly similar to KIAA0309 [H.sapiens]	65
1102	ACCCACGTCAG	24,00	6,84	Hs.198951	jun B proto-oncogene	
1103	TAATCCCAGCT	14,00	4,18	Hs.238384	EST	

	1104	ATTGCACCACT	46,00	12,50	Hs.117582	CGI-43 protein
	1105	AGGACCAAGGA	1,00	0,37	Hs.99539	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ
5	1106	TAAGCTACTAA	1,00	0,37	Hs.97469	ESTs, Weakly similar to I49698 alpha- 1,3-galactosylt
	1107	CTCCATTGTCT	1,00	0,37	Hs.93005	slug (chicken homolog), zinc finger prote- in
10	1108	TGACATTAAAC	1,00	0,37	Hs.87432	ESTs
	1109	GGATTCAAGAG	1,00	0,37	Hs.86947	a disintegrin and metalloproteinase domain 8
	1110	ATGTTATCATA	1,00	0,37	Hs.8325	mitogen-activated protein kinase 9
15	1111	TACTCTGTTGA	1,00	0,37	Hs.82587	phospholipase D1, phosphatidylcholine- specific
	1112	GGAAAAGAAAA	1,00	0,37	Hs.82141	Human clone 23612 mRNA sequence
20	1113	TATACGTTATG	1,00	0,37	Hs.78894	KIAA0161 gene product
	1114	CACTTGGTGAT	1,00	0,37	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(NAD)
	1115	ATGAATGTAAA	1,00	0,37	Hs.76853	Homo sapiens mRNA full length insert cDNA clone EURO
25	1116	TGTTTTCATAA	1,00	0,37	Hs.75703	small inducible cytokine A4 (homologous to mouse Mip)
	1117	AGTTTACGATT	1,00	0,37	Hs.74649	cytochrome c oxidase subunit VIc
30	1118	GTGGTTCATTC	1,00	0,37	Hs.6853	carbohydrate (N-acetylglucosamine 6-O) sulfotransfer
	1119	CAACAAAAGCA	1,00	0,37	Hs.66450	ESTs
	1120	CATTTTTTTCG	1,00	0,37	Hs.59525	ESTs
	1121	CTGCTAAACTA	1,00	0,37	Hs.46826	ESTs
35	1122	ACCCTGAATGG	1,00	0,37	Hs.43086	ESTs
	1123	TTGTAACAAAA	1,00	0,37	Hs.40154	jumonji (mouse) homolog
	1124	TGCTGTTTATA	1,00	0,37	Hs.37958	ESTs
	1125	TATGTGGGTTA	1,00	0,37	Hs.34359	ESTs
40	1126	CAGCAATTATA	1,00	0,37	Hs.32309	inositol polyphosphate-1-phosphatase
	1127	CTCCATTGCCA	1,00	0,37	Hs.31869	ESTs
	1128	GGGTGGGTCAC	1,00	0,37	Hs.31500	ESTs
	1129	ATTCCACCACT	1,00	0,37	Hs.2934	ribonucleotide reductase M1 polypeptide
45	1130	TCTTACTCAGA	1,00	0,37	Hs.285081	ESTs
	1131	AATAAAAAATA	1,00	0,37	Hs.284275	Homo sapiens PAK2 mRNA, complete cds
	1132	GAGACAGTGAC	1,00	0,37	Hs.284146	hypothetical protein DKFZp762N0610
50	1133	CCTGGGCAACA	1,00	0,37	Hs.273683	EST
	1134	CCTTTGCACTC	1,00	0,37	Hs.265124	ESTs
	1135	TGCAGACAGGG	1,00	0,37	Hs.264363	hypothetical protein FLJ10110
55	1136	TTGGCCCAGTC	1,00	0,37	Hs.25951	Rho guanine nucleotide exchange factor (GEF) 3
	1137	TCTTTAAAGTA	1,00	0,37	Hs.25155	guanine nucleotide regulatory protein (oncogene)
	1138	ATATTGGTGGT	1,00	0,37	Hs.250692	hepatic leukemia factor
60	1139	GTGGCGAATGC	1,00	0,37	Hs.230479	EST
	1140	TATTAACATTC	1,00	0,37	Hs.226573	inhibitor of kappa light polypeptide gene enhancer i

1141	TCTCCATTCCT	1,00	0,37	Hs.226573	inhibitor of kappa light polypeptide gene enhancer i
1142	TATATAGAATG	1,00	0,37	Hs.22581	ESTs
1143	GCGAGATCCTG	1,00	0,37	Hs.22529	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
1144	CACTCCAACCT	1,00	0,37	Hs.205899	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC
1145	CGATGTAAAA	1,00	0,37	Hs.20072	myosin regulatory light chain interacting protein
1146	CCTTCTGAATA	1,00	0,37	Hs.194660	ceroid-lipofuscinosis, neuronal 3, juvenile (Batten,
1147	TGAGGATCCAG	1,00	0,37	Hs.191621	ESTs
1148	ATTGTACAACA	1,00	0,37	Hs.184326	CDC10 (cell division cycle 10, S. cere- visiae, homolo
1149	AGCCTATTTAA	1,00	0,37	Hs.183593	zinc finger protein 24 (KOX 17)
1150	GCCCCGCGCC	1,00	0,37	Hs.183202	ESTs
1151	GTGAATGCACT	1,00	0,37	Hs.176065	ESTs
1152	TTCATTAAGAA	1,00	0,37	Hs.17411	KIAA0699 protein
1153	ACCGAGGTGCA	1,00	0,37	Hs.171882	ESTs
1154	TTGGTATTGCA	1,00	0,37	Hs.163541	ESTs
1155	ATGTATTTTCA	1,00	0,37	Hs.161554	hypothetical protein FLJ20159
1156	GTTGAATTGCA	1,00	0,37	Hs.156828	Homo sapiens cDNA FLJ10522 fis, clone NT2RP2000845
1157	TCTGTCATCCC	1,00	0,37	Hs.150158	ESTs
1158	GTGGTGCAAAC	1,00	0,37	Hs.149852	EST, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE
1159	GGCTTTGGAAT	1,00	0,37	Hs.146481	ESTs
1160	TTTGCTTTTGA	1,00	0,37	Hs.144504	hypothetical protein FLJ10624
1161	AAAGCATTAGA	1,00	0,37	Hs.14155	KIAA0653 protein
1162	AAACAACCCCA	1,00	0,37	Hs.1369	decay accelerating factor for complement (CD55, Crom
1163	CTCCTTGTC	1,00	0,37	Hs.135530	EST
1164	GTGCTGCACAC	1,00	0,37	Hs.133272	ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C
1165	TTTAAACTTGG	1,00	0,37	Hs.12431	ESTs
1166	CGGCCCAGGTT	1,00	0,37	Hs.122823	thousand and one amino acid protein kinase
1167	CTGACTGATGG	1,00	0,37	Hs.121509	collagen, type XI, alpha 2
1168	ATAGATACACA	1,00	0,37	Hs.120850	ESTs
1169	TGGCAGTAGTG	1,00	0,37	Hs.120644	ESTs
1170	AAATCCTTCTA	1,00	0,37	Hs.119301	S100 calcium-binding protein A10 (an- nexin II ligand,
1171	TCAAACCTTGT	1,00	0,37	Hs.117582	CGI-43 protein
1172	TACACCTGGAA	1,00	0,37	Hs.114624	ESTs
1173	CAAGGATTTTT	1,00	0,37	Hs.111323	Protein inhibitor of activated STAT X
1174	CTAGTATAAAA	1,00	0,37	Hs.106650	hypothetical protein FLJ20533
1175	AATATAAAAAA	1,00	0,37	Hs.103548	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
1176	CAAATATGGTT	1,00	0,37	Hs.10351	KIAA0308 protein
1177	CAAGAACAGGG	1,00	0,37	Hs.102135	signal sequence receptor, delta (translo-

					con-associat
	1178 TCACCGGTCAG	61,00	16,20	Hs.80562	gelsolin (amyloidosis, Finnish type)
5	1179 GTGAAAACCCC	4,00	1,38	Hs.277213	EST, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ S
	1180 GTGGTGGGCAC	60,00	15,85	Hs.77510	isovaleryl Coenzyme A dehydrogenase
	1181 GTGGTGGGTGC	60,00	15,81	Hs.136509	EST
10	1182 CCGTTGCACTC	6,00	1,96	Hs.278329	ESTs
	1183 CATCACGGATC	3,00	1,08	Hs.82112	interleukin 1 receptor, type I
	1184 GTATGTACAGG	3,00	1,08	Hs.164255	ESTs, Moderately similar to ALU2_HUMAN ALU SUBFAMILY
15	1185 CCCTTTATATC	3,00	1,08	Hs.13766	ESTs
	1186 GCTCGTGGTCA	3,00	1,08	Hs.119475	cold inducible RNA-binding protein
	1187 CCCATCTAGCT	3,00	1,08	Hs.106070	cyclin-dependent kinase inhibitor 1C (p57, Kip2)
20	1188 TCTCAAAAAA	8,00	2,52	Hs.194841	ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY
	1189 CCCCTGGCTGG	5,00	1,68	Hs.920	modulator recognition factor I
	1190 GGTTATTTAGT	5,00	1,68	Hs.8110	adducin 3 (gamma)
25	1191 GCAAAACCTCA	7,00	2,24	Hs.156596	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ
	1192 AGTTGTTTGGT	2,00	0,75	Hs.96418	ESTs
	1193 TCATAGCCTTG	2,00	0,75	Hs.78846	heat shock 27kD protein 2
30	1194 AGGACTGGACT	2,00	0,75	Hs.75258	H2A histone family, member Y
	1195 TAAACCTAGGA	2,00	0,75	Hs.56186	EGF-like-domain, multiple 3
	1196 GTGGCTCACTT	2,00	0,75	Hs.285616	ESTs
	1197 TCATTTGGTGT	2,00	0,75	Hs.285439	ESTs
35	1198 GCCTTGGCAGT	2,00	0,75	Hs.25351	iroquois-class homeodomain protein
	1199 CCCTTGTTCTT	2,00	0,75	Hs.250723	FK506 binding protein 12-rapamycin associated protei
	1200 GAACAGTATGA	2,00	0,75	Hs.189762	ESTs
40	1201 ATGGCAGGCGG	2,00	0,75	Hs.161554	hypothetical protein FLJ20159
	1202 ACACAGCAAGA	136,00	34,48	Hs.80562	gelsolin (amyloidosis, Finnish type)
	1203 GATCAGGCCAG	30,00	8,16	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danlos syndrome)
45	1204 GTGAAACTCTG	32,00	8,57	Hs.188853	Homo sapiens cDNA FLJ10150 fis, clone HEMBA1003395
	1205 GGCCTGCAGGA	6,00	1,93	Hs.71869	apoptosis-associated speck-like protein containing a
50	1206 AAATCAATACA	7,00	2,21	Hs.94953	ESTs, Highly similar to C1QC_HUMAN COMPLEMENT C1Q SU
	1207 ATTGTACCACT	7,00	2,21	Hs.7099	hypothetical protein FLJ20265
	1208 CGCCTGTAGTC	29,00	7,81	Hs.60088	ESTs
55	1209 GCAAAACCCAG	4,00	1,35	Hs.210610	ESTs, Moderately similar to ALU6_HUMAN ALU SUBFAMILY
	1210 CTTTGATGCGG	4,00	1,35	Hs.183601	regulator of G-protein signalling 16
	1211 GGCCCTAGGCA	33,00	8,73	Hs.78909	butyrate response factor 2 (EGF- response factor 2)
60	1212 CCTGGCTAATT	29,00	7,72	Hs.25661	ESTs, Weakly similar to ALUF_HUMAN !!!! ALU CLASS F
	1213 CTTCTGTCCT	10,00	2,96	Hs.83623	nuclear receptor subfamily 1, group I,

					member 3
1214	GCGGGGTGGAG	37,00	9,65	Hs.85155	butyrate response factor 1 (EGF-response factor 1)
1215	GTGGCAGGCGC	85,00	21,18	Hs.48604	DKFZP434B168 protein
1216	AGCCCAGGAGG	9,00	2,69	Hs.136340	ESTs, Weakly similar to unnamed protein product [H.s]
1217	ATAGTGCCACT	6,00	1,90	Hs.246717	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ
1218	CATTTGTAAAA	3,00	1,05	Hs.84429	KIAA0971 protein
1219	CGTACAGCCCC	3,00	1,05	Hs.32580	KIAA1448 protein
1220	GGGCTACGTCC	3,00	1,05	Hs.123107	kallikrein 1, renal/pancreas/salivary
1221	ATCACACCACT	27,00	7,14	Hs.234786	KIAA0707 protein
1222	CACTCCAGCCT	13,00	3,69	Hs.193451	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ
1223	CTTGTAATCCC	46,00	11,69	Hs.183253	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
1224	GTGAAACCTCA	47,00	11,91	Hs.153029	ESTs
1225	ATCTCAGCTCA	12,00	3,43	Hs.246192	ESTs, Weakly similar to RMS1_HUMAN REGULATOR OF MITO
1226	TATGTGCTGTA	5,00	1,61	Hs.20084	retinoid X receptor, alpha
1227	ACTCGAATATC	4,00	1,32	Hs.95655	secreted and transmembrane 1
1228	GAGTCCCTGGT	4,00	1,32	Hs.68398	period (Drosophila) homolog 1
1229	TGCAATATGCC	6,00	1,87	Hs.750	fibrillin 1 (Marfan syndrome)
1230	GAAGCAATAAA	6,00	1,87	Hs.198253	major histocompatibility complex, class II, DQ alpha
1231	GTGAAACTCCG	37,00	9,36	Hs.261734	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY
1232	GGCTGCCGAGT	2,00	0,72	Hs.99829	hypothetical protein FLJ20565
1233	CTTAGCCCCAG	2,00	0,72	Hs.96908	ESTs
1234	TTATTCCACAA	2,00	0,72	Hs.93765	lipoma HMGIC fusion partner
1235	TCACAGCCCCC	2,00	0,72	Hs.8619	SRY (sex determining region Y)-box 18
1236	TTTTCTTTTG	2,00	0,72	Hs.78546	ATPase, Ca++ transporting, plasma membrane 1
1237	CTTGCATAAGA	2,00	0,72	Hs.72912	cytochrome P450, subfamily I (aromatic compound-indu
1238	TATGTGTTCTC	2,00	0,72	Hs.3353	beta-1,3-glucuronyltransferase 1 (glucuronosyltransf
1239	ACTATCATCTT	2,00	0,72	Hs.29117	H.sapiens mRNA for pur alpha extended 3'untranslated
1240	CGCCTATAGTC	2,00	0,72	Hs.271166	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY
1241	CCCGCCAGTGC	2,00	0,72	Hs.256297	integrin, alpha 11
1242	TTCTAATTTTT	2,00	0,72	Hs.170414	paired basic amino acid cleaving system 4
1243	CGGGAAGACAT	2,00	0,72	Hs.154525	KIAA1076 protein
1244	CCAGTAGTCCC	2,00	0,72	Hs.147959	EST
1245	CAGTTTGTGTT	2,00	0,72	Hs.144477	hypothetical protein PRO2975
1246	TCCTTTAAAT	2,00	0,72	Hs.10587	KIAA0353 protein
1247	GTGCTAAGCGG	46,00	11,41	Hs.4217	collagen, type VI, alpha 2
1248	AGAATCACTTG	41,00	10,16	Hs.117582	CGI-43 protein

	1249	GTGGTGTACGC	9,00	2,60	Hs.182225	RNA binding motif protein 3
	1250	GCCCCAGAATC	3,00	1,02	Hs.8682	ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY
5	1251	TTGGGAGGCTG	3,00	1,02	Hs.118269	ESTs, Weakly similar to A46010 X-linked retinopathy
	1252	GTGGCACGCGC	19,00	5,01	Hs.187346	ESTs
10	1253	CAAGCGCTCTA	4,00	1,29	Hs.23598	CREB binding protein (Rubinstein-Taybi syndrome)
	1254	AGTTCGAGACC	4,00	1,29	Hs.232540	ESTs
	1255	AGAACCAAAAA	4,00	1,29	Hs.181244	major histocompatibility complex, class I, A
15	1256	CTGGCTATCCG	4,00	1,29	Hs.10784	hypothetical protein FLJ20037
	1257	TAGTCCCAGCT	11,00	3,08	Hs.274579	ancient conserved domain protein 1
	1258	GTGAAATCCTG	28,00	7,06	Hs.53531	lipoic acid synthetase
20	1259	CCTGTAATTCC	47,00	11,36	Hs.23582	tumor-associated calcium signal transducer 2
	1260	CTTCTTGCCCC	20,00	5,17	Hs.251577	hemoglobin, alpha 1
	1261	TGGTTGGTGGT	11,00	3,05	Hs.12701	plasmolipin
25	1262	CCCGTAATCCC	17,00	4,46	Hs.274168	Homo sapiens mRNA; cDNA DKFZp761P0212 (from clone DK
	1263	CCTGGCCAGAA	5,00	1,55	Hs.261734	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY
	1264	CGTGTAATCCC	12,00	3,28	Hs.187761	ESTs
30	1265	GCGAAACCTCA	6,00	1,81	Hs.42644	thioredoxin-like
	1266	TGGTTACAAAA	6,00	1,81	Hs.3850	Homo sapiens clone 23596 mRNA sequence
	1267	CCACAGCACTC	7,00	2,06	Hs.273828	ESTs
35	1268	GTGGCACGTGC	103,00	23,64	Hs.278588	ESTs, Weakly similar to ALU2_HUMAN ALU SUBFAMILY SB
	1269	ATGTCTTTTCT	18,00	4,66	Hs.1516	insulin-like growth factor-binding protein 4
40	1270	CTTGTAAGTCCC	11,00	3,02	Hs.272202	hypothetical protein FLJ20825
	1271	CTCATCTGCTG	10,00	2,78	Hs.82109	syndecan 1
	1272	AGGACATAATT	1,00	0,34	Hs.93454	ESTs
45	1273	GAGCTACACCA	1,00	0,34	Hs.82171	Human clone 191B7 placenta expressed mRNA from chrom
	1274	TTGCTACTAAA	1,00	0,34	Hs.7790	ESTs
	1275	CTTAGTGTTTT	1,00	0,34	Hs.7720	dynein, cytoplasmic, heavy polypeptide 1
	1276	CTGGTCCTGGA	1,00	0,34	Hs.76476	cathepsin H
50	1277	GGTGGCAGTTG	1,00	0,34	Hs.75794	endothelial differentiation, lysophosphatidic acid G
	1278	CTGATATAGAC	1,00	0,34	Hs.74002	nuclear receptor coactivator 1
	1279	TGGAAATCATT	1,00	0,34	Hs.5028	DKFZP564O0423 protein
55	1280	ACTTTGAAAGG	1,00	0,34	Hs.44077	hypothetical protein FLJ10793
	1281	AAAGGCACTGA	1,00	0,34	Hs.3994	ESTs
	1282	GTTCTCTTTT	1,00	0,34	Hs.3843	dual specificity phosphatase 7
	1283	AGCGCAGCTGT	1,00	0,34	Hs.34771	ESTs
60	1284	ATTGTGAAGAG	1,00	0,34	Hs.34578	alpha2,3-sialyltransferase
	1285	GCCTTCGGAAA	1,00	0,34	Hs.33104	Homo sapiens mRNA; cDNA DKFZp434H2121 (from clone DK

1286	GCTATTTTGAT	1,00	0,34	Hs.32250	ESTs
1287	TATCTCTTAAA	1,00	0,34	Hs.286228	ESTs
1288	TGTGATTTTAA	1,00	0,34	Hs.286163	ESTs
1289	TATTTTCAGATT	1,00	0,34	Hs.285585	ESTs
1290	ATGATTTTGAG	1,00	0,34	Hs.285306	putative selenocysteine lyase
1291	AATATTCATAT	1,00	0,34	Hs.284311	Homo sapiens clone 25038 mRNA sequence
1292	AGACCCCATTT	1,00	0,34	Hs.279297	EST
1293	CACCCATAGTC	1,00	0,34	Hs.278018	EST
1294	GTCTTGCTGCA	1,00	0,34	Hs.26966	KIAA1171 protein
1295	CGGCCCCATCTG	1,00	0,34	Hs.26290	ESTs
1296	CAATCTGATGC	1,00	0,34	Hs.26176	hypothetical protein FLJ10261
1297	ATGTTGGGTGT	1,00	0,34	Hs.260855	Homo sapiens mRNA; cDNA DKFZp761G2311 (from clone DK
1298	ACTCTGTCTCC	1,00	0,34	Hs.259339	EST
1299	GGAATACAGAA	1,00	0,34	Hs.250825	ESTs, Highly similar to vacuolar protein sorting hom
1300	ACTGGGCAAGC	1,00	0,34	Hs.240062	hypothetical protein
1301	GGTCAGAAATT	1,00	0,34	Hs.211581	metal-regulatory transcription factor 1
1302	AACCGAAGGGA	1,00	0,34	Hs.20596	ESTs
1303	GGGATAGAGAC	1,00	0,34	Hs.202955	hypothetical protein FLJ20507
1304	TTTCAGTTAGT	1,00	0,34	Hs.196284	ESTs
1305	GCTATTGATGT	1,00	0,34	Hs.193398	ESTs
1306	AAGAGGAGGCC	1,00	0,34	Hs.183639	hypothetical protein FLJ10210
1307	TAATACACTAA	1,00	0,34	Hs.183475	Homo sapiens clone 25061 mRNA sequence
1308	GCAGATGCTTT	1,00	0,34	Hs.180799	ESTs, Moderately similar to ALU5 HUMAN ALU SUBFAMILY
1309	TCACAAGGCTG	1,00	0,34	Hs.17998	ESTs
1310	TGCGAGCTGGG	1,00	0,34	Hs.179573	collagen, type I, alpha 2
1311	GGATTTGCTGC	1,00	0,34	Hs.177956	Homo sapiens mRNA; cDNA DKFZp434C0926 (from clone DK
1312	CACGCACACAC	1,00	0,34	Hs.177664	KIAA0914 gene product
1313	ATGTGGACTGA	1,00	0,34	Hs.174905	KIAA0033 protein
1314	GGAGGCAGAGC	1,00	0,34	Hs.172838	Human clone Z'3-1 placenta expressed mRNA from chrom
1315	GCTTTCTGTAA	1,00	0,34	Hs.172674	nuclear factor of activated T-cells, cytoplasmic 3
1316	TGATTATTTAC	1,00	0,34	Hs.16930	ESTs
1317	ACATCTGCCTG	1,00	0,34	Hs.161554	hypothetical protein FLJ20159
1318	CTTAGTTTTAA	1,00	0,34	Hs.161554	hypothetical protein FLJ20159
1319	AGGAAGAGTCA	1,00	0,34	Hs.154655	imogen 38
1320	CAATGCAGAGG	1,00	0,34	Hs.150748	malonyl-CoA decarboxylase
1321	TAATTCTTGTA	1,00	0,34	Hs.146123	ESTs
1322	CAAGGGCCCAC	1,00	0,34	Hs.14587	ESTs, Weakly similar to AF151859_1 CGI-101 protein [
1323	TTTTGAAGAAA	1,00	0,34	Hs.144465	ESTs
1324	TGTCTCCGTCT	1,00	0,34	Hs.135150	lung type-I cell membrane-associated glycoprotein
1325	TTTTCTTCAGG	1,00	0,34	Hs.125753	chromosome 2 open reading frame 2

5	1326	TTCCTCCCTCT	1,00	0,34	Hs.125384	ESTs
	1327	TCTGCCTTTCT	1,00	0,34	Hs.125019	ESTs, Highly similar to KIAA0886 protein [H.sapiens]
	1328	ATAACTGTCAG	1,00	0,34	Hs.12040	STE20-like kinase
	1329	TTGCAGTTTTT	1,00	0,34	Hs.117582	CGI-43 protein
	1330	TATTTAAAAAA	1,00	0,34	Hs.117304	ESTs
10	1331	GGCTCAGGGGC	1,00	0,34	Hs.116489	ESTs, Weakly similar to GCP170 [H.sapiens]
	1332	TTTATTGAAAC	1,00	0,34	Hs.112193	mutS (E. coli) homolog 5
	1333	CTGGCTTAAAT	1,00	0,34	Hs.11171	APG5 (autophagy 5, S. cerevisiae)-like
15	1334	GCTTTATGTGG	1,00	0,34	Hs.111460	ESTs, Weakly similar to Con1 [H.sapiens]
	1335	GCATACTTTAT	1,00	0,34	Hs.109370	ESTs
	1336	AGAATACTGAG	1,00	0,34	Hs.106705	neuronal PAS domain protein 2
20	1337	ACCCAAAAAAA	1,00	0,34	Hs.101840	major histocompatibility complex, class I-like seque
	1338	GGACATTAGGG	1,00	0,34	Hs.101265	(Manual assignment) MEMOREC NSM2 (CCA1) sphingomyeli
25	1339	AAAAATAAATT	1,00	0,34	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (from clone DKF
	1340	AGATACATAGC	5,00	1,53	Hs.84045	Homo sapiens cDNA FLJ20288 fis, clone HEP04414
30	1341	TGGATATCAGT	5,00	1,53	Hs.7327	claudin 1
	1342	TTTTCCACTTT	5,00	1,53	Hs.6900	ring finger protein 13
	1343	GTGGCTCAGGC	4,00	1,26	Hs.259047	ESTs
	1344	CCTGTGATTCC	4,00	1,26	Hs.227961	EST
35	1345	GGCGACAGAGC	11,00	2,99	Hs.92254	hypothetical protein FLJ20163
	1346	CCTGTGGTCCT	11,00	2,99	Hs.120769	Homo sapiens cDNA FLJ20463 fis, clone KAT06143
	1347	TGCCTGTGGTC	16,00	4,15	Hs.277100	ESTs, Weakly similar to ALU2_HUMAN ALU SUBFAMILY SB
40	1348	GTAAAAAAGCC	3,00	0,99	Hs.98988	ESTs
	1349	TGTGAACACAT	3,00	0,99	Hs.80645	interferon regulatory factor 1
	1350	AAACGAAGTTG	3,00	0,99	Hs.78353	SFRS protein kinase 2
45	1351	TACATCAGTAA	3,00	0,99	Hs.65029	growth arrest-specific 1
	1352	CCTGTAGGCC	3,00	0,99	Hs.207938	EST
	1353	GTGAGACCTCG	3,00	0,99	Hs.203206	ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY
50	1354	TGCCACCACAC	9,00	2,51	Hs.239993	ESTs
	1355	GCTGGATTTTG	2,00	0,69	Hs.82124	laminin, beta 1
	1356	TCACTTTTTTA	2,00	0,69	Hs.8045	ESTs
	1357	ATTATCCTCAG	2,00	0,69	Hs.7987	DKFZP434F162 protein
55	1358	GGATCCAATTT	2,00	0,69	Hs.61796	transcription factor AP-2 gamma (activating enhancer
	1359	CCAATTGAAGA	2,00	0,69	Hs.40328	ESTs
	1360	TTACTTTTGGT	2,00	0,69	Hs.285861	hypothetical protein FLJ10359
60	1361	GAGAGCTTTGC	2,00	0,69	Hs.275374	aldo-keto reductase family 1, member C1 (dihydrodiol
	1362	TACCCCCAAAC	2,00	0,69	Hs.241926	ESTs
	1363	GGGCAGACACT	2,00	0,69	Hs.18878	ESTs, Weakly similar to dJ876B10.4

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					[H.sapiens]
1364	ATGGCGCACGC	2,00	0,69	Hs.124984	ESTs, Moderately similar to unnamed protein product
1365	AGGTTGCCGAG	2,00	0,69	Hs.105399	KIAA0809 protein
1366	CCACTGCACCC	20,00	5,00	Hs.6853	carbohydrate (N-acetylglucosamine 6-O) sulfotransfer
1367	ATGGTGGGGGA	18,00	4,55	Hs.1665	zinc finger protein homologous to Zfp-36 in mouse
1368	CCCTCTCCCTT	8,00	2,24	Hs.85087	latent transforming growth factor beta binding prote
1369	TCACCAAAAAA	6,00	1,75	Hs.84753	KIAA0246 protein
1370	GTGAAACCCCC	59,00	13,37	Hs.265865	EST
1371	CCTGCAATCCC	34,00	7,97	Hs.3280	caspase 6, apoptosis-related cysteine protease
1372	GTGAAGCCCCG	22,00	5,34	Hs.285592	Homo sapiens mRNA; cDNA DKFZp564M113 (from clone DKF
1373	CCACTGTACTC	53,00	11,94	Hs.220261	ESTs, Moderately similar to ALU4_HUMAN ALU SUBFAMILY
1374	GTGGTGGGCGC	50,00	11,28	Hs.136810	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
1375	AGTATGACCTA	3,00	0,96	Hs.74649	cytochrome c oxidase subunit VIc
1376	GTGACAGCCAC	3,00	0,96	Hs.74441	chromodomain helicase DNA binding protein 4
1377	GGGCTTTTGAG	3,00	0,96	Hs.29893	Homo sapiens mRNA full length insert cDNA clone EURO
1378	GTGAGACCCCT	3,00	0,96	Hs.269952	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
1379	GTGGTGCACAT	3,00	0,96	Hs.269030	ESTs
1380	CCTGTAGTCAC	3,00	0,96	Hs.268900	ESTs
1381	TGGTAACTGGC	3,00	0,96	Hs.108741	ESTs
1382	GTGGTATGTGC	5,00	1,47	Hs.277102	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
1383	GTAAGATTAGC	5,00	1,47	Hs.250705	ESTs
1384	GCGAAACCCCA	72,00	15,71	Hs.210682	ESTs, Weakly similar to ALU6_HUMAN ALU SUBFAMILY SP
1385	ATCGTGCCACT	20,00	4,81	Hs.7615	Homo sapiens mRNA; cDNA DKFZp434N2030 (from clone DK
1386	TCTGTAATCCC	44,00	9,85	Hs.142	sulfotransferase family, cytosolic, 1A, phenol-prefe
1387	TTAGCCAGGCT	11,00	2,85	Hs.71367	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY
1388	ACAAAACCCTG	4,00	1,21	Hs.268591	ESTs
1389	ATCTCGGCTCA	14,00	3,49	Hs.29809	Homo sapiens mRNA; cDNA DKFZp434C185 (from clone DKF
1390	CCTGTAATGCC	13,00	3,26	Hs.7179	RAD1 (S. pombe) homolog
1391	CCACCGCACTC	22,00	5,18	Hs.222669	ESTs, Moderately similar to ALU4_HUMAN ALU SUBFAMILY
1392	GTGGTGTGTGC	38,00	8,50	Hs.27038	Homo sapiens mRNA; cDNA DKFZp434G2127 (from clone DK
1393	ATGAAACCCCA	27,00	6,22	Hs.285341	ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C

1394	CCTGTAGCCCC	7,00	1,92	Hs.277320	EST, Weakly similar to ALU6_HUMAN ALU SUBFAMILY SP S
1395	TTTTTAAAAA	2,00	0,66	Hs.77840	annexin A4
1396	AAGGAGCAAGT	2,00	0,66	Hs.76688	carboxylesterase 1 (mono- cyte/macrophage serine ester
1397	ACTTTTTTATG	2,00	0,66	Hs.697	cytochrome c-1
1398	ATTGAGCCACA	2,00	0,66	Hs.63290	2-hydroxyphytanoyl-CoA lyase
1399	ACCACAAAAA	2,00	0,66	Hs.469	succinate dehydrogenase complex, subunit A, flavopro
1400	ATCACAGCTCA	2,00	0,66	Hs.29590	ESTs
1401	TGGTTCCAGCT	2,00	0,66	Hs.278541	ESTs, Weakly similar to alternatively spliced produc
1402	TGACTGGCTTT	2,00	0,66	Hs.274439	Homo sapiens cDNA FLJ11265 fis, clone PLACE1009158
1403	GTGGTGGACCC	2,00	0,66	Hs.270901	ESTs
1404	CTGCTGTACTC	2,00	0,66	Hs.22826	tropomodulin 3 (ubiquitous)
1405	ATGATAATTAA	2,00	0,66	Hs.170142	ESTs
1406	TAAAATAAGGG	2,00	0,66	Hs.169487	Kreisler (mouse) maf-related leucine zipper homolog
1407	GAGAGAGAGAA	2,00	0,66	Hs.169391	ESTs
1408	TACCCTGAAAC	2,00	0,66	Hs.144018	ESTs
1409	ACTGCCCGCTG	12,00	3,03	Hs.81071	extracellular matrix protein 1
1410	GGTGAGCGTGT	5,00	1,44	Hs.2913	EphB3
1411	GTGGTGGATGC	5,00	1,44	Hs.277904	EST
1412	ACTGTGCCACT	5,00	1,44	Hs.161554	hypothetical protein FLJ20159
1413	GTGGCAGGCAC	68,00	14,52	Hs.246935	ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C
1414	CCCACTTGTA	12,00	3,00	Hs.75922	brain protein I3
1415	GCCCTTTCTCT	13,00	3,21	Hs.7835	endocytic receptor (macrophage man- nose receptor fami
1416	AGACCTCCTTC	6,00	1,67	Hs.281706	sortilin 1
1417	AGTGGTGGCTA	6,00	1,67	Hs.230	fibromodulin
1418	GGACAGATGTA	3,00	0,93	Hs.75356	transcription factor 4
1419	GTGGCGAGCAC	3,00	0,93	Hs.261831	EST
1420	ATGGTGTGTGC	3,00	0,93	Hs.193347	ESTs
1421	GGA CTGAGTCA	3,00	0,93	Hs.18387	transcription factor AP-2 alpha (activating enhancer
1422	GTGAGTGCCCT	3,00	0,93	Hs.171872	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 8 (RNA
1423	GCGGAACCTCA	3,00	0,93	Hs.10700	hypothetical protein
1424	GTGTGGGGGGC	41,00	8,95	Hs.2340	junction plakoglobin
1425	GTGAAACTCCA	32,00	7,12	Hs.140002	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY
1426	CCACTACACTC	29,00	6,50	Hs.83429	tumor necrosis factor (ligand) super- family, member 1
1427	ACGGAAGTTTT	4,00	1,18	Hs.144974	ESTs, Highly similar to unnamed protein product [H.s
1428	GTGAAACCCGT	13,00	3,18	Hs.278577	Homo sapiens mRNA; cDNA DKFZp564P073 (from clone DKF
1429	TCAA ACTGTGA	5,00	1,42	Hs.94881	ESTs

1430	CATCGAAAGTT	2,00	0,64	Hs.80618	hypothetical protein
1431	AGTAATCATCA	2,00	0,64	Hs.75925	proteasome (prosome, macropain) inhibitor subunit 1
1432	AATAATCCTGG	2,00	0,64	Hs.62908	ESTs
1433	GTATTCCTAAA	2,00	0,64	Hs.5724	ESTs, Weakly similar to multi PDZ domain protein MUP
1434	CTGGGAAGCAT	2,00	0,64	Hs.42311	ESTs
1435	GATCAAAACTG	2,00	0,64	Hs.41267	c21orf7 form A-D
1436	GTGACAGGCGC	2,00	0,64	Hs.278879	ESTs, Moderately similar to ALUA_HUMAN !!!! ALU CLAS
1437	GCACCGTGGAA	2,00	0,64	Hs.27299	transcriptional regulator protein
1438	TTAACTGTATT	2,00	0,64	Hs.180952	actin, beta
1439	ATGTTAGAGAC	2,00	0,64	Hs.1592	CDC16 (cell division cycle 16, S. cerevisiae, homolo
1440	ATCGCATCACT	2,00	0,64	Hs.158126	ESTs
1441	GACTCTGGAGA	2,00	0,64	Hs.154567	supervillin
1442	AAACTGTTCAA	2,00	0,64	Hs.118978	KIAA0256 gene product
1443	ACCAACACGGG	2,00	0,64	Hs.109005	ESTs
1444	AAAGATGTATC	1,00	0,32	Hs.979	pyruvate dehydrogenase (lipoamide) beta
1445	AAAACAGCAAG	1,00	0,32	Hs.92909	SON DNA binding protein
1446	TTTTCAGGTAA	1,00	0,32	Hs.91773	protein phosphatase 2 (formerly 2A), catalytic subun
1447	TGCCTCCCAGC	1,00	0,32	Hs.90527	HSPC128 protein
1448	TAAGTGAACAT	1,00	0,32	Hs.83164	collagen, type XV, alpha 1
1449	TTTTGCTCAGA	1,00	0,32	Hs.8102	ribosomal protein S20
1450	CATTCTCCCAG	1,00	0,32	Hs.79110	nucleolin
1451	GTTTCAGCACT	1,00	0,32	Hs.77502	methionine adenosyltransferase II, alpha
1452	GTAACCTCTATG	1,00	0,32	Hs.7277	peroxisomal biogenesis factor 3
1453	GTTCTATTGTA	1,00	0,32	Hs.6909	DKFZP564G202 protein
1454	CTATATTGTAA	1,00	0,32	Hs.65919	ESTs
1455	GTGAAACATTG	1,00	0,32	Hs.6567	Homo sapiens mRNA; cDNA DKFZp434C136 (from clone DKF
1456	GTATTGAAGTT	1,00	0,32	Hs.6079	B cell RAG associated protein
1457	CTTTAGAAGCA	1,00	0,32	Hs.5669	ESTs
1458	TGACTCCTCAA	1,00	0,32	Hs.47007	mitogen-activated protein kinase kinase kinase 14
1459	CTTTTATGGAC	1,00	0,32	Hs.44833	ESTs
1460	TAAATCTACAA	1,00	0,32	Hs.44701	ESTs
1461	TTCCCAAATGA	1,00	0,32	Hs.44257	Homo sapiens mRNA; cDNA DKFZp762O2215 (from clone DK
1462	GTAAGAGTTCT	1,00	0,32	Hs.4084	KIAA1025 protein
1463	ATGCCATTGGA	1,00	0,32	Hs.30213	ceroid-lipofuscinosis, neuronal 5
1464	AGGAAATGGAT	1,00	0,32	Hs.30194	ESTs
1465	AACAAGCTGGG	1,00	0,32	Hs.29759	RNA POLYMERASE I AND TRANSCRIPT RELEASE FACTOR
1466	TGCACTTGAGA	1,00	0,32	Hs.29055	ESTs
1467	GCATTCTGGTT	1,00	0,32	Hs.286261	ESTs
1468	GTGGCCACCCT	1,00	0,32	Hs.286217	KIAA0685 gene product
1469	AAGGTGGTTGT	1,00	0,32	Hs.285999	trinucleotide repeat containing 15

5	1470	AGAACTACGTG	1,00	0,32	Hs.284176	hypothetical protein PRO2221
	1471	AATTTGGGAGA	1,00	0,32	Hs.279882	PC326 prote
	1472	GGGAAACCCCT	1,00	0,32	Hs.279408	EST
	1473	CTTACTCTTGA	1,00	0,32	Hs.27342	ESTs
	1474	ACCGTGCCACT	1,00	0,32	Hs.270667	ESTs
	1475	AGGCTGGTTTA	1,00	0,32	Hs.26322	cell cycle related kinase
10	1476	TCTTTTGGGAG	1,00	0,32	Hs.257312	EST
	1477	ACTGATCTTGT	1,00	0,32	Hs.251871	CTP synthase
	1478	AAGTCTGTAGA	1,00	0,32	Hs.250863	ESTs
	1479	ATGGGGAAAGA	1,00	0,32	Hs.24989	ESTs
15	1480	ACAGTGCCACT	1,00	0,32	Hs.246374	ESTs
	1481	TGTGGGGACAA	1,00	0,32	Hs.245017	EST
	1482	CAAGTCTCCAG	1,00	0,32	Hs.241515	COX11 (yeast) homolog, cytochrome c oxidase assembly
20	1483	TTCCCTCCAAA	1,00	0,32	Hs.239727	desmocollin 2
	1484	ATGTATAGGGC	1,00	0,32	Hs.238809	ESTs
	1485	GGTTGTTGCGG	1,00	0,32	Hs.23823	ESTs
	1486	TCTTCTTAATA	1,00	0,32	Hs.23047	ESTs, Weakly similar to predicted using Genefinder [
25	1487	GCTCATTTT CAG	1,00	0,32	Hs.22870	Homo sapiens mRNA full length insert cDNA clone EURO
	1488	AGTTCCAGACC	1,00	0,32	Hs.223935	EST
30	1489	AGTCAGTGGGA	1,00	0,32	Hs.21943	ESTs, Weakly similar to ORF YGL221c [S.cerevisiae]
	1490	TTTCCAATGGA	1,00	0,32	Hs.21756	translation factor sui1 homolog
	1491	TACATTTGAAT	1,00	0,32	Hs.21537	protein phosphatase 1, catalytic subunit, beta isofo
35	1492	TTTTCTGTATT	1,00	0,32	Hs.21356	hypothetical protein DKFZp762K2015
	1493	AGAAAGATGGA	1,00	0,32	Hs.211577	kinectin 1 (kinesin receptor)
	1494	TTTACCTTTGG	1,00	0,32	Hs.21108	ESTs
40	1495	TACGATATTCA	1,00	0,32	Hs.207776	aspartylglucosaminidase
	1496	GCACTGGGGCA	1,00	0,32	Hs.206259	Homo sapiens mRNA for KIAA1190 protein, partial cds
	1497	GCTGCTAGAAA	1,00	0,32	Hs.197751	KIAA0666 protein
45	1498	GGGTAGAGAGT	1,00	0,32	Hs.196437	hypothetical protein FLJ10788
	1499	ATCGGCTCCCA	1,00	0,32	Hs.194478	Homo sapiens mRNA; cDNA DKFZp434O1572 (from clone DK
	1500	ATAATGGAGTG	1,00	0,32	Hs.17850	ESTs
50	1501	GAAGAAAGACT	1,00	0,32	Hs.172506	myosin VB
	1502	TGCCTGACAAG	1,00	0,32	Hs.169160	ESTs
	1503	TTCTGTAAATC	1,00	0,32	Hs.167106	proteasome (prosome, macropain) subunit, alpha type,
55	1504	AAATATTAAAC	1,00	0,32	Hs.16364	hypothetical protein FLJ10955
	1505	ATAAAGCCGAA	1,00	0,32	Hs.159471	ZAP3 protein
	1506	AGGCTGAGGCG	1,00	0,32	Hs.156292	ESTs
	1507	TAGTGCTCTCA	1,00	0,32	Hs.154424	deiodinase, iodothyronine, type II
60	1508	TTCATAAAAAA	1,00	0,32	Hs.154057	matrix metalloproteinase 19
	1509	GTGGCTACAGT	1,00	0,32	Hs.151251	ESTs
	1510	TAATCTTTCTT	1,00	0,32	Hs.151236	highly charged protein
65	1511	GATGGGGAAAT	1,00	0,32	Hs.14520	eukaryotic translation initiation factor 2C,

					1
1512	ACTAAGTGCTA	1,00	0,32	Hs.132739	I-mfa domain-containing protein
1513	CGGTTATTAA	1,00	0,32	Hs.119488	cystein-rich hydrophobic domain 2
1514	AGTGTGGGACT	1,00	0,32	Hs.118821	CGI-62 protein
1515	ATAGTTTAGCA	1,00	0,32	Hs.112157	ESTs
1516	CACCGAGACCA	1,00	0,32	Hs.107169	insulin-like growth factor binding protein 5
1517	AAATGACAATA	1,00	0,32	Hs.104904	ESTs
1518	TGACCAGGCGC	1,00	0,32	Hs.1019	parathyroid hormone receptor 1
1519	GGGCATCTCTT	38,00	8,11	Hs.76807	major histocompatibility complex, class II, DR alpha
1520	GTGGCGGGAGC	6,00	1,62	Hs.68257	general transcription factor IIF, polypeptide 1 (74k
1521	GAGAAACCCCG	40,00	8,44	Hs.5486	clone FLB5214
1522	AAATGCGAACA	4,00	1,16	Hs.5672	ESTs, Weakly similar to Similarity to Yeast D-lactat
1523	ATCCACCTGCC	3,00	0,91	Hs.231656	EST
1524	GCCAGCTGACA	3,00	0,91	Hs.118913	ESTs
1525	AGAAAGAATCT	3,00	0,91	Hs.107979	small membrane protein 1
1526	TGCCCCCTGCC	3,00	0,91	Hs.105700	secreted frizzled-related protein 4
1527	GAGAAACCTG	35,00	7,42	Hs.194359	ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C
1528	TTGCTGACTTT	36,00	7,54	Hs.108885	collagen, type VI, alpha 1
1529	AGGCTGAGGCA	11,00	2,64	Hs.17834	downstream neighbor of SON
1530	TCACTGCATTC	5,00	1,37	Hs.235587	EST
1531	CTTAAAAAAA	5,00	1,37	Hs.176626	hypothetical protein EDAG-1
1532	GTGAAAACCTG	9,00	2,22	Hs.283606	ESTs, Moderately similar to ALU5_HUMAN ALU SUBFAMILY
1533	AGCCACCGTGC	31,00	6,52	Hs.240845	DKFZP434D146 protein
1534	GTGGCACATAC	6,00	1,57	Hs.205353	ectonucleoside triphosphate diphosphohydrolase 1
1535	CCATTGTACTC	15,00	3,39	Hs.108740	DKFZP586A0522 protein
1536	TGCCTGTAATC	51,00	10,11	Hs.167135	Homo sapiens cDNA FLJ10728 fis, clone NT2RP3001236
1537	TTAGCCAGGAT	19,00	4,15	Hs.211457	EST
1538	TAGGGAATGAA	3,00	4,35	Hs.59545	ring finger protein 15
1539	AAAGCATTTCT	3,00	4,35	Hs.36688	ESTs, Moderately similar to WAP four-disulfide core
1540	ATGACCCGCAG	3,00	4,35	Hs.286254	ESTs, Weakly similar to AF170723_1 protein kinase ST
1541	ATTTTTTTCAG	3,00	4,35	Hs.278004	EST
1542	GCAAGCCATTT	3,00	4,35	Hs.272813	dual oxidase 1
1543	GATTTTTTTTT	3,00	4,35	Hs.227913	API5-like 1
1544	TCTCTTGGGGT	3,00	4,35	Hs.16740	hypothetical protein FLJ11036
1545	TGTGTGTAACA	3,00	4,35	Hs.156457	ESTs
1546	CCTTTGTCTTT	3,00	0,88	Hs.99654	protein-O-mannosyltransferase 1
1547	AATTGTAGTTA	3,00	0,88	Hs.6809	RAP2A, member of RAS oncogene family
1548	AGCCACTGTAC	3,00	0,88	Hs.55346	ESTs, Weakly similar to Z141_HUMAN ZINC FINGER PROTE

1549	CAAAC TCAAAA	3,00	0,88	Hs.279809	hypothetical protein PRO1741
1550	GAGCACTTGGG	3,00	0,88	Hs.182937	peptidylprolyl isomerase A (cyclophilin A)
1551	AAGTTTTTAGT	3,00	0,88	Hs.149917	ESTs
1552	TTTGAGGATTG	3,00	0,88	Hs.147916	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3
1553	TAGTTGGAAC T	3,00	0,88	Hs.1119	nuclear receptor subfamily 4, group A, member 1
1554	TTGACCAGGCT	13,00	2,98	Hs.285080	ESTs
1555	CTTATTTGTTT	5,00	1,34	Hs.4114	plastin 3 (T isoform)
1556	AGCTTCCAGCC	5,00	1,34	Hs.144974	ESTs, Highly similar to unnamed protein product [H.s
1557	CACCCCTCGC	2,00	0,61	Hs.91246	hypothetical protein DKFZp5470146
1558	TCTCCAGGACA	2,00	0,61	Hs.8025	Homo sapiens clone 23767 and 23782 mRNA sequences
1559	TATTTCAATTG	2,00	0,61	Hs.79507	KIAA0582 protein
1560	CAGGTTGAAGT	2,00	0,61	Hs.79219	RaIGDS-like gene; KIAA0959 protein
1561	TATGTTAATGT	2,00	0,61	Hs.7341	ESTs, Weakly similar to DUS8_HUMAN DUAL SPECIFICITY
1562	GACTGCTCTGG	2,00	0,61	Hs.36475	ESTs
1563	GAAGAGTGCTC	2,00	0,61	Hs.32204	ESTs
1564	GAGCCAAAGAA	2,00	0,61	Hs.29423	ESTs, Weakly similar to macrophage lectin 2 [H.sapie
1565	CTTGTAATCTC	2,00	0,61	Hs.278002	EST
1566	TTACAATCACA	2,00	0,61	Hs.21276	ESTs
1567	GTGAAATCCAG	2,00	0,61	Hs.183275	ESTs
1568	CCTGTAATACC	9,00	2,17	Hs.92254	hypothetical protein FLJ20163
1569	AAAAGCAGAAA	4,00	1,11	Hs.84728	Kruppel-like factor 5 (intestinal)
1570	TTTGGGCCTAA	18,00	3,88	Hs.230320	EST
1571	CCTGTGGTCCC	52,00	10,04	Hs.249373	Homo sapiens clone FLB2543
1572	TAGCTCCCTTG	5,00	1,32	Hs.199160	myeloid/lymphoid or mixed-lineage leukemia (trithora
1573	GTGAGACCCTG	22,00	4,58	Hs.135756	polymerase (DNA-directed) kappa
1574	GCGAAACCCCG	65,00	12,25	Hs.30376	hypothetical protein
1575	CCACTGCATTC	38,00	7,45	Hs.270403	ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C
1576	GGGATCGCCCC	6,00	1,52	Hs.12865	p47
1577	TTCCAAGGCAG	9,00	2,13	Hs.317	topoisomerase (DNA) I
1578	ATGGTGGGTGC	9,00	2,13	Hs.209602	ESTs, Weakly similar to ubiquitous TPR motif, Y isof
1579	ATCTTGGCTCA	7,00	1,72	Hs.86958	interferon (alpha, beta and omega) receptor 2
1580	GTGAAACACCG	10,00	2,32	Hs.207766	EST
1581	CGTTCATTCAT	3,00	0,86	Hs.6139	synaptogyrin 1
1582	CCATAATGTTG	3,00	0,86	Hs.39957	pleckstrin 2 (mouse) homolog
1583	CTCTACGCATT	3,00	0,86	Hs.278573	H-2K binding factor-2
1584	ATGCAGAGGTG	3,00	0,86	Hs.210706	ESTs, Weakly similar to AF211175_1 unknown [H.sapien
1585	GCCAACAGCAT	3,00	0,86	Hs.155606	paired mesoderm homeo box 1
1586	CCTGTAATCAC	8,00	1,92	Hs.266136	ESTs
1587	GGATATGTGGT	21,00	4,34	Hs.738	early growth response 1

1588	GCTCACACCTG	4,00	1,09	Hs.60617	sialyltransferase 4A (beta-galactosidase alpha-2,3-s
1589	CATACAGAAAA	4,00	1,09	Hs.3107	CD97 antigen
1590	TATCCCAGAAC	27,00	5,40	Hs.169286	crystallin, beta B2
1591	CGCCTGTAATC	33,00	6,46	Hs.235083	EST
1592	GTGGCACACAC	49,00	9,23	Hs.71475	hypothetical protein
1593	ATCATACCACT	6,00	1,50	Hs.224071	EST, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C W
1594	GTGGCGTGCAC	19,00	3,94	Hs.228163	EST
1595	TTGCCCAGGCT	50,00	9,38	Hs.56027	Homo sapiens mRNA; cDNA DKFZp586J1717 (from clone DK
1596	CCGGTAATCCC	7,00	1,70	Hs.272813	dual oxidase 1
1597	AGCCACTGTGC	24,00	4,81	Hs.180606	EST
1598	GTGGTGCACAC	48,00	8,93	Hs.272173	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
1599	CCCACTCTTTG	3,00	0,84	Hs.9414	KIAA1488 protein
1600	CAAATCTTGA	3,00	0,84	Hs.75431	fibrinogen, gamma polypeptide
1601	CCTGTAGACCC	3,00	0,84	Hs.5123	inorganic pyrophosphatase
1602	TCCTGGTTATT	3,00	0,84	Hs.4084	KIAA1025 protein
1603	TGCTAGATTGG	3,00	0,84	Hs.239663	myeloid/lymphoid or mixed-lineage leu- kemia (trithora
1604	AACCCGGGAGA	3,00	0,84	Hs.236241	EST
1605	TACTCGGTTGT	3,00	0,84	Hs.119394	ESTs
1606	GACGGGGTGGA	3,00	0,84	Hs.111279	hypothetical protein
1607	ATTTGTGTGTA	2,00	0,59	Hs.94499	ESTs
1608	GTTCCAAGCAA	2,00	0,59	Hs.94011	ESTs, Weakly similar to MAGE-B4 [H.sapiens]
1609	CTATCTGTGGA	2,00	0,59	Hs.9176	ESTs
1610	GGCCCAGAGCC	2,00	0,59	Hs.91246	hypothetical protein DKFZp547O146
1611	TTGATGCCCAG	2,00	0,59	Hs.8503	ESTs
1612	TATTGTAAAA	2,00	0,59	Hs.7984	ESTs
1613	CAATCTTCAA	2,00	0,59	Hs.78909	butyrate response factor 2 (EGF- response factor 2)
1614	CTTCCTTGTGT	2,00	0,59	Hs.6298	KIAA1151 protein
1615	GACAGTGATAG	2,00	0,59	Hs.53913	hypothetical protein FLJ10252
1616	GGCCTCTGATG	2,00	0,59	Hs.46670	PRO1575 protein
1617	GCCTCCCCCAC	2,00	0,59	Hs.40109	KIAA0872 protein
1618	GGAGCAGACGC	2,00	0,59	Hs.31718	Homo sapiens cDNA FLJ11034 fis, clone PLACE1004258
1619	CTGCCCTCTGC	2,00	0,59	Hs.27801	zinc finger protein 278
1620	GGCTCTTCTGG	2,00	0,59	Hs.27721	hypothetical protein FLJ20353
1621	TTGCAATAGGT	2,00	0,59	Hs.25625	hypothetical protein FLJ11323
1622	TGATGATCATT	2,00	0,59	Hs.22394	hypothetical protein FLJ10893
1623	CCCAAACGGTA	2,00	0,59	Hs.195453	ribosomal protein S27 (metalloproteinase 1)
1624	TTGGCCAAGAT	2,00	0,59	Hs.19522	hypothetical protein PRO2849
1625	TTTACCTGTTG	2,00	0,59	Hs.173381	dihydropyrimidinase-like 2
1626	TGTCAATGGGG	2,00	0,59	Hs.169055	golgi autoantigen, golgin subfamily a, 2
1627	CTTCCGGGTAA	2,00	0,59	Hs.108924	DKFZP586P1422 protein
1628	AAGGTTCTTCT	1,00	0,29	Hs.89695	insulin rec ptor

1629	TAATTTTAAAC	1,00	0,29	Hs.8861	ESTs
1630	TTAAATGCTCT	1,00	0,29	Hs.82501	similar to mouse Xrn1 / Dhms2 protein
1631	AGCTCCCAAGA	1,00	0,29	Hs.80475	polymerase (RNA) II (DNA directed) polypeptide J (13)
1632	TGCTGCGGAAG	1,00	0,29	Hs.80306	Homo sapiens mRNA, clone:RES4-4
1633	GAGCAGTGCTG	1,00	0,29	Hs.7636	feline sarcoma (Snyder-Theilen) viral (v-fes)/Fujina
1634	CAAGGAAATGT	1,00	0,29	Hs.64840	ESTs
1635	GCAACACCGGA	1,00	0,29	Hs.63525	poly(rC)-binding protein 2
1636	GCCAAAGATGT	1,00	0,29	Hs.58636	squamous cell carcinoma antigen recognized by T cell
1637	GTTGCAGGCGC	1,00	0,29	Hs.5811	hypothetical protein FLJ20467
1638	TCTTTAAAAA	1,00	0,29	Hs.55999	ESTs
1639	TGTGCTTCTAG	1,00	0,29	Hs.38613	ESTs
1640	TATCAAAAAA	1,00	0,29	Hs.32491	ESTs
1641	TAACTCCTAGT	1,00	0,29	Hs.31845	ESTs
1642	TGATATTAAAG	1,00	0,29	Hs.30661	electron-transferring-flavoprotein dehydrogenase
1643	AAACCAATTTT	1,00	0,29	Hs.30483	Homo sapiens mRNA; cDNA DKFZp434O1311 (from clone DK
1644	AAGAACTCAGG	1,00	0,29	Hs.30250	v-maf musculoaponeurotic fibrosarcoma (avian) oncogene
1645	CAGTCCCAAAA	1,00	0,29	Hs.29846	Human DNA sequence from clone 717M23 on chromosome 2
1646	AAACCGGTCCC	1,00	0,29	Hs.285490	ESTs, Weakly similar to unnamed protein product [H.s
1647	AACATTCCTAA	1,00	0,29	Hs.285429	ESTs
1648	TTAACATTTAT	1,00	0,29	Hs.279763	hypothetical protein FLJ10504
1649	ATGGCGTGTGC	1,00	0,29	Hs.278880	ESTs
1650	GAGCTCTTCCT	1,00	0,29	Hs.274598	cytochrome P450, subfamily IID (debrisoquine, sparte
1651	GCAAGACCTTG	1,00	0,29	Hs.273603	ESTs
1652	AGGTAAAGAGA	1,00	0,29	Hs.272046	ESTs
1653	CCCGTAATCTC	1,00	0,29	Hs.270062	Homo sapiens mRNA; cDNA DKFZp586D0924 (from clone DK
1654	GCGGCACGCAC	1,00	0,29	Hs.269867	ESTs
1655	GACTTCAGCA	1,00	0,29	Hs.265168	ESTs, Moderately similar to T10_MOUSE SER/THR-RICH P
1656	GCTGTTCTAAG	1,00	0,29	Hs.24422	regulatory factor X-associated protein
1657	GCACTGAGAAG	1,00	0,29	Hs.239499	KIAA0185 protein
1658	GCGAGACCTTG	1,00	0,29	Hs.232157	ESTs
1659	TTGCATTCTCC	1,00	0,29	Hs.21379	ESTs
1660	TGCTTGATGTC	1,00	0,29	Hs.209680	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
1661	AACGCAGCCTT	1,00	0,29	Hs.20060	KIAA0229 protein
1662	TAGGAAACCTG	1,00	0,29	Hs.200596	KIAA0547 gene product
1663	GGCTTTATTCT	1,00	0,29	Hs.200412	Homo sapiens mRNA; cDNA DKFZp434G0719 (from clone DK
1664	AATACTTCTCT	1,00	0,29	Hs.2003	T cell receptor beta locus
1665	GGTGACAGAGG	1,00	0,29	Hs.200235	ESTs



1666	AGAAAAAAAT	1,00	0,29	Hs.200057	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC
1667	CATTGGCACTC	1,00	0,29	Hs.195614	splicing factor 3b, subunit 3, 130kD
1668	TTAATTAGCAA	1,00	0,29	Hs.183085	Homo sapiens mRNA; cDNA DKFZp434K098 (from clone DKF
1669	CGCGTCAGAGC	1,00	0,29	Hs.182982	golgin-67
1670	AAACTCGCCG	1,00	0,29	Hs.17969	KIAA0663 gene product
1671	TGTACTTTCCT	1,00	0,29	Hs.179661	tubulin, beta polypeptide
1672	CAGACTGGGAG	1,00	0,29	Hs.1790	nuclear receptor subfamily 3, group C, member 2
1673	TTTCTGAAGGG	1,00	0,29	Hs.172910	ESTs, Highly similar to unnamed protein product [H.s
1674	TAAATAAGGAA	1,00	0,29	Hs.17235	ESTs
1675	GATGACAGAGT	1,00	0,29	Hs.171995	kallikrein 3, (prostate specific antigen)
1676	GTTACCGAGTG	1,00	0,29	Hs.171637	ESTs, Weakly similar to KIAA1317 pro- tein [H.sapiens]
1677	GGTCAAATCAT	1,00	0,29	Hs.170162	KIAA1357 protein
1678	GCTTCACTTCC	1,00	0,29	Hs.164303	ESTs
1679	GACAATACACC	1,00	0,29	Hs.161554	hypothetical protein FLJ20159
1680	TTCCAAAAAA	1,00	0,29	Hs.159971	SWI/SNF related, matrix associated, actin dependent
1681	TGTGACCCCTC	1,00	0,29	Hs.159237	hexokinase 3 (white cell)
1682	TTTGTGCCATT	1,00	0,29	Hs.155507	ESTs
1683	CCTTGCCCTAT	1,00	0,29	Hs.143746	ESTs
1684	AGAACAATAA	1,00	0,29	Hs.135721	ESTs
1685	AGACTGTACTG	1,00	0,29	Hs.132348	ESTs, Weakly similar to diaphanous 1 [H.sapiens]
1686	CCATCCCAGTG	1,00	0,29	Hs.127863	ESTs
1687	ACAGACTGTTA	1,00	0,29	Hs.125036	tumor endothelial marker 7 precursor
1688	GGCGACCCATT	1,00	0,29	Hs.12451	echinoderm microtubule-associated protein-like
1689	CAGGTCCCATT	1,00	0,29	Hs.11924	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
1690	ACAAAGAAAAG	1,00	0,29	Hs.118578	Homo sapiens cDNA FLJ20053 fis, clone COL00809
1691	ACTGATGCTCA	1,00	0,29	Hs.115467	ESTs
1692	TCCTCTTTCAA	1,00	0,29	Hs.113987	lectin, galactoside-binding, soluble, 2 (galectin 2)
1693	AGGCAGCACTG	1,00	0,29	Hs.11112	ESTs
1694	CTACTGCACTC	22,00	4,42	Hs.185989	ESTs
1695	CCCAGCTAATT	29,00	5,59	Hs.251235	EST
1696	GTGGCACGCAC	22,00	4,35	Hs.228343	EST
1697	GCAAAATCCCA	9,00	2,04	Hs.268051	ESTs, Weakly similar to ALU2_HUMAN ALU SUBFAMILY SB
1698	GTGAAACCTTG	35,00	6,56	Hs.161554	hypothetical protein FLJ20159
1699	ACTGTAATCCC	10,00	2,23	Hs.127809	ESTs
1700	ATCGCACCAC	19,00	3,81	Hs.142569	ESTs
1701	GGGAAACCCCA	10,00	2,20	Hs.278281	ESTs, Weakly similar to alternatively spliced produc
1702	GTGAAACCCCT	27,00	5,16	Hs.229364	ESTs

5	1703	CAGCAGCAAAA	5,00	1,25	Hs.285090	ESTs
	1704	TAGAAGCCAAC	7,00	1,63	Hs.7905	SH3 and PX domain-containing protein SH3PX1
	1705	TTCTTTTCTT	4,00	1,04	Hs.250722	(Manual assignment) MUG, Myeloid-upregulated protein
10	1706	CCTATAATCCT	4,00	1,04	Hs.158164	ATP-binding cassette, sub-family B (MDR/TAP), member
	1707	TAAACGTGGCA	3,00	0,82	Hs.284146	hypothetical protein DKFZp762N0610
	1708	CAGAAGTCTTC	3,00	0,82	Hs.23921	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ
15	1709	ACCAGCCAAAG	3,00	0,82	Hs.193090	ESTs, Highly similar to AF161437_1 HSPC319 [H.sapien]
	1710	GAAATGGGGAA	3,00	0,82	Hs.173933	Homo sapiens mRNA for KIAA1439 protein, partial cds
	1711	GTGTGGTATTC	3,00	0,82	Hs.172140	ESTs
20	1712	CCGAGTTTTTG	3,00	0,82	Hs.139709	ESTs
	1713	GGCAAACCTTA	3,00	0,82	Hs.102497	paxillin
	1714	CCACAGGGGAT	15,00	3,05	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danlos syndrome)
25	1715	CCTGTGGTCTC	6,00	1,44	Hs.236504	EST, Weakly similar to ALU6_HUMAN ALU SUBFAMILY SP S
	1716	CACCACCACGC	5,00	1,23	Hs.5862	hypothetical protein
	1717	GTGAAACCCGG	12,00	2,51	Hs.229170	ESTs
30	1718	GTGAAACCCTA	29,00	5,33	Hs.152081	ESTs
	1719	ATATGTATATT	4,00	1,02	Hs.75839	zinc finger protein 6 (CMPX1)
	1720	GTGAAACCACA	4,00	1,02	Hs.283788	hypothetical protein DKFZp547A023
	1721	GGGATTAAAGC	4,00	1,02	Hs.211579	melanoma adhesion molecule
35	1722	TACCTTTGCTA	4,00	1,02	Hs.120980	nuclear receptor co-repressor 2
	1723	AATGAATGAAA	2,00	0,57	Hs.8986	complement component 1, q subcomponent, beta polypep
40	1724	ATATTTTCATTC	2,00	0,57	Hs.79402	polymerase (RNA) II (DNA directed) polypeptide C (33)
	1725	TGGAGGGGCGAG	2,00	0,57	Hs.7306	secreted frizzled-related protein 1
	1726	TCGCGCAATAA	2,00	0,57	Hs.72249	protease-activated receptor 3
	1727	CTCAAAATCAA	2,00	0,57	Hs.72165	hypothetical protein FLJ20283
45	1728	TGTACATATGT	2,00	0,57	Hs.268384	homolog of yeast CDH1/HCT1
	1729	TGCAATGTTGT	2,00	0,57	Hs.171957	triple functional domain (PTPRF interacting)
	1730	TCATTTTGTGA	2,00	0,57	Hs.154567	supervillin
50	1731	TAAAACGTGAA	2,00	0,57	Hs.12592	period (Drosophila) homolog 3
	1732	TCATCTGCAAA	2,00	0,57	Hs.105189	ESTs, Weakly similar to AF148856_2 unknown [H.sapien]
55	1733	GGCAAAATCTA	2,00	0,57	Hs.104627	Homo sapiens cDNA FLJ10158 fis, clone HEMBA1003463
	1734	GACCTATCTCT	8,00	1,78	Hs.194431	palladin
	1735	GTGGTGCGTGC	29,00	5,23	Hs.129727	X-ray repair complementing defective repair in China
60	1736	TCTTGAACAGC	3,00	0,80	Hs.72249	protease-activated receptor 3
	1737	GGCTTTGGTCT	3,00	0,80	Hs.177592	ribosomal protein, large, P1
	1738	CCACCACACCC	3,00	0,80	Hs.117582	CGI-43 protein

65

1739	ATGAAACCCCG	25,00	4,58	Hs.226396	hypothetical protein FLJ11126
1740	CCACTGCACTG	31,00	5,53	Hs.193220	ESTs
1741	CCACTGCGCTC	12,00	2,45	Hs.260287	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ
1742	GAGAAACCCCA	30,00	5,36	Hs.5719	chromosome condensation-related SMC- associated prote
1743	CCTGTAATCCT	63,00	10,50	Hs.165954	ESTs
1744	GACAGTCGGTG	4,00	1,00	Hs.8203	endomembrane protein emp70 precursor isolog
1745	TTTTCTCTGAA	4,00	1,00	Hs.75516	tyrosine kinase 2
1746	TTGGCTAGGCC	7,00	1,57	Hs.211539	eukaryotic translation initiation factor 2, subunit
1747	CCCTTGTCCGA	7,00	1,57	Hs.127824	ESTs, Weakly similar to weak similarity to collagens
1748	AGCCCAGGAGT	9,00	1,91	Hs.274813	EST
1749	GTGGTGTGCAC	17,00	3,18	Hs.20126	KIAA0317 gene product
1750	CCTGTGATCCT	5,00	1,17	Hs.240395	potassium channel, subfamily K, member 6 (TWIK-2)
1751	CCTGTAAACCC	5,00	1,17	Hs.161554	hypothetical protein FLJ20159
1752	TCAATAAAACC	4,00	0,98	Hs.151411	KIAA0916 protein
1753	ACGAAACCCCA	4,00	0,98	Hs.117582	CGI-43 protein
1754	TGACCACCCTT	3,00	0,78	Hs.42390	nasopharyngeal carcinoma susceptibility protein
1755	CTCGAATAAAA	3,00	0,78	Hs.34871	KIAA0569 gene product
1756	CGACTGCACTC	3,00	0,78	Hs.182061	Novel human gene mapping to chomo- some 22
1757	CAGAATAATGT	3,00	0,78	Hs.125031	choline/ethanolaminephosphotransferase
1758	CAGAAGGCCAC	2,00	0,55	Hs.8268	ESTs
1759	GAAAGAGCTCT	2,00	0,55	Hs.7337	hypothetical protein FLJ10936
1760	AAAAATTATCTT	2,00	0,55	Hs.63657	hypothetical protein FLJ11005
1761	GGTGTCTGTGG	2,00	0,55	Hs.5889	ESTs, Weakly similar to AC004876_5 similar to predic
1762	AACTGAGAAGT	2,00	0,55	Hs.56406	ESTs, Highly similar to unnamed protein product [H.s
1763	TGAGTGGTTTG	2,00	0,55	Hs.29672	ESTs
1764	GAAGTTGCCTT	2,00	0,55	Hs.26777	KIAA0843 protein
1765	TTGTTAAGCCT	2,00	0,55	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PLACE1007402
1766	TATCTCAGAAC	2,00	0,55	Hs.223142	ESTs
1767	GGTGAATTTTA	2,00	0,55	Hs.210866	EST
1768	TGAGCACATAA	2,00	0,55	Hs.194208	suc1-associated neurotrophic factor target 2 (FGFR s
1769	GTGCGTGCCTG	2,00	0,55	Hs.182354	ESTs
1770	ATTATCCAGCG	2,00	0,55	Hs.182225	RNA binding motif protein 3
1771	TCTTCTTTCAG	2,00	0,55	Hs.17757	Homo sapiens mRNA; cDNA DKFZp434E1515 (from clone DK
1772	CTCTCCAAACC	2,00	0,55	Hs.151242	complement component 1 inhibitor (an- gioedema, heredi
1773	CCATTGCTCTC	2,00	0,55	Hs.117582	CGI-43 protein
1774	AAGATCCTTGT	2,00	0,55	Hs.113503	karyopherin (importin) beta 3

5	1775	GGAACCTGGCT	2,00	0,55	Hs.105613	ESTs
	1776	AGTTTGTACC	2,00	0,55	Hs.10130	ESTs
	1777	TCCACAGTGGG	1,00	0,27	Hs.99636	ESTs, Weakly similar to I54197 hypothetical protein
	1778	TACCCCTCTCA	1,00	0,27	Hs.994	phospholipase C, beta 2
10	1779	AAAGATGTACA	1,00	0,27	Hs.95243	transcription elongation factor A (SII)-like 1
	1780	ATTTATAATCC	1,00	0,27	Hs.914	major histocompatibility complex, class II, DP alpha
	1781	ACTGTTTGTTT	1,00	0,27	Hs.814	major histocompatibility complex, class II, DP beta
15	1782	TCGATGTGGCG	1,00	0,27	Hs.81248	CUG triplet repeat, RNA-binding protein 1
	1783	TTAAGATCTTC	1,00	0,27	Hs.79404	neuron-specific protein
20	1784	TTCTTGTGATA	1,00	0,27	Hs.79081	protein phosphatase 1, catalytic subunit, gamma isof
	1785	AACAATTATCA	1,00	0,27	Hs.7845	Homo sapiens cDNA FLJ20820 fis, clone ADSE00490
25	1786	AGAAACACTCA	1,00	0,27	Hs.75782	general transcription factor IIIC, polypeptide 2 (be
	1787	AGAAATAAAAA	1,00	0,27	Hs.74649	cytochrome c oxidase subunit VIc
	1788	TAAGTGTGGTT	1,00	0,27	Hs.7327	claudin 1
30	1789	AGGAGAGAGCC	1,00	0,27	Hs.6932	Homo sapiens clone 23809 mRNA sequence
	1790	TGGACAAGTCA	1,00	0,27	Hs.64988	ESTs
	1791	TTAAACTGCTG	1,00	0,27	Hs.6232	KIAA0764 gene product
	1792	AGACCTCACTG	1,00	0,27	Hs.49763	ESTs
35	1793	TATTTGTATTT	1,00	0,27	Hs.4764	KIAA0763 gene product
	1794	TGGATAGATTC	1,00	0,27	Hs.45519	ESTs
	1795	TTGATTGATTT	1,00	0,27	Hs.42927	Homo sapiens cDNA FLJ11298 fis, clone PLACE1009794
40	1796	ACTATATTGTG	1,00	0,27	Hs.42532	ESTs
	1797	GAGTCCGCGCT	1,00	0,27	Hs.4069	glucocorticoid modulatory element binding protein 1
45	1798	TATTTATTTTT	1,00	0,27	Hs.39143	ESTs, Weakly similar to predicted using Genefinder [
	1799	TGACATCCTGA	1,00	0,27	Hs.285056	ESTs
	1800	CTGCAAGGACA	1,00	0,27	Hs.284135	Homo sapiens HSPC295 mRNA, partial cds
50	1801	ATCCCCCAGAA	1,00	0,27	Hs.278386	ESTs
	1802	CCACTGCGCTT	1,00	0,27	Hs.252836	EST, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE
	1803	TGCCAGACCCT	1,00	0,27	Hs.249721	ESTs
55	1804	GGTGTGCACCT	1,00	0,27	Hs.24587	signal transduction protein (SH3 containing)
	1805	CTTTTATTTTT	1,00	0,27	Hs.245710	heterogeneous nuclear ribonucleoprotein H1 (H)
60	1806	AGCGCTGGGGA	1,00	0,27	Hs.241471	RNB6
	1807	CTAGGACCTGT	1,00	0,27	Hs.240112	KIAA0276 protein
	1808	TAGTCCTAGCT	1,00	0,27	Hs.237372	EST

1809	ATTTAATTTTA	1,00	0,27	Hs.235883	ESTs
1810	GGCAACAAAGT	1,00	0,27	Hs.233364	ESTs
1811	CTGTAAGGATC	1,00	0,27	Hs.227730	integrin, alpha 6
1812	AGTCTTCCAGT	1,00	0,27	Hs.226213	cytochrome P450, 51 (lanosterol 14-alpha-demethylase)
1813	GCTCCCCCTCC	1,00	0,27	Hs.2157	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)
1814	AGTATTTATGA	1,00	0,27	Hs.203838	ESTs
1815	GCTAAACCCTG	1,00	0,27	Hs.202781	ESTs, Moderately similar to ALU5 HUMAN ALU SUBFAMILY
1816	CCAGCATTACC	1,00	0,27	Hs.20082	Homo sapiens zinc finger protein NY-REN-21 antigen m
1817	CCTGCAATCTC	1,00	0,27	Hs.197793	ESTs
1818	GAAAAATGCGC	1,00	0,27	Hs.193398	ESTs
1819	GCCAGGGCTCA	1,00	0,27	Hs.187913	ESTs, Moderately similar to MRP3 [H.sapiens]
1820	TAAAACTTACA	1,00	0,27	Hs.184075	ESTs
1821	ACCCTTTTTAT	1,00	0,27	Hs.183153	ADP-ribosylation factor 4-like
1822	GTTTCAAACGA	1,00	0,27	Hs.180535	ESTs, Weakly similar to S69890 mitogen inducible gen
1823	CAGTCTCAGTG	1,00	0,27	Hs.17767	Homo sapiens mRNA; cDNA DKFZp761N07121 (from clone D
1824	AAAAATTCATC	1,00	0,27	Hs.170328	moesin
1825	TAAATAAACAA	1,00	0,27	Hs.16755	MBIP protein
1826	CACCTCAAACA	1,00	0,27	Hs.157150	ESTs, Weakly similar to zinc finger protein 106 [M.m
1827	AATGTCCTCGG	1,00	0,27	Hs.155987	KIAA0645 gene product
1828	TGTACCCCGCT	1,00	0,27	Hs.155975	protein tyrosine phosphatase, receptor type, C-assoc
1829	CGGGTTTGTGC	1,00	0,27	Hs.155482	hydroxyacyl glutathione hydrolase
1830	GTCCATCTTAA	1,00	0,27	Hs.153177	ribosomal protein S28
1831	TTTATTTTATAG	1,00	0,27	Hs.152250	ESTs
1832	CCTAAAAAAA	1,00	0,27	Hs.148907	Homo sapiens mRNA; cDNA DKFZp564G223 (from clone DKF
1833	TGATCGAGCTT	1,00	0,27	Hs.145867	ESTs
1834	GAAGATATTCC	1,00	0,27	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol
1835	ATGGAGCTGCA	1,00	0,27	Hs.142779	ESTs
1836	ATAAGACCTTA	1,00	0,27	Hs.142296	jerky (mouse) homolog
1837	CAAGCCAAAAA	1,00	0,27	Hs.14229	hypothetical protein FLJ10379
1838	CAAATGGCAAA	1,00	0,27	Hs.134292	ESTs
1839	GAAGTTTAAAT	1,00	0,27	Hs.132463	phosphoinositide-3-kinase, class 2, beta polypeptide
1840	GAAGGCAAGAT	1,00	0,27	Hs.1321	coagulation factor XII (Hageman factor)
1841	TTAGTTATGAC	1,00	0,27	Hs.13063	transcription factor CA150
1842	CTGTATGTTTA	1,00	0,27	Hs.128777	ESTs
1843	ACCTGCATTCC	1,00	0,27	Hs.125034	Homo sapiens cDNA FLJ10733 fis, clone NT2RP3001392
1844	CCAGCTGCCTG	1,00	0,27	Hs.11782	ESTs
1845	AAAAGTGGTGT	1,00	0,27	Hs.117582	CGI-43 protein

1846	TTTATCTGATA	1,00	0,27	Hs.117582	CGI-43 protein
1847	TATTTTACCTA	1,00	0,27	Hs.114765	myeloid/lymphoid or mixed-lineage leukemia (trithora)
1848	ACCTCCACACG	1,00	0,27	Hs.108947	KIAA0050 gene product
1849	GATTGCTGTGC	1,00	0,27	Hs.100555	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 18 (Myc)
1850	TGAAGCAGAAA	1,00	0,27	Hs.100407	Homo sapiens mRNA; cDNA DKFZp564H2416 (from clone DK)
1851	ATTGTGCCACT	28,00	4,88	Hs.272324	Homo sapiens mRNA; cDNA DKFZp566G231 (from clone DKF)
1852	TCGGAGCTGTT	11,00	2,20	Hs.4055	chromosome 21 open reading frame 50
1853	GTGGTGTGCGC	9,00	1,87	Hs.278038	ESTs, Highly similar to PMM2_HUMAN PHOSPHOMANNOMUTAS
1854	TGCTACGAAAA	7,00	1,53	Hs.146550	myosin, heavy polypeptide 9, non-muscle
1855	CCTGGCCTAAA	7,00	1,53	Hs.111676	protein kinase H11; small stress protein-like protein
1856	TTCAGTGTGAG	56,00	8,99	Hs.621	lectin, galactoside-binding, soluble, 3 (galectin 3)
1857	CCCTACCCTGT	30,00	5,10	Hs.75736	apolipoprotein D
1858	GTGGCGTGCGC	6,00	1,34	Hs.117582	CGI-43 protein
1859	AGCCACCACAC	20,00	3,57	Hs.170310	cat eye syndrome chromosome region, candidate 1
1860	TCTACTAAAAA	5,00	1,15	Hs.48802	Homo sapiens clone 23632 mRNA sequence
1861	GCCGGGCACGG	5,00	1,15	Hs.271480	hypothetical protein FLJ20686
1862	GTGCTCAAACC	5,00	1,15	Hs.103915	KIAA0346 protein
1863	CCACTGCACTT	35,00	5,78	Hs.194300	ESTs
1864	GTGGCGGACGC	4,00	0,96	Hs.182577	inositol polyphosphate-5-phosphatase, 75kD
1865	CCACTGCCCTC	12,00	2,31	Hs.1010	regulator of mitotic spindle assembly 1
1866	GTGGCGTGTGC	30,00	4,99	Hs.278627	prenylcysteine lyase
1867	TCTGTAGTCCC	6,00	1,32	Hs.7358	Homo sapiens mRNA; cDNA DKFZp566D1146 (from clone DK)
1868	CTAATTTAACT	3,00	0,76	Hs.9194	putative glioblastoma cell differentiation-related
1869	GTCTCAGTCAT	3,00	0,76	Hs.78943	bleomycin hydrolase
1870	GACAGTCACTC	3,00	0,76	Hs.6066	Rho guanine nucleotide exchange factor (GEF) 4
1871	CCTGTAGTCCA	3,00	0,76	Hs.277028	EST
1872	CAGAGTTGTAT	3,00	0,76	Hs.109144	ESTs
1873	GGCTGAGCTCA	5,00	1,13	Hs.83004	interleukin 14
1874	GCTTTCTCAA	5,00	1,13	Hs.177153	EST
1875	CCTGTAGTCCT	20,00	3,48	Hs.179657	plasminogen activator, urokinase receptor
1876	GTGAAACACTG	8,00	1,65	Hs.145357	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY
1877	GTGAAGCCCCA	13,00	2,41	Hs.171501	ubiquitin specific protease 11
1878	CCTGTATTCCC	8,00	1,63	Hs.249718	ESTs
1879	TTCAGTGCCTG	6,00	1,30	Hs.180933	CpG binding protein

1880	GGGAAACAGGT	4,00	0,94	Hs.18368	DKFZP564B0769 protein	
1881	CCTTTTTTTTT	2,00	0,53	Hs.9956	hypothetical protein FLJ20259	
1882	GGGGCTTAGGA	2,00	0,53	Hs.89135	KIAA1528 protein	5
1883	CTAGACAGTAA	2,00	0,53	Hs.52526	KIAA0669 gene product	
1884	GTGTTCTGTGC	2,00	0,53	Hs.241567	RNA binding motif, single stranded inter- acting prote	
1885	TGCTGTAAAGG	2,00	0,53	Hs.23856	Homo sapiens HSPC091 mRNA, partial cds	10
1886	GAGGAGTGGGT	2,00	0,53	Hs.206770	zinc finger protein 297	
1887	GTAAGACCCTG	2,00	0,53	Hs.164177	ESTs	
1888	GGCCGTTAGAA	2,00	0,53	Hs.135	methylnalonate-semialdehyde dehydro- genase	15
1889	AGGCTAAAAGC	2,00	0,53	Hs.113029	ribosomal protein S25	
1890	CTGTGTAATTT	2,00	0,53	Hs.109731	ESTs	
1891	CTGAAGCGTGC	2,00	0,53	Hs.103391	Human insulin-like growth factor binding protein 5 (	20
1892	AGAACCTTCAA	9,00	1,78	Hs.181244	major histocompatibility complex, class I, A	
1893	TTCTGTGCTGG	16,00	2,84	Hs.1279	complement component 1, r subcompo- nent	25
1894	TTAGCTGAGTC	5,00	1,12	Hs.153028	cytochrome b-561	
1895	TTGGCCAGACT	9,00	1,76	Hs.91728	polymyositis/scleroderma autoantigen 1 (75kD)	
1896	TTTCATTGCCT	9,00	1,76	Hs.173159	transforming, acidic coiled-coil containing protein	30
1897	GTGGCCAGAGG	9,00	1,76	Hs.1420	fibroblast growth factor receptor 3 (achondroplasia,	
1898	ACCGTTCTGTA	6,00	1,28	Hs.117582	CGI-43 protein	35
1899	TAAGTCCAAAG	3,00	0,74	Hs.24743	hypothetical protein FLJ20171	
1900	TGCCGTAAATG	3,00	0,74	Hs.199067	v-erb-b2 avian erythroblastic leukemia viral oncogen	
1901	TGAACTTTCCT	3,00	0,74	Hs.17567	ESTs	40
1902	TAAAGATCCTC	3,00	0,74	Hs.100407	Homo sapiens mRNA; cDNA DKFZp564H2416 (from clone DK	
1903	GTGGCTCACAC	55,00	8,11	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (from clone DK	45
1904	GTGGTACACAC	5,00	1,10	Hs.250419	ESTs	
1905	GATCTCTTGGG	5,00	1,10	Hs.115947	keratin 16 (focal non-epidermolytic pal- moplantar ker	
1906	GAGGAACTCAA	7,00	1,40	Hs.5008	CGI-87 protein	50
1907	AATAAAGCCTT	6,00	1,24	Hs.3314	selenoprotein P, plasma, 1	
1908	TTTACAAGTTA	4,00	0,91	Hs.91246	hypothetical protein DKFZp547O146	
1909	AGGTCAAAAAA	4,00	0,91	Hs.149570	actin related protein 2/3 complex, subunit 4 (20 kD)	55
1910	GAGCCCCCGTG	4,00	0,91	Hs.12908	CDC42-binding protein kinase beta (DMPK-like)	
1911	GAGTAGCTGAG	3,00	0,72	Hs.260039	sarcospan (Kras oncogene-associated gene)	60
1912	GTGCTGCTCCA	2,00	0,52	Hs.7936	BAI1-associated protein 2	
1913	GAGATTGTGTT	2,00	0,52	Hs.75452	heat shock 70kD protein 2	

1914	GAAGGGGTGCT	2,00	0,52	Hs.61950	DKFZp434A0131 protein
1915	GCCACAGTACA	2,00	0,52	Hs.55044	DKFZP586H2123 protein
1916	TAATTTTACT	2,00	0,52	Hs.52256	hypothetical protein FLJ20624
1917	ACTGTTTGGCA	2,00	0,52	Hs.286110	translocase of inner mitochondrial membrane 9 (yeast)
1918	TCTGGCTAATT	2,00	0,52	Hs.262198	ESTs
1919	GTGGAAACCCA	2,00	0,52	Hs.243818	ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY
1920	TTGCCCAAGCT	2,00	0,52	Hs.213469	EST
1921	AAAACAGTGGC	2,00	0,52	Hs.184109	ribosomal protein L37a
1922	TGATGTGATAG	2,00	0,52	Hs.181159	Homo sapiens mRNA; cDNA DKFZp434F0217 (from clone DK
1923	TTTGAACCCTT	2,00	0,52	Hs.16206	uncharacterized hypothalamus protein HT008
1924	CCTATAATAAA	2,00	0,52	Hs.13885	ESTs, Weakly similar to T09A5.6 [C.elegans]
1925	AGAATCACTTA	2,00	0,52	Hs.130815	ESTs
1926	TATTTTGCAA	2,00	0,52	Hs.11449	DKFZP564O123 protein
1927	CCTATAACCCC	1,00	0,26	Hs.99410	ESTs
1928	TCCAACCTACAC	1,00	0,26	Hs.94581	sulfotransferase family, cytosolic, 2B, member 1
1929	TACCCAAAGAA	1,00	0,26	Hs.9436	ESTs, Weakly similar to NC5R_RAT NADH-CYTOCHROME B5
1930	TGTTTGTA AAA	1,00	0,26	Hs.9271	KIAA1071 protein
1931	TTTTTTTTTTC	1,00	0,26	Hs.90797	Homo sapiens clone 23620 mRNA sequence
1932	TATCTCTGCAA	1,00	0,26	Hs.82985	collagen, type V, alpha 2
1933	TTCTTCTGAAA	1,00	0,26	Hs.8087	NAG-5 protein
1934	CAGATGTTTAA	1,00	0,26	Hs.77631	glycine cleavage system protein H (aminomethyl carrier)
1935	TTTGTAATATT	1,00	0,26	Hs.75546	capping protein (actin filament) muscle Z-line, alpha
1936	ACCCAGTTGTT	1,00	0,26	Hs.75410	heat shock 70kD protein 5 (glucose-regulated protein)
1937	CTCATTGGTGG	1,00	0,26	Hs.6580	Homo sapiens clone 23718 mRNA sequence
1938	TCTTCTCACAA	1,00	0,26	Hs.656	cell division cycle 25C
1939	CCTTTGTTCAA	1,00	0,26	Hs.6107	ESTs
1940	TTAGAGATTCC	1,00	0,26	Hs.5947	mel transforming oncogene (derived from cell line NK)
1941	TCCACACCAAA	1,00	0,26	Hs.53656	ESTs, Weakly similar to D29149 proline-rich protein
1942	TGTAATGGTTT	1,00	0,26	Hs.4930	low density lipoprotein receptor-related protein 4
1943	GTA CTTACCTT	1,00	0,26	Hs.3454	ESTs, Weakly similar to KIAA0665 protein [H.sapiens]
1944	CTTAAATGGTT	1,00	0,26	Hs.29679	cofactor required for Sp1 transcriptional activation
1945	CTCCAACCTGA	1,00	0,26	Hs.285999	trinucleotide repeat containing 15
1946	TTAGGCTTTAG	1,00	0,26	Hs.285698	hypothetical protein FLJ20392
1947	GAAGATGTACG	1,00	0,26	Hs.285077	ESTs



1948	TGCCACCATAC	1,00	0,26	Hs.284138	ESTs
1949	TGTCTGTAGTC	1,00	0,26	Hs.282837	ESTs
1950	TAAAGTCCATT	1,00	0,26	Hs.278398	KIAA1117 protein
1951	CCAAGTCACTT	1,00	0,26	Hs.277543	KIAA0631 protein
1952	ATGGAATGCTA	1,00	0,26	Hs.268551	receptor-interacting serine-threonine kinase 3
1953	TTGAAACCTCG	1,00	0,26	Hs.267148	ESTs
1954	TATATCATATT	1,00	0,26	Hs.266914	hypothetical protein FLJ10355
1955	TGGCACGCTGC	1,00	0,26	Hs.250890	ESTs, Weakly similar to TOM1 [H.sapiens]
1956	ACAGAGTCTCA	1,00	0,26	Hs.249031	EST
1957	GAAATATTGAT	1,00	0,26	Hs.247043	type 1 tumor necrosis factor receptor shedding amino
1958	GTGAAACCTGA	1,00	0,26	Hs.242076	EST
1959	ATGTCAACCAA	1,00	0,26	Hs.241558	ariadne (Drosophila) homolog 2
1960	GAAAAGGGCAC	1,00	0,26	Hs.23440	KIAA1105 protein
1961	TGCAGTCTTTG	1,00	0,26	Hs.232111	ESTs
1962	CAGATTTCCAG	1,00	0,26	Hs.21893	ESTs, Weakly similar to AF121081_1 cAMP inducible 2
1963	AAAAGGAAACC	1,00	0,26	Hs.21415	Homo sapiens mRNA; cDNA DKFZp761K2024 (from clone DK
1964	ATTGTAAGCTT	1,00	0,26	Hs.210232	ESTs
1965	GTCTTAAATA	1,00	0,26	Hs.187991	DKFZP564A122 protein
1966	TCCGCAGGGAA	1,00	0,26	Hs.184592	Human clone A9A2BRB5 (CAC)n/(GTG)n repeat-containing
1967	GCTGGAGCTCA	1,00	0,26	Hs.181315	ESTs, Moderately similar to ALU4_HUMAN ALU SUBFAMILY
1968	TGTTGTAAATA	1,00	0,26	Hs.171501	ubiquitin specific protease 11
1969	GCTCCTACATT	1,00	0,26	Hs.169488	dentatorubral-pallidoluysian atrophy (atrophin-1)
1970	CAGGTGCCAAA	1,00	0,26	Hs.168350	KIAA0554 protein
1971	TGCTGCTGCCC	1,00	0,26	Hs.167046	ESTs
1972	GCCTGGGCTGA	1,00	0,26	Hs.164476	hypothetical protein FLJ20626
1973	GTATGAGGTGG	1,00	0,26	Hs.164464	ESTs
1974	GTAAACAGAAA	1,00	0,26	Hs.161554	hypothetical protein FLJ20159
1975	TGAAATAAACT	1,00	0,26	Hs.155212	methylmalonyl Coenzyme A mutase
1976	TTTTGTCAACA	1,00	0,26	Hs.154645	ESTs, Weakly similar to tyrosine kinase [H.sapiens]
1977	GCACGTGTTCT	1,00	0,26	Hs.152096	cytochrome P450, subfamily IIJ (arachidonic acid epo
1978	TTAGTCCACAG	1,00	0,26	Hs.150390	zinc finger protein 262
1979	AAATTTCAAGC	1,00	0,26	Hs.146401	small inducible cytokine subfamily E, member 1 (endo
1980	CCCAGCTACTT	1,00	0,26	Hs.143961	ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY
1981	AAACCAGGAAA	1,00	0,26	Hs.139120	ribonuclease P (30kD)
1982	AATTTCAAGAA	1,00	0,26	Hs.119591	adaptor-related protein complex 2, sigma 1 subunit
1983	TACCCTAAAAT	1,00	0,26	Hs.117325	Homo sapiens cDNA FLJ11166 fis, clone PLACE1007242

1984	GGACTGTAGTG	1,00	0,26	Hs.11711	KIAA0329 gene product
1985	CTCCCGCCGGA	1,00	0,26	Hs.109445	KIAA1020 protein
1986	TGAAGTGCCCT	1,00	0,26	Hs.106932	ESTs
1987	GAAGAGGCTGG	1,00	0,26	Hs.105962	ESTs
1988	TTCCCTTCTTC	9,00	1,69	Hs.814	major histocompatibility complex, class II, DP beta
1989	AACCCGGAAGG	8,00	1,54	Hs.87497	butyrophilin, subfamily 3, member A2
1990	GTGGCGCGTGC	16,00	2,66	Hs.24135	hypothetical protein DKFZp761C241
1991	TACCCTAAAC	103,00	13,65	Hs.165662	KIAA0675 gene product
1992	CCTGTGATCCC	40,00	5,77	Hs.249982	cathepsin B
1993	CCGGCCCTACC	4,00	0,89	Hs.271473	epithelial protein up-regulated in carcinoma, membra
1994	GCACGCGTAAC	4,00	0,89	Hs.169552	ESTs, Weakly similar to BRDT [H.sapiens]
1995	AACAAGGTGAG	3,00	0,71	Hs.94952	ESTs, Highly similar to transcription elongation fac
1996	TGCGTCCCTCC	3,00	0,71	Hs.6179	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17 (72k
1997	GACCCTTTTGG	3,00	0,71	Hs.272848	Homo sapiens mRNA; cDNA DKFZp434G1310 (from clone DK
1998	GATTTTTCTGA	3,00	0,71	Hs.241567	RNA binding motif, single stranded interacting prote
1999	TGATTCTGTTT	3,00	0,71	Hs.146428	collagen, type V, alpha 1
2000	CCCGGCTAATT	14,00	2,35	Hs.102926	ESTs
2001	GTGAAGCCCTG	16,00	2,61	Hs.105407	ectodermal dysplasia 1, anhidrotic
2002	ACTGAAAGAAG	5,00	1,05	Hs.169756	complement component 1, s subcomponent
2003	CTGAGAGCTGG	14,00	2,31	Hs.78501	growth arrest-specific 6
2004	GTTCCAGCAGC	4,00	0,88	Hs.23918	Homo sapiens clone 25116 mRNA sequence
2005	CCATTGCGCTC	4,00	0,88	Hs.204299	ESTs, Moderately similar to alternatively spliced pr
2006	GGATGCGCAGG	4,00	0,88	Hs.168541	Homo sapiens mRNA full length insert cDNA clone EURO
2007	TTGGTGGAGGT	2,00	0,50	Hs.76294	CD63 antigen (melanoma 1 antigen)
2008	AGAATTATGGG	2,00	0,50	Hs.6975	PRO1073 protein
2009	TGTGGTGGCAC	2,00	0,50	Hs.46624	HSPC043 protein
2010	CAGTTCTTGAT	2,00	0,50	Hs.284217	serologically defined colon cancer antigen 33
2011	GCAAGACCCCG	2,00	0,50	Hs.262335	ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C
2012	AAAACAAAACA	2,00	0,50	Hs.24734	oxysterol binding protein
2013	AAGACTGACAA	2,00	0,50	Hs.225951	topoisomerase-related function protein 4
2014	TTCTCCTCTTT	2,00	0,50	Hs.22451	hypothetical protein FLJ10357
2015	TCAATCAGTGA	2,00	0,50	Hs.127270	ESTs
2016	TGGGGTCCCCA	2,00	0,50	Hs.123661	ESTs
2017	CCATTGCACTG	11,00	1,90	Hs.142457	ESTs, Moderately similar to alternatively spliced pr
2018	AATAAATTCCT	14,00	2,30	Hs.76307	neuroblastoma, suppression of tumorigenicity 1

2019	GTGGCAGATGC	7,00	1,34	Hs.273539	ESTs, Weakly similar to ALU2_HUMAN ALU SUBFAMILY SB	
2020	CCTGTTATCCC	7,00	1,34	Hs.228142	EST	
2021	GCGAAACTCCA	7,00	1,34	Hs.112860	KIAA1353 protein	5
2022	GTGAAACCTCG	38,00	5,28	Hs.194408	KIAA1244 protein	
2023	GGCAGACACAT	3,00	0,69	Hs.33287	nuclear factor I/B	
2024	AAAGAGAAGAG	3,00	0,69	Hs.22969	ESTs	
2025	ACAAAGCATTT	40,00	5,46	Hs.103391	Human insulin-like growth factor binding protein 5 (	10
2026	TTTAGTGACGT	7,00	1,32	Hs.7104	Kruppel-like factor 13	
2027	AGCCACCACGC	17,00	2,63	Hs.60772	ESTs	
2028	GCGAAACCTCG	8,00	1,46	Hs.210473	ESTs, Weakly similar to GELS_HUMAN GELSOLIN PRECURSO	15
2029	GCAGTTGGATC	4,00	0,86	Hs.284932	Homo sapiens clone 24650 ubiquitin hydrolase mRNA, p	
2030	CTTGTGAAGTG	4,00	0,86	Hs.283681	ESTs	20
2031	GTGGCTCACGC	56,00	7,21	Hs.228230	EST	
2032	CAGCTATTTCA	10,00	1,69	Hs.153179	fatty acid binding protein 5 (psoriasis- associated)	
2033	CACACACACAC	4,00	0,84	Hs.63984	cadherin 13, H-cadherin (heart)	25
2034	CCACCACACTC	4,00	0,84	Hs.256696	EST, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	
2035	CAAGGGTGACA	4,00	0,84	Hs.170222	solute carrier family 9 (sodium/hydrogen exchanger),	30
2036	GCAGCACTTAT	2,00	0,48	Hs.82035	GAP-like protein	
2037	CCTGACCTCAA	2,00	0,48	Hs.7874	muskelin 1, intracellular mediator con- taining kelch	
2038	GGGGTATGGTT	2,00	0,48	Hs.76144	platelet-derived growth factor receptor, beta polype	35
2039	AGCAGCCGCTC	2,00	0,48	Hs.7104	Kruppel-like factor 13	
2040	CTCCTGGCCCA	2,00	0,48	Hs.5321	ARP3 (actin-related protein 3, yeast) homolog	40
2041	TTATGCCTCCA	2,00	0,48	Hs.43314	ESTs	
2042	TACTTCCTGCG	2,00	0,48	Hs.38039	ESTs	
2043	CCTTGCCCAGG	2,00	0,48	Hs.3144	Cas-Br-M (murine) ectropic retroviral transforming s	45
2044	GTAGGGTTCCT	2,00	0,48	Hs.278597	protein tyrosine phosphatase, non- receptor type 18 (	
2045	ATAACCAAATG	2,00	0,48	Hs.25726	transposon-derived Buster1 transpo- sase-like protein	50
2046	CCTGTGAATAG	2,00	0,48	Hs.200647	EST	
2047	TGACCAGGGTC	2,00	0,48	Hs.167827	Homo sapiens clone HH419 unknown mRNA	
2048	CAGACCCAAAA	2,00	0,48	Hs.167558	zinc finger protein 161	55
2049	TTCTCATAATC	2,00	0,48	Hs.164919	ESTs, Highly similar to KPC2_HUMAN PROTEIN KINASE C,	
2050	ACTGATGCAAG	2,00	0,48	Hs.161049	ESTs	
2051	AACTCTGATAT	2,00	0,48	Hs.151046	hypothetical protein FLJ11193	60
2052	GGGCATCTCCA	2,00	0,48	Hs.107000	ESTs	
2053	TGGATGTCTGT	1,00	0,24	Hs.96716	ESTs	

2054	TATTAGAAGCA	1,00	0,24	Hs.91065	hypothetical protein DKFZp761B2423
2055	CACTGAATATG	1,00	0,24	Hs.86948	small nuclear ribonucleoprotein D1 polypeptide (16kD)
2056	AGTTAATAAAG	1,00	0,24	Hs.8065	Homo sapiens mRNA full length insert cDNA clone EURO
2057	TTATATTTTCT	1,00	0,24	Hs.8021	KIAA1058 protein
2058	GTCACCAAACA	1,00	0,24	Hs.79283	selectin P ligand
2059	TTACACTGTAA	1,00	0,24	Hs.78687	neutral sphingomyelinase (N-SMase) activation associ
2060	AAGTTGCATCT	1,00	0,24	Hs.74649	cytochrome c oxidase subunit VIc
2061	TAGACATTTGA	1,00	0,24	Hs.74649	cytochrome c oxidase subunit VIc
2062	TTCATAGGTAA	1,00	0,24	Hs.7312	ESTs
2063	CATTTTAGGCA	1,00	0,24	Hs.72782	hypothetical protein FLJ11171
2064	ATACTATAATT	1,00	0,24	Hs.6966	Human DNA sequence from clone RP1-187J11 on chromoso
2065	CTTCGCTTTGT	1,00	0,24	Hs.69485	ESTs, Weakly similar to similar to other protein pho
2066	ATGATATATGC	1,00	0,24	Hs.6831	Homo sapiens clone 1400 unknown protein mRNA, partia
2067	GCCCCCTTACA	1,00	0,24	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat region mRNA
2068	TCAGTCCCTGT	1,00	0,24	Hs.3685	hypothetical protein FLJ20209
2069	AATTTTCATTA	1,00	0,24	Hs.35092	ESTs
2070	GCCAGTCCACT	1,00	0,24	Hs.34782	ESTs, Moderately similar to transducin [H.sapiens]
2071	TAGAGAGTTTA	1,00	0,24	Hs.29643	ESTs
2072	GCTGTCCCCTC	1,00	0,24	Hs.278422	DKFZP586G1122 protein
2073	GTGAAAGCCGT	1,00	0,24	Hs.270662	ESTs, Weakly similar to transformation-related prote
2074	TCTTCCAGAAA	1,00	0,24	Hs.256585	ESTs
2075	TTGGCCGGGAT	1,00	0,24	Hs.254900	ESTs
2076	GTAAAGAATGT	1,00	0,24	Hs.24790	ESTs
2077	AAATTTTGTGA	1,00	0,24	Hs.24650	ESTs, Moderately similar to AF133913_1 ARL-6 interac
2078	AACGCTGCAAA	1,00	0,24	Hs.24174	KIAA0876 protein
2079	GTACCCTAAAA	1,00	0,24	Hs.239970	ESTs, Weakly similar to b34I8.1 [H.sapiens]
2080	TAATCTTTTTT	1,00	0,24	Hs.231463	EST
2081	AAATTGTATGT	1,00	0,24	Hs.22826	tropomodulin 3 (ubiquitous)
2082	CCACTACATTC	1,00	0,24	Hs.22573	ESTs
2083	GCCGCACTCAG	1,00	0,24	Hs.200577	ESTs
2084	TCTTGTCATAC	1,00	0,24	Hs.198998	conserved helix-loop-helix ubiquitous kinase
2085	CAGCACCTGAT	1,00	0,24	Hs.198281	pyruvate kinase, muscle
2086	TTGAATAAAAG	1,00	0,24	Hs.198161	phospholipase A2, group IVB (cytosolic)
2087	GGGAAGTGTGC	1,00	0,24	Hs.197733	ESTs, Weakly similar to TRP7_HUMAN TRANSIENT RECEPTO
2088	CCTGGCCTACC	1,00	0,24	Hs.19585	KRAB-zinc finger protein SZF1-1
2089	TTATTTTCAA	1,00	0,24	Hs.194293	ESTs
2090	TCTCTCTGCCT	1,00	0,24	Hs.184987	ESTs

2091	AGAGGAAGTAA	1,00	0,24	Hs.177537	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
2092	ACCAAAAAAAAA	1,00	0,24	Hs.173724	creatine kinase, brain
2093	GGGACATTTAT	1,00	0,24	Hs.173108	Homo sapiens clone 24523 mRNA se- quence
2094	TACCATCCATA	1,00	0,24	Hs.169476	glyceraldehyde-3-phosphate dehydroge- nase
2095	TTGATGAAGAA	1,00	0,24	Hs.168075	karyopherin (importin) beta 2
2096	GCCCGGTGCCC	1,00	0,24	Hs.1665	zinc finger protein homologous to Zfp-36 in mouse
2097	AAGAACTGTTT	1,00	0,24	Hs.159456	zinc finger protein 288
2098	CCAGCAACTGT	1,00	0,24	Hs.145279	SET translocation (myeloid leukemia- associated)
2099	ATGGTGCGTGC	1,00	0,24	Hs.140498	ESTs, Weakly similar to ALUE_HUMAN !!!! ALU CLASS E
2100	CTCTTCAGGGT	1,00	0,24	Hs.13781	Homo sapiens cDNA FLJ11302 fis, clone PLACE1009971
2101	TCAATGTGAAA	1,00	0,24	Hs.13467	Homo sapiens BAC clone RP11-121A8 from 7p14-p13
2102	CTTAATACTAC	1,00	0,24	Hs.13273	KIAA0592 protein
2103	GGCTGCAGTAT	1,00	0,24	Hs.129892	KIAA0522 protein
2104	GGAAGCTGAAG	1,00	0,24	Hs.128629	ESTs
2105	CCTCGGGCATC	1,00	0,24	Hs.126735	ESTs
2106	TTTTCTTGCTG	1,00	0,24	Hs.120907	Homo sapiens mRNA; cDNA DKFZp547D135 (from clone DKF
2107	GCCTTGCCTCT	1,00	0,24	Hs.118837	ESTs
2108	CTTTAAAAAAA	1,00	0,24	Hs.118162	fibronectin 1
2109	TGCGGAAAAAA	1,00	0,24	Hs.113207	G protein-coupled receptor 30
2110	TGACTTTCTGC	1,00	0,24	Hs.11123	ESTs, Weakly similar to B38919 hypo- thetical protein
2111	CATTACATAT	1,00	0,24	Hs.109438	Homo sapiens clone 24775 mRNA se- quence
2112	AATGTGTTACT	1,00	0,24	Hs.105751	Ste20-related serine/threonine kinase
2113	ATCTTTATTCC	1,00	0,24	Hs.10351	KIAA0308 protein
2114	TGTTTGAATTC	1,00	0,24	Hs.103422	Homo sapiens mRNA; cDNA DKFZp434F1622 (from clone DK
2115	ACAACACCCCA	5,00	1,00	Hs.21453	Homo sapiens mRNA for inositol 1,4,5- trisphosphate 3
2116	CTGGAAATAAA	3,00	0,67	Hs.69745	ferredoxin reductase
2117	TTATTTATGAA	3,00	0,67	Hs.245188	tissue inhibitor of metalloproteinase 3 (Sorsby fund
2118	TACCAAGGATT	3,00	0,67	Hs.21729	splicing factor 3a, subunit 1, 120kD
2119	GTGCCAAACAC	3,00	0,67	Hs.172216	chromogranin A (parathyroid secretory protein 1)
2120	CCCGGCCCAAA	3,00	0,67	Hs.133207	PTPRF interacting protein, binding pro- tein 1 (liprin
2121	AGAATTGCTTG	37,00	4,88	Hs.56542	X-prolyl aminopeptidase (aminopepti- dase P) 1, solubl
2122	TCTCTGATGCT	34,00	4,52	Hs.6441	tissue inhibitor of metalloproteinase 2
2123	ACACTGCACTC	7,00	1,27	Hs.200454	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S

2124	GAAATGAGCAG	6,00	1,13	Hs.77293	KIAA0127 gene product
2125	GCTGGATGCGG	6,00	1,13	Hs.18075	chromosome 9 open reading frame 3
2126	GCAAAACCCCTA	6,00	1,13	Hs.108740	DKFZP586A0522 protein
2127	TTTGCTCTCCC	15,00	2,28	Hs.75350	vinculin
2128	GGAGGCTGAGG	48,00	6,01	Hs.185973	membrane fatty acid (lipid) desaturase
2129	GTAAAACCCCA	21,00	2,98	Hs.18955	Homo sapiens cDNA FLJ20667 fis, clone KAIA596
2130	GGAGGGGGGCTT	30,00	3,99	Hs.77886	lamin A/C
2131	AGCTAAGTTTG	4,00	0,83	Hs.19447	ESTs, Weakly similar to CL36_HUMAN LIM DOMAIN PROTEI
2132	CACACAGTTTT	18,00	2,62	Hs.204354	ras homolog gene family, member B
2133	ATGGCGGGTGC	9,00	1,52	Hs.172382	hypothetical protein FLJ20001
2134	GACTTGTATAT	6,00	1,12	Hs.81328	nuclear factor of kappa light polypeptide gene enhan
2135	ATAGTACAGCC	3,00	0,66	Hs.6361	MEK partner 1
2136	AGCCACCGCTC	3,00	0,66	Hs.6195	ESTs
2137	GGCAGGATGAT	3,00	0,66	Hs.274319	hypothetical protein FLJ10509
2138	GCCTGGGACCT	3,00	0,66	Hs.180871	protein kinase C, alpha binding protein
2139	ACAGCCGTGGG	3,00	0,66	Hs.123090	SWI/SNF related, matrix associated, actin dependent
2140	AGCCGAGATCA	5,00	0,97	Hs.277663	EST, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE
2141	AGCCTTTGTTG	26,00	3,47	Hs.9930	collagen-binding protein 2 (colligen 2)
2142	GTGTGCCTCCA	6,00	1,10	Hs.75254	interferon regulatory factor 3
2143	TGGAGAAGAGC	8,00	1,37	Hs.179526	upregulated by 1,25-dihydroxyvitamin D-3
2144	GGCCCCATTGC	4,00	0,81	Hs.173421	Human clone CE29 8.1 (CAC)n/(GTG)n repeat-containing
2145	AATATTCATAG	2,00	0,47	Hs.8583	similar to APOBEC1
2146	GCTCCGTAAGG	2,00	0,47	Hs.80712	KIAA0202 protein
2147	GAGGTGCCCCA	2,00	0,47	Hs.77955	ESTs
2148	AGTGTATTTTT	2,00	0,47	Hs.76473	insulin-like growth factor 2 receptor
2149	TAAACCTAAAG	2,00	0,47	Hs.60548	hypothetical protein PRO1635
2150	AGTCAAGCCCC	2,00	0,47	Hs.57687	four and a half LIM domains 3
2151	TATCAAAACAT	2,00	0,47	Hs.258939	EST
2152	ATCCTACTGTT	2,00	0,47	Hs.239218	uncharacterized hypothalamus protein HCDASE
2153	GCACCAAATGA	2,00	0,47	Hs.23585	KIAA1078 protein
2154	CCAATGCTATG	2,00	0,47	Hs.22753	Homo sapiens mRNA; cDNA DKFZp434K0926 (from clone DK
2155	CATCGTTACAT	2,00	0,47	Hs.173802	KIAA0603 gene product
2156	TAACCAAAAAC	2,00	0,47	Hs.169241	ELK4, ETS-domain protein (SRF accessory protein 1)
2157	CTGAAACCCCA	2,00	0,47	Hs.162132	ESTs
2158	GGAAGGCAAGC	2,00	0,47	Hs.144998	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ
2159	GAAAGGTGGTT	2,00	0,47	Hs.14394	hypothetical protein FLJ20157
2160	TCATAACCTTG	2,00	0,47	Hs.124029	inositol polyphosphate-5-phosphatase, 40kD
2161	TACCCCATAAA	5,00	0,96	Hs.281083	ESTs

2162	CGCCCCCTGCG	6,00	1,09	Hs.135805	ESTs, Weakly similar to KIAA1323 protein [H.sapiens]	
2163	ACAAAGCCCCA	3,00	0,65	Hs.8583	similar to APOBEC1	
2164	CCTATAGTCCT	3,00	0,65	Hs.41694	origin recognition complex, subunit 2 (yeast homolog)	5
2165	CCAGTACAGCC	3,00	0,65	Hs.140978	Homo sapiens mRNA; cDNA DKFZp762H106 (from clone DKF	
2166	CTGCTGCTGGT	3,00	0,65	Hs.12289	Cdc42 effector protein 2	10
2167	CTTAATCTTGT	4,00	0,80	Hs.75462	BTG family, member 2	
2168	GCCACACCCCC	4,00	0,80	Hs.113916	Burkitt lymphoma receptor 1, GTP-binding protein	
2169	TCCTCCCTACT	14,00	2,04	Hs.70266	yeast Sec31p homolog	15
2170	GTGAGACCCCA	12,00	1,80	Hs.198671	ESTs	
2171	CAGATGCAAAA	11,00	1,68	Hs.89506	paired box gene 6 (aniridia, keratitis)	
2172	CCCCAGGAGAA	5,00	0,93	Hs.169902	solute carrier family 2 (facilitated glucose transpo	20
2173	CTTCTGGGGAC	6,00	1,06	Hs.75082	ras homolog gene family, member G (rho G)	
2174	GTGGCTTACAC	4,00	0,79	Hs.264482	Homo sapiens mRNA; cDNA DKFZp761A0411 (from clone DK	25
2175	GCGAGACCCCA	4,00	0,79	Hs.15681	ESTs	
2176	TAAACTATTGG	3,00	0,63	Hs.78851	KIAA0217 protein	
2177	GACGGCTGCAA	3,00	0,63	Hs.4909	dickkopf (Xenopus laevis) homolog 3	30
2178	GTGAAACCGTC	3,00	0,63	Hs.30596	Homo sapiens mRNA full length insert cDNA clone EURO	
2179	CCACTGGACTC	3,00	0,63	Hs.253913	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S	
2180	TGTTAGCAAAT	3,00	0,63	Hs.22666	ESTs	35
2181	AAGTACGAGGA	3,00	0,63	Hs.22660	ESTs	
2182	CTGTTGGAAAA	3,00	0,63	Hs.209863	ESTs	
2183	AACCACTGTGC	3,00	0,63	Hs.188037	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY	40
2184	CTTCTCCAAAA	2,00	0,46	Hs.99949	prolactin-induced protein	
2185	GTGGTCAAGTT	2,00	0,46	Hs.92127	ESTs	
2186	CCTTTGCTGAG	2,00	0,46	Hs.7442	Human DNA sequence from clone 742C19 on chromosome 2	45
2187	TTGCTGCCAGC	2,00	0,46	Hs.5566	gap junction protein, beta 2, 26kD (connexin 26)	
2188	TGAATTTCCTG	2,00	0,46	Hs.30057	Homo sapiens clone 24749 and 24750 mRNA sequences	50
2189	GTGGTATATGC	2,00	0,46	Hs.279893	hypothetical protein FLJ20342	
2190	GTGGTGCACTC	2,00	0,46	Hs.268573	Homo sapiens mRNA; cDNA DKFZp762N226 (from clone DKF	
2191	GTGGCACAAAGC	2,00	0,46	Hs.258487	EST	55
2192	AGCCACCATAC	2,00	0,46	Hs.236051	EST	
2193	TAAAACCGTTT	2,00	0,46	Hs.182280	MADS box transcription enhancer factor 2, polypeptid	
2194	CCTTGTTTAAC	2,00	0,46	Hs.173965	ribosomal protein S6 kinase, 90kD, polypeptide 3	60
2195	GCTCACTGCAA	2,00	0,46	Hs.163385	EST	

2196	TGCCTTGGGCT	2,00	0,46	Hs.1497	retinoic acid receptor, gamma
2197	TTATTGTTCCC	2,00	0,46	Hs.12126	hepatocellular carcinoma-associated antigen 112
2198	GGGACAACCCA	2,00	0,46	Hs.11530	ESTs
2199	GTTTCTTACTG	2,00	0,46	Hs.106204	KIAA1327 protein
2200	TTTTGCTTTT	2,00	0,46	Hs.102267	lysyl oxidase
2201	ATTTTCATCAA	2,00	0,46	Hs.101282	Homo sapiens mRNA; cDNA DKFZp434B102 (from clone DKF
2202	TACAGAATGTG	1,00	0,23	Hs.99196	ESTs
2203	TTGTATTGTTG	1,00	0,23	Hs.98445	ESTs
2204	GGGCAGAAGGC	1,00	0,23	Hs.9585	ESTs
2205	TATTGGCCTGG	1,00	0,23	Hs.79572	cathepsin D (lysosomal aspartyl protease)
2206	TGACTGTAAAA	1,00	0,23	Hs.75621	protease inhibitor 1 (anti-elastase), alpha-1-antitr
2207	ACCTGCTTCCC	1,00	0,23	Hs.75458	ribosomal protein L18
2208	TGATACAGAAA	1,00	0,23	Hs.69504	ESTs
2209	AATGAATTCTT	1,00	0,23	Hs.5613	Homo sapiens mRNA; cDNA DKFZp564E2222 (from clone DK
2210	ATTTTGTCACT	1,00	0,23	Hs.5459	KIAA1436 protein
2211	CACCCCTTACT	1,00	0,23	Hs.5437	Tax1 (human T-cell leukemia virus type I) binding pr
2212	CTGGTGGGCCA	1,00	0,23	Hs.5338	carbonic anhydrase XII
2213	CTTTGAAATAG	1,00	0,23	Hs.50476	ESTs
2214	AGTCCTGCTTC	1,00	0,23	Hs.44565	ESTs
2215	TAACATTGAGA	1,00	0,23	Hs.43756	ESTs
2216	CTGAGAAGCGG	1,00	0,23	Hs.41055	ESTs, Highly similar to RL2A_HUMAN 60S RIBOSOMAL PRO
2217	TATATATAGAG	1,00	0,23	Hs.34853	inhibitor of DNA binding 4, dominant negative helix-
2218	GTCTGCTCCAG	1,00	0,23	Hs.32978	proprotein convertase subtilisin/kexin type 7
2219	CCCCCGAGGCT	1,00	0,23	Hs.31019	ESTs
2220	AATGAAAAATT	1,00	0,23	Hs.30888	cytochrome c oxidase subunit VIIa polypeptide 2 like
2221	TTTGTACTAAT	1,00	0,23	Hs.29846	Human DNA sequence from clone 717M23 on chromosome 2
2222	TTCCATTATCA	1,00	0,23	Hs.29356	ESTs
2223	GTTTAAAAAGC	1,00	0,23	Hs.29032	ESTs
2224	CAATTTAAAGT	1,00	0,23	Hs.286249	ESTs
2225	TGTATTTGTAA	1,00	0,23	Hs.286056	ESTs
2226	GTGGCGTGCCT	1,00	0,23	Hs.282652	EST
2227	TAAAATGTGAC	1,00	0,23	Hs.268447	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX
2228	AACAATAAAAA	1,00	0,23	Hs.268135	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAMILY SB2
2229	GAAACACGTAG	1,00	0,23	Hs.26407	ESTs
2230	ACTTTAACAGG	1,00	0,23	Hs.252387	cadherin EGF LAG seven-pass G-type receptor 1
2231	AGCCCCACAAA	1,00	0,23	Hs.250570	ESTs



2232	TGGTGAGATGA	1,00	0,23	Hs.224829	ESTs
2233	GGCACC GCGTG	1,00	0,23	Hs.20677	KIAA1303 protein
2234	CAAGGATAAGA	1,00	0,23	Hs.2001	thromboxane A synthase 1 (platelet, cytochrome P450,
2235	CGCCCCGGCGG	1,00	0,23	Hs.196244	ESTs
2236	GAAGAGAAGGT	1,00	0,23	Hs.180455	RAD23 (S. cerevisiae) homolog A
2237	CAGATTTTGTG	1,00	0,23	Hs.177656	calmodulin 1 (phosphorylase kinase, delta)
2238	ATTAGTTACAA	1,00	0,23	Hs.177635	KIAA1095 protein
2239	CCCACCACATT	1,00	0,23	Hs.170610	ESTs
2240	CTGCTAACCCA	1,00	0,23	Hs.170310	cat eye syndrome chromosome region, candidate 1
2241	GTTCTCTGCTT	1,00	0,23	Hs.169078	Human clone A9A2BRB6 (CAC)n/(GTG)n repeat-containing
2242	TATGTACAGTT	1,00	0,23	Hs.163001	hypothetical protein PRO0907
2243	AACCCGGGAGT	1,00	0,23	Hs.161974	EST
2244	GTAACCTCAAA	1,00	0,23	Hs.161930	EST
2245	TTCAATTTCTT	1,00	0,23	Hs.159971	SWI/SNF related, matrix associated, actin dependent
2246	AGCTAAAAAAA	1,00	0,23	Hs.15953	hypothetical protein FLJ10120
2247	TTATTTAAAG	1,00	0,23	Hs.158135	KIAA0981 protein
2248	GACTCCACATT	1,00	0,23	Hs.156637	Cas-Br-M (murine) ectropic retroviral transforming s
2249	AGACAAAATTA	1,00	0,23	Hs.153487	signal transducing adaptor molecule (SH3 domain and
2250	ACTGAGAAGAG	1,00	0,23	Hs.130761	ESTs, Moderately similar to AF151803_1 CGI-45 protei
2251	GGTGCTGAATA	1,00	0,23	Hs.12489	ESTs
2252	GATTTCTTTGA	1,00	0,23	Hs.119651	glypican 3
2253	TGTCAAAAGAG	1,00	0,23	Hs.118578	Homo sapiens cDNA FLJ20053 fis, clone COL00809
2254	ACGGGGAGAGT	1,00	0,23	Hs.117582	CGI-43 protein
2255	TGGCTTTATCC	1,00	0,23	Hs.11506	Human clone 23589 mRNA sequence
2256	GTTGCGTGTCC	1,00	0,23	Hs.108300	NOT3 (negative regulator of transcription 3, yeast)
2257	TAAACGGCCTC	1,00	0,23	Hs.10632	hypothetical protein DKFZp762M136
2258	GGCCAGAATGA	1,00	0,23	Hs.102708	DKFZP434A043 protein
2259	TGAAGCAAAAA	1,00	0,23	Hs.100407	Homo sapiens mRNA; cDNA DKFZp564H2416 (from clone DK
2260	TCACAGCTGTG	19,00	2,52	Hs.77054	B-cell translocation gene 1, anti-proliferative
2261	AGAAAAAAAAA	70,00	7,56	Hs.251680	(Manual assignment) not unique, contains loricrin
2262	GTGGCGCACGC	11,00	1,65	Hs.135723	glycolipid transfer protein
2263	TCTGTACACCT	19,00	2,51	Hs.182740	ribosomal protein S11
2264	AGGGAGGGGCC	6,00	1,05	Hs.172153	glutathione peroxidase 3 (plasma)
2265	AGGACACCGCC	5,00	0,91	Hs.77793	c-src tyrosine kinase
2266	CGAGGGCACTC	5,00	0,91	Hs.26915	spectrin, beta, non-erythrocytic 2
2267	TGCTGCCAGAC	4,00	0,77	Hs.79219	RaIGDS-like gene; KIAA0959 protein
2268	TACTGGTTTAT	4,00	0,77	Hs.30299	IGF-II mRNA-binding protein 2

2269	CCCCACCTAA	15,00	2,04	Hs.77422	proteolipid protein 2 (colonic epithelium-enriched)
2270	TGAATGATACG	4,00	0,76	Hs.278614	protease, serine, 15
2271	TGAAACTGCAA	4,00	0,76	Hs.147189	HYA22 protein
2272	TGAGTCTGGCT	10,00	1,48	Hs.4055	chromosome 21 open reading frame 50
2273	GGAGTGTGCTC	29,00	3,36	Hs.9615	myosin regulatory light chain 2, smooth muscle isofo
2274	TCATCGGGCTG	2,00	0,44	Hs.78335	microtubule-associated protein, RP/EB family, member
2275	GAGACCTTGGA	2,00	0,44	Hs.72249	protease-activated receptor 3
2276	CACTGGACGAG	2,00	0,44	Hs.71574	ESTs
2277	TGTACTTATTA	2,00	0,44	Hs.6906	v-ral simian leukemia viral oncogene homolog A (ras
2278	ACCACCCTGTT	2,00	0,44	Hs.4864	KIAA0892 protein
2279	ATTTCTCATTC	2,00	0,44	Hs.36794	D-type cyclin-interacting protein 1
2280	GGACATTTTTC	2,00	0,44	Hs.16986	hypothetical protein FLJ11046
2281	CATCTTAAATG	2,00	0,44	Hs.15467	hypothetical protein FLJ20725
2282	GAATCATTTAT	2,00	0,44	Hs.154668	KIAA0391 gene product
2283	ATCAAATGCAA	9,00	1,36	Hs.79070	v-myc avian myelocytomatosis viral oncogene homolog
2284	AGCACCAGAAC	3,00	0,61	Hs.60103	KIAA0690 protein
2285	TCCTGACCACC	3,00	0,61	Hs.26002	LIM domain binding 1
2286	CTTATAATCCC	3,00	0,61	Hs.259541	ESTs
2287	ACCCATCGCCT	3,00	0,61	Hs.165428	ESTs
2288	CCATTGCACTA	3,00	0,61	Hs.115140	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
2289	TACCCAGAAC	9,00	1,35	Hs.145320	ESTs
2290	CTCTCACCCTG	18,00	2,27	Hs.75108	ribonuclease/angiogenin inhibitor
2291	CAAGGGCTTGC	15,00	1,96	Hs.156764	RAP1B, member of RAS oncogene family
2292	TTTGCACCTGT	7,00	1,12	Hs.75188	wee1+ (S. pombe) homolog
2293	GCCAGGAGCTA	7,00	1,12	Hs.18141	ladinin 1
2294	TAAAATACTCC	4,00	0,75	Hs.8125	Homo sapiens mRNA; cDNA DKFZp586E1521 (from clone DK
2295	TGATTGATTTG	4,00	0,75	Hs.5912	F-box only protein 7
2296	TAAAACTTTC	4,00	0,75	Hs.204096	lipophilin B (uteroglobin family member), prostatein
2297	TCCTGCACTC	16,00	2,06	Hs.261038	ESTs
2298	ACCAAAGCCCC	10,00	1,43	Hs.284281	Human putative ribosomal protein S1 mRNA
2299	AATAGGGTCAA	8,00	1,22	Hs.64797	amyloid beta (A4) precursor-like protein 2
2300	CCTATAGTCCC	11,00	1,53	Hs.140697	ESTs, Weakly similar to unnamed protein product [H.s
2301	CCTCCCTGCTC	3,00	0,59	Hs.90790	ESTs
2302	ACCTAGCCACT	3,00	0,59	Hs.89463	potassium large conductance calcium-activated channe
2303	CAGCTCAGCTG	3,00	0,59	Hs.58414	filamin C, gamma (actin-binding protein-280)
2304	TCAATAAATGT	3,00	0,59	Hs.106747	ESTs, Weakly similar to AF217508_1

					uncharacterized b
2305	CACTCACACCC	4,00	0,73	Hs.24447	sigma receptor (SR31747 binding protein 1)
2306	GTGAAACCTGT	7,00	1,10	Hs.272795	hypothetical protein FLJ20359
2307	ATCATACCACG	2,00	2,80	Hs.97259	ESTs
2308	AACGGGGGCCCT	2,00	2,80	Hs.97203	small inducible cytokine subfamily A (Cys-Cys), memb
2309	TCCCCGGTCAG	2,00	2,80	Hs.80562	gelsolin (amyloidosis, Finnish type)
2310	GCGCATCAAAA	2,00	2,80	Hs.59761	ESTs
2311	AATTTTCAGGCA	2,00	2,80	Hs.5476	serine protease inhibitor, Kazal type, 5
2312	ATCCCACTACT	2,00	2,80	Hs.3991	ESTs
2313	ATCCGCTGGGG	2,00	2,80	Hs.30954	phosphomevalonate kinase
2314	ACTGTGGACTG	2,00	2,80	Hs.285122	ESTs, Weakly similar to S53869 laminin beta-2 chain
2315	AGAGAAGAATG	2,00	2,80	Hs.2841	neuromedin U
2316	AGGATTGTTTG	2,00	2,80	Hs.283545	ESTs
2317	GTAAAGATTTG	2,00	2,80	Hs.278629	ESTs
2318	ACTATGGATAG	2,00	2,80	Hs.275511	EST
2319	GTTAGGCACGA	2,00	2,80	Hs.272800	hypothetical protein FLJ20456
2320	TGCCACCAACA	2,00	2,80	Hs.271411	beta-site APP-cleaving enzyme 2
2321	AAATGGGAACA	2,00	2,80	Hs.271226	ESTs
2322	GGGGTTTGT	2,00	2,80	Hs.258455	EST
2323	ACATAGTCTGA	2,00	2,80	Hs.25766	ESTs
2324	TATGCTGAAAT	2,00	2,80	Hs.255277	ESTs
2325	TTCACCTCATT	2,00	2,80	Hs.254914	EST, Weakly similar to NICE-1 protein [H.sapiens]
2326	TCTTGCAACA	2,00	2,80	Hs.25431	KIAA1219 protein
2327	CAATAAAATTC	2,00	2,80	Hs.250236	EST
2328	GGCTTTTGTT	2,00	2,80	Hs.230730	EST, Moderately similar to RLA1 HUMAN 60S ACIDIC RIB
2329	AGTTTGTTTTA	2,00	2,80	Hs.212570	EST
2330	TTCCACTGTGA	2,00	2,80	Hs.198862	fibulin 2
2331	CAAGTGGGTGT	2,00	2,80	Hs.187685	ESTs
2332	TGCAGGGACCT	2,00	2,80	Hs.173043	metastasis-associated 1-like 1
2333	TACTTCACCCA	2,00	2,80	Hs.169517	aldehyde dehydrogenase 5
2334	CTTTGATTTAT	2,00	2,80	Hs.165590	ribosomal protein S13
2335	TGTTGTTTTT	2,00	2,80	Hs.145211	Homo sapiens mRNA; cDNA DKFZp434K1111 (from clone DK
2336	GTAGCGCCTCC	2,00	2,80	Hs.143212	cystatin F (leukocystatin)
2337	CTAGTGGCGGC	2,00	2,80	Hs.142043	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX
2338	ACCTCACCTGG	2,00	2,80	Hs.137585	UDP glycosyltransferase 2 family, polypeptide B11
2339	CTTGTTCAAAA	2,00	2,80	Hs.137560	ESTs, Moderately similar to AMSH [H.sapiens]
2340	CCTCTTTCCAG	2,00	2,80	Hs.134615	ESTs
2341	TCTTAGTTCTA	2,00	2,80	Hs.130729	ESTs
2342	CACCTTATAGT	2,00	2,80	Hs.117582	CGI-43 protein
2343	AGCTTCTACCA	2,00	2,80	Hs.11261	small proline-rich protein 2A
2344	GTCAAGCCCAA	2,00	2,80	Hs.105033	ESTs, Weakly similar to SPR2J protein

					[M.musculus]
	2345 AACTTATCATT	2,00	2,80	Hs.103368	ESTs
5	2346 ATGTGCTTCCG	2,00	0,43	Hs.76494	proline arginine-rich end leucine-rich repeat protei
	2347 CCTTTTTGTCC	2,00	0,43	Hs.62601	Homo sapiens mRNA; cDNA DKFZp586K1318 (from clone DK
10	2348 CTCTGTTTACA	2,00	0,43	Hs.5947	mel transforming oncogene (derived from cell line NK
	2349 GAAGTGCTGCT	2,00	0,43	Hs.21812	ESTs
	2350 CCATTGCAGTC	2,00	0,43	Hs.207659	EST
15	2351 CCACTGCACGC	2,00	0,43	Hs.202669	thiopurine S-methyltransferase
	2352 GTGGTGTACAC	2,00	0,43	Hs.168102	Human proteinase activated receptor-2 mRNA, 3'UTR
	2353 ATAAATAAATT	2,00	0,43	Hs.16677	hypothetical protein FLJ10506
20	2354 TTGATAAATAA	2,00	0,43	Hs.139226	replication factor C (activator 1) 2 (40kD)
	2355 GCAAAAGCCCG	2,00	0,43	Hs.109798	G8 protein
	2356 TAAAATATGGG	1,00	0,22	Hs.98401	Homo sapiens mRNA full length insert cDNA clone EURO
25	2357 CTTTGGTTTGC	1,00	0,22	Hs.8895	ESTs
	2358 CCAAAGGAGAA	1,00	0,22	Hs.8889	serine hydroxymethyltransferase 1 (soluble)
	2359 TGTACCTTTTC	1,00	0,22	Hs.8172	ESTs
30	2360 TGTTAAGTGTT	1,00	0,22	Hs.78825	matrin 3
	2361 TACAAGCTGAG	1,00	0,22	Hs.77508	glutamate dehydrogenase 1
	2362 TCTGCGGGTGG	1,00	0,22	Hs.76159	ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton
35	2363 TATCAATATTC	1,00	0,22	Hs.7306	secreted frizzled-related protein 1
	2364 ATGTTTTGTAA	1,00	0,22	Hs.6853	carbohydrate (N-acetylglucosamine 6-O) sulfotransfer
	2365 GCTTTTTGTTG	1,00	0,22	Hs.6048	FEM-1-like death receptor binding protein
40	2366 CTGGAGACCCA	1,00	0,22	Hs.56729	lymphocyte-specific protein 1
	2367 TTCAGAATAAA	1,00	0,22	Hs.50848	hypothetical protein FLJ20331
	2368 ACAATGAAGCA	1,00	0,22	Hs.285665	Homo sapiens mRNA; cDNA DKFZp564P013 (from clone DKF
45	2369 GCCTGTGGGGT	1,00	0,22	Hs.285565	ESTs
	2370 CAGCAAGGCTT	1,00	0,22	Hs.283714	30 kDa protein
	2371 CAAGGCACCAA	1,00	0,22	Hs.28107	ESTs
50	2372 TACCAGAGTCC	1,00	0,22	Hs.279927	hypothetical protein
	2373 ATTTTTGTAAA	1,00	0,22	Hs.27413	adaptor protein containing pH domain, PTB domain and
	2374 TCTGTTACACC	1,00	0,22	Hs.272759	KIAA1457 protein
55	2375 ACGTTTGATTT	1,00	0,22	Hs.27263	KIAA1458 protein
	2376 AAGAGATGTTC	1,00	0,22	Hs.26799	DKFZP564D0764 protein
	2377 TTGGTCAGGGT	1,00	0,22	Hs.264381	EST
	2378 TGGAGCTATGA	1,00	0,22	Hs.261655	EST
60	2379 AGACTCAGGCC	1,00	0,22	Hs.24305	ESTs
	2380 GTTCATCCTTG	1,00	0,22	Hs.236894	ESTs, Highly similar to LRP1_HUMAN LOW-DENSITY LIPOP
	2381 TATCTTGTTGC	1,00	0,22	Hs.23296	ESTs

2382	GTTTGTTCCT	1,00	0,22	Hs.21143	ESTs, Weakly similar to KIAA1532 protein [H.sapiens]
2383	AAGACACTGTT	1,00	0,22	Hs.20707	hypothetical protein R31240_1
2384	CCTAGAATCTG	1,00	0,22	Hs.20196	adenylate cyclase 9
2385	GTCGGGGGAGA	1,00	0,22	Hs.18844	ESTs
2386	ATGTTGTCAAT	1,00	0,22	Hs.1845	MHC class I region ORF
2387	TTTTCCCTCAG	1,00	0,22	Hs.184242	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase)
2388	ACATTTCATTA	1,00	0,22	Hs.18192	Ser/Arg-related nuclear matrix protein (plenty of pr
2389	TTAGCCAGGGT	1,00	0,22	Hs.180610	splicing factor proline/glutamine rich (polypyrimidi
2390	GGTGGAAAAA	1,00	0,22	Hs.178728	methyl-CpG binding domain protein 3
2391	GGGCAGAATAA	1,00	0,22	Hs.164690	ESTs
2392	GGTGCCCGGCA	1,00	0,22	Hs.163593	ribosomal protein L18a
2393	TAGCTGAGGCA	1,00	0,22	Hs.159557	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
2394	CGGATTCAATT	1,00	0,22	Hs.14763	ESTs
2395	AAGAAAGGGAA	1,00	0,22	Hs.140908	ESTs
2396	TCAAAAGGGCA	1,00	0,22	Hs.125158	ESTs
2397	CTCTCCTTGCC	1,00	0,22	Hs.118738	KIAA0800 gene product
2398	TTGCAGAGGGG	1,00	0,22	Hs.110373	ESTs
2399	TGTCTGCAGAA	1,00	0,22	Hs.107418	ESTs
2400	AGCTTCCGCTT	1,00	0,22	Hs.106529	CGI-65 protein
2401	CTCACACACAC	1,00	0,22	Hs.104311	novel protein with MAM domain
2402	GCCTACCCGAG	15,00	1,89	Hs.23582	tumor-associated calcium signal transducer 2
2403	GCCCACAGTAG	4,00	0,72	Hs.76122	splicing factor, arginine/serine-rich 4
2404	ACTGCAGAGCG	4,00	0,72	Hs.12186	Homo sapiens cDNA FLJ20792 fis, clone COL01292
2405	GGCCCCCTCACC	11,00	1,48	Hs.274313	insulin-like growth factor binding protein 6
2406	AACAGATATTG	3,00	0,58	Hs.190161	LR8 protein
2407	GTGGCAGACGC	3,00	0,58	Hs.116506	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ
2408	GAAAATAAAGT	3,00	0,58	Hs.111334	ferritin, light polypeptide
2409	TTAGTGTCGTA	11,00	1,47	Hs.74649	cytochrome c oxidase subunit VIc
2410	CTTCCTTGCCCT	18,00	2,10	Hs.2785	keratin 17
2411	TTCATAGCTGC	8,00	1,16	Hs.155481	cartilage associated protein
2412	CCCTAGGTTGG	13,00	1,64	Hs.3989	plexin B2
2413	AAGATATCAGT	2,00	0,42	Hs.74122	caspase 4, apoptosis-related cysteine protease
2414	TTTGTTGAATG	2,00	0,42	Hs.44856	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ
2415	CAACGTCCTGA	2,00	0,42	Hs.29068	ESTs
2416	GAATTGACGCC	2,00	0,42	Hs.21851	Homo sapiens mRNA; cDNA DKFZp586J2118 (from clone DK
2417	AACCCATTGTG	2,00	0,42	Hs.184326	CDC10 (cell division cycle 10, S. cerevisiae, homolo
2418	ACCACTTCCTC	2,00	0,42	Hs.173421	Human clon CE29 8.1 (CAC)n/(GTG)n

					repeat-containing
5	2419	GCCCATCGTAC	2,00	0,42	Hs.103441 ESTs, Weakly similar to testicular tektin B1-like pr
	2420	CCTACTCCCAG	2,00	0,42	Hs.10071 seven transmembrane protein TM7SF3
	2421	GCCTGGTGACC	5,00	0,83	Hs.180224 death-associated protein 6
10	2422	ATGGCAACAGA	13,00	1,62	Hs.149609 integrin, alpha 5 (fibronectin receptor, alpha polyp
	2423	CAGGCCTGGCC	8,00	1,15	Hs.74649 cytochrome c oxidase subunit VIc
	2424	GTGAGACCCCG	8,00	1,15	Hs.210717 ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY
15	2425	GAGCTGGTGAA	3,00	0,57	Hs.6163 ESTs, Weakly similar to myotonic dystrophy kinase [H
	2426	TCTGTTGAGTG	3,00	0,57	Hs.46679 ESTs
	2427	CTCAACCCCCC	15,00	1,78	Hs.89137 low density lipoprotein-related protein 1 (alpha-2-m
20	2428	ATCACTAAAGA	4,00	0,70	Hs.75888 phosphogluconate dehydrogenase
	2429	CCCCTGCACTC	4,00	0,70	Hs.235213 ESTs
	2430	CCCTCTGTCAG	4,00	0,70	Hs.110095 Homo sapiens mRNA; cDNA DKFZp761E0711 (from clone DK
25	2431	CACTGCCTTTG	4,00	0,70	Hs.106019 protein phosphatase 1, regulatory subunit 10
	2432	AAGATCAAGAT	10,00	1,32	Hs.1288 actin, alpha 1, skeletal muscle
30	2433	GCGAGACCCTG	8,00	1,13	Hs.278531 Homo sapiens mRNA; cDNA DKFZp434A1014 (from clone DK
	2434	TTTGCCTGGAT	2,00	0,41	Hs.95260 Autosomal Highly Conserved Protein
	2435	GTCCCAACACA	2,00	0,41	Hs.8961 ESTs
35	2436	TTGGGGTGCCT	2,00	0,41	Hs.85279 hydroxysteroid (17-beta) dehydrogenase 1
	2437	AAAAGGCACTT	2,00	0,41	Hs.82425 actin related protein 2/3 complex, subunit 5 (16 kD)
40	2438	TCTTACGCGTT	2,00	0,41	Hs.7905 SH3 and PX domain-containing protein SH3PX1
	2439	ATGCAGTTCAA	2,00	0,41	Hs.65135 Homo sapiens mRNA; cDNA DKFZp434E0121 (from clone DK
45	2440	ATGCTGAGAGG	2,00	0,41	Hs.6185 ESTs, Weakly similar to BcDNA.GH12174 [D.melanogaste
	2441	CATCACACTCC	2,00	0,41	Hs.56729 lymphocyte-specific protein 1
	2442	TGCTGTTGCTG	2,00	0,41	Hs.55923 ESTs, Highly similar to lin-10 protein homolog [R.no
50	2443	ATTGTTTCTTG	2,00	0,41	Hs.52081 KIAA0867 protein
	2444	AGGGAGACCTG	2,00	0,41	Hs.40154 jumonji (mouse) homolog
	2445	CTACAAAAAGA	2,00	0,41	Hs.279609 mitochondrial carrier homolog 2
	2446	TGTGTTAAGAG	2,00	0,41	Hs.275221 hypothetical protein FLJ20061
55	2447	CCACTATACTC	2,00	0,41	Hs.269404 ESTs
	2448	GAATGTCCTTT	2,00	0,41	Hs.172674 nuclear factor of activated T-cells, cytoplasmic 3
60	2449	GAACGACCTAG	2,00	0,41	Hs.15783 Homo sapiens mRNA; cDNA DKFZp434P1115 (from clone DK
	2450	AAGAAGGCAAG	2,00	0,41	Hs.155402 D site of albumin promoter (albumin D-box) binding p
65	2451	ATCTATTGAAA	2,00	0,41	Hs.15386 ESTs

2452	TCCTATGCAGA	2,00	0,41	Hs.108924	DKFZP586P1422 protein
2453	GAGACCCTGGA	3,00	0,56	Hs.8088	similar to S. cerevisiae Sec6p and R. norvegicus rse
2454	TAGCTCGATCC	3,00	0,56	Hs.58372	ESTs
2455	TTGTCCAGGCT	7,00	1,02	Hs.99423	ATP-dependent RNA helicase
2456	ACCCTTTAACA	11,00	1,39	Hs.181392	major histocompatibility complex, class I, E
2457	TTTTTGTATTA	4,00	0,69	Hs.179526	upregulated by 1,25-dihydroxyvitamin D-3
2458	GGAGATGAGGA	5,00	0,81	Hs.83419	KIAA0252 protein
2459	AGCCTGGGAGG	5,00	0,81	Hs.117582	CGI-43 protein
2460	TCCCTGGGGGT	1,00	0,20	Hs.94875	ESTs
2461	ATCAAAGGTTT	1,00	0,20	Hs.94795	Homo sapiens mRNA; cDNA DKFZp564O222 (from clone DKF
2462	TAACCTTTATAA	1,00	0,20	Hs.81505	KIAA0579 protein
2463	TTGTCCTGACC	1,00	0,20	Hs.80181	ESTs
2464	AACTATGCCAG	1,00	0,20	Hs.7905	SH3 and PX domain-containing protein SH3PX1
2465	CTGCTGTAATA	1,00	0,20	Hs.77508	glutamate dehydrogenase 1
2466	GGGTCCTCTCC	1,00	0,20	Hs.76064	ribosomal protein L27a
2467	AGGGCAGTGCC	1,00	0,20	Hs.74649	cytochrome c oxidase subunit VIc
2468	TCACCGTGGAC	1,00	0,20	Hs.73800	selectin P (granule membrane protein 140kD, antigen
2469	AACCCGGTAGG	1,00	0,20	Hs.69707	H.sapiens HCG II mRNA
2470	AACTGATTAA	1,00	0,20	Hs.59838	hypothetical protein FLJ10808
2471	GGGTTGGGGTC	1,00	0,20	Hs.58014	G protein-coupled receptor, family C, group 5, membe
2472	GCATTGTGGTG	1,00	0,20	Hs.5534	ESTs
2473	GATTATGTAAT	1,00	0,20	Hs.5056	CGI-41 protein
2474	TATGAGCAGAA	1,00	0,20	Hs.5010	Homo sapiens clone 24672 mRNA se- quence
2475	TAAAGGCACAG	1,00	0,20	Hs.4980	LIM domain binding 2
2476	AGCAAACTGG	1,00	0,20	Hs.46489	ESTs
2477	TGGAAGTGAAGT	1,00	0,20	Hs.43899	Homo sapiens mRNA; cDNA DKFZp434C1714 (from clone DK
2478	CTGATTCAACT	1,00	0,20	Hs.30818	ESTs
2479	GGTGAGCTACT	1,00	0,20	Hs.29874	ESTs, Weakly similar to A49656 estrogen-responsive f
2480	CCCCAAAAAAA	1,00	0,20	Hs.29595	JM4 protein
2481	GGTTATTGTAT	1,00	0,20	Hs.286184	Homo sapiens mRNA; cDNA DKFZp566C114 (from clone DKF
2482	GAGAACTGTAG	1,00	0,20	Hs.286169	ESTs
2483	TCTGAAAAAAA	1,00	0,20	Hs.285112	ESTs
2484	GGGACGGGGTG	1,00	0,20	Hs.284161	Homo sapiens mRNA for KIAA1532 protein, partial cds
2485	TGTAGGGGTTA	1,00	0,20	Hs.267289	polymerase (DNA directed), alpha
2486	AAGCTGGAGGC	1,00	0,20	Hs.265327	Human DNA sequence from clone RP4-756G23 on chromoso
2487	TACAAAGCATA	1,00	0,20	Hs.26484	HIRA-interacting protein 3
2488	AATTAAAAAAA	1,00	0,20	Hs.257515	EST

2489	GAACACCGTCC	1,00	0,20	Hs.25300	hypothetical protein DKFZp761G1923
2490	GCAAACTGTC	1,00	0,20	Hs.252721	ESTs
2491	GCCGCCCTACG	1,00	0,20	Hs.24907	coronin, actin-binding protein, 2B
2492	GGGCCTTGGAG	1,00	0,20	Hs.227789	mitogen-activated protein kinase-activated protein k
2493	GGAAGACCAGA	1,00	0,20	Hs.209464	ESTs, Weakly similar to cDNA EST yk282b7.5 comes fro
2494	GTGGCTGACGC	1,00	0,20	Hs.202234	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAMILY SB2
2495	TCAAGTTTAAA	1,00	0,20	Hs.199160	myeloid/lymphoid or mixed-lineage leukemia (trithora
2496	AAACTATCACA	1,00	0,20	Hs.194693	solute carrier family 7 (cationic amino acid transpo
2497	GGGTAGTGTCA	1,00	0,20	Hs.183738	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein
2498	TTTTATTATCC	1,00	0,20	Hs.182485	actinin, alpha 4
2499	GCCTTTCCTCA	1,00	0,20	Hs.180669	conserved gene amplified in osteosarcoma
2500	CATTTACTCTA	1,00	0,20	Hs.17109	integral membrane protein 2A
2501	CTGCCATCTTT	1,00	0,20	Hs.165433	Homo sapiens mRNA; cDNA DKFZp586K1924 (from clone DK
2502	TCTTCTTTGTA	1,00	0,20	Hs.160711	ESTs
2503	GGCAAATGAAG	1,00	0,20	Hs.15589	PPAR binding protein
2504	GTGGTTTGTTG	1,00	0,20	Hs.15099	KIAA0740 gene product
2505	TTAGGGCCCCAG	1,00	0,20	Hs.137313	ESTs
2506	GCCCTTCTCAG	1,00	0,20	Hs.136506	beta V spectrin
2507	CTTGCTGAAGA	1,00	0,20	Hs.13619	ESTs
2508	AAGTAAGTCTA	1,00	0,20	Hs.117582	CGI-43 protein
2509	GCACCAGGAGC	1,00	0,20	Hs.110533	Homo sapiens mRNA; cDNA DKFZp761H172 (from clone DKF
2510	TTACCCAGTGT	1,00	0,20	Hs.10888	ESTs
2511	TTTGAATCAGT	1,00	0,20	Hs.10784	hypothetical protein FLJ20037
2512	TTTTGTGTTGG	1,00	0,20	Hs.107233	ESTs
2513	CAAACCTTTAA	9,00	1,20	Hs.105379	unknown
2514	CTAAAAA	31,00	2,97	Hs.23740	KIAA1598 protein
2515	CCAGTAATCCC	7,00	1,01	Hs.237078	ESTs
2516	CCCATAATCCC	7,00	1,01	Hs.111256	arachidonate 15-lipoxygenase, second type
2517	ATGGCACCCT	5,00	0,79	Hs.161554	hypothetical protein FLJ20159
2518	CAGCTGGCCAT	9,00	1,19	Hs.79732	fibulin 1
2519	CTGCTGCACTC	9,00	1,19	Hs.193974	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
2520	AATGGCATTGA	4,00	0,68	Hs.31431	ESTs
2521	CTCCCCTGCCC	9,00	1,18	Hs.82422	capping protein (actin filament), gelsolin-like
2522	ATGTCCAATTT	3,00	0,55	Hs.247309	succinate-CoA ligase, GDP-forming, beta subunit
2523	CTACAATTTTC	3,00	0,55	Hs.24307	f-box and WD-40 domain protein 3
2524	CTGTAAAACAA	3,00	0,55	Hs.180686	ubiquitin protein ligase E3A (human papilloma virus



2525	TGAGGGATGGA	3,00	0,55	Hs.172740	microtubule-associated protein, RP/EB family, member
2526	AGGCAGAGGTT	3,00	0,55	Hs.164129	ESTs, Weakly similar to ALU6_HUMAN ALU SUBFAMILY SP
2527	GAAAATATCAA	3,00	0,55	Hs.15423	hypothetical protein HDCMC04P
2528	ATGAAACCCTG	27,00	2,59	Hs.187991	DKFZP564A122 protein
2529	GTCTTCGAAGT	2,00	0,40	Hs.78353	SFRS protein kinase 2
2530	CTGAAGGCTGA	2,00	0,40	Hs.78146	platelet/endothelial cell adhesion molecule (CD31 an
2531	TGACAATTTTG	2,00	0,40	Hs.75912	KIAA0257 protein
2532	TGCATCTGTGC	2,00	0,40	Hs.58589	glycogenin 2
2533	ACCGAAACTTG	2,00	0,40	Hs.38041	pyridoxal (pyridoxine, vitamin B6) kinase
2534	AAGGGGCCTTT	2,00	0,40	Hs.26208	collagen, type XVI, alpha 1
2535	CCACTGTACTT	2,00	0,40	Hs.183475	Homo sapiens clone 25061 mRNA sequence
2536	ATGCTTTTCAC	2,00	0,40	Hs.181357	laminin receptor 1 (67kD, ribosomal protein SA)
2537	GGGTCAGGAGA	2,00	0,40	Hs.181271	CGI-120 protein
2538	CACATCCTTAC	2,00	0,40	Hs.173717	phosphatidic acid phosphatase type 2B
2539	AATATTAAAAA	2,00	0,40	Hs.168103	prp28, U5 snRNP 100 kd protein
2540	GGCCCCCCTCC	2,00	0,40	Hs.155979	KIAA0295 protein
2541	TCTAAAAAAA	2,00	0,40	Hs.13328	ESTs
2542	CGCCTATAATC	6,00	0,88	Hs.194110	Homo sapiens mRNA; cDNA DKFZp434C0814 (from clone DK
2543	AAGGATGCCAA	10,00	1,25	Hs.169946	GATA-binding protein 3
2544	GTCCCTGCCTT	4,00	0,67	Hs.279837	glutathione S-transferase M2 (muscle)
2545	CACCCAATGGG	4,00	0,67	Hs.110121	SEC7 homolog
2546	CAGGAGGAAAG	5,00	0,77	Hs.177425	KIAA0964 protein
2547	TGGGCCCGTGT	5,00	0,77	Hs.11607	ESTs
2548	TGTGACCTCTC	5,00	0,77	Hs.108973	dolichyl-phosphate mannosyltransferase polypeptide 2
2549	GGAGGCGGAGG	6,00	0,87	Hs.15562	hypothetical protein FLJ10871
2550	GGACAGCTCAG	3,00	0,54	Hs.286242	ESTs, Weakly similar to hypothetical protein [H.sapi
2551	GTTACCAGTTT	3,00	0,54	Hs.28264	Homo sapiens mRNA; cDNA DKFZp564L0822 (from clone DK
2552	CAACTTAAGTG	3,00	0,54	Hs.16492	DKFZP564G2022 protein
2553	CCAGTGCACTC	10,00	1,23	Hs.254856	EST
2554	TGCACACACAC	4,00	0,66	Hs.99816	beta-catenin-interacting protein ICAT
2555	CCTCTAATCCC	4,00	0,66	Hs.236150	ESTs, Weakly similar to AF090942_1 PRO0657 [H.sapien
2556	AAGCGCTCTCG	6,00	0,86	Hs.168913	serine/threonine kinase 24 (Ste20, yeast homolog)
2557	CTTGTGTGTAG	6,00	0,86	Hs.158203	actin binding LIM protein 1
2558	GAAATCTGTCC	2,00	0,39	Hs.8710	ESTs
2559	CAAGGAGATCT	2,00	0,39	Hs.7471	ESTs, Weakly similar to homology with GTP binding pr
2560	CAAATACTGC	2,00	0,39	Hs.6557	ESTs
2561	AGATAGCATTA	2,00	0,39	Hs.6241	phosphoinositide-3-kinase, regulatory subunit, polyp

2562	AGAATGTACGG	2,00	0,39	Hs.57973	hypothetical protein
2563	CCACGCACTGT	2,00	0,39	Hs.48778	Homo sapiens mRNA; cDNA DKFZp586O0221 (from clone DK
2564	CACCCCTCAGG	2,00	0,39	Hs.26369	hypothetical protein FLJ20287
2565	ATTACACCACT	2,00	0,39	Hs.254565	EST, Weakly similar to A46010 X-linked retinopathy p
2566	AACCCAGAAGG	2,00	0,39	Hs.229985	EST, Weakly similar to ALU2_HUMAN ALU SUBFAMILY SB S
2567	GTGGTGTATGC	2,00	0,39	Hs.229244	ESTs
2568	AACTATAAACG	2,00	0,39	Hs.22393	density-regulated protein
2569	AAGTTTATAGA	2,00	0,39	Hs.206097	oncogene TC21
2570	GTGAAGTTGCG	2,00	0,39	Hs.123178	translocase of inner mitochondrial mem- brane 44 (yeas
2571	CCCTCCTGCTC	3,00	0,53	Hs.96731	huntingtin interacting protein-1-related
2572	AACCCAACTC	3,00	0,53	Hs.11184	hypothetical protein FLJ20419
2573	GTTGGGACATC	4,00	0,65	Hs.9663	programmed cell death 6-interacting protein
2574	CCGCTGATCCA	4,00	0,65	Hs.184161	exostoses (multiple) 1
2575	GGATACAACCT	4,00	0,65	Hs.173993	RNA binding motif protein 6
2576	ATTTAAAAAAA	4,00	0,65	Hs.1139	cold shock domain protein A
2577	CATTTAAAAAA	1,00	0,19	Hs.9443	zinc finger protein 202
2578	TATACCTGTGT	1,00	0,19	Hs.92200	KIAA0480 gene product
2579	GTGAATGACAA	1,00	0,19	Hs.8834	ring finger protein 3
2580	CCCCTCCCCTC	1,00	0,19	Hs.83429	tumor necrosis factor (ligand) super- family, member 1
2581	CAATTTATATC	1,00	0,19	Hs.8294	KIAA0196 gene product
2582	ACAGATTCAAT	1,00	0,19	Hs.8248	NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD
2583	AGTGTATCACA	1,00	0,19	Hs.79844	DKFZP564M1416 protein
2584	GAGGGAGTTGG	1,00	0,19	Hs.77810	nuclear factor of activated T-cells, cyto- plasmic 4
2585	TAACATCCCTG	1,00	0,19	Hs.75400	KIAA0280 protein
2586	GGGAGCTTGTA	1,00	0,19	Hs.74649	cytochrome c oxidase subunit VIc
2587	TAGATGTGATT	1,00	0,19	Hs.62112	zinc finger protein 207
2588	TATAGATCGTC	1,00	0,19	Hs.59757	zinc finger protein 281
2589	AAGTTTTGATT	1,00	0,19	Hs.58382	hypothetical protein FLJ11101
2590	CCAATAGGGCC	1,00	0,19	Hs.5555	ESTs, Weakly similar to TERA_HUMAN TRANSITIONAL ENDO
2591	TCGCACACTTT	1,00	0,19	Hs.48998	fibronectin leucine rich transmembrane protein 2
2592	AAAGGTTGCAG	1,00	0,19	Hs.47367	Homo sapiens mRNA; cDNA DKFZp434O031 (from clone DKF
2593	AGCTTTCCAAT	1,00	0,19	Hs.45109	ESTs
2594	TAGCTTCCTTA	1,00	0,19	Hs.44276	homeo box C10
2595	CTGTTACCTTC	1,00	0,19	Hs.38178	ESTs
2596	CTTATGTATTA	1,00	0,19	Hs.30861	ESTs
2597	TCAACACAGTT	1,00	0,19	Hs.285874	ESTs
2598	TATTTCTGAAA	1,00	0,19	Hs.285533	ESTs
2599	TACCTGTAATC	1,00	0,19	Hs.284555	ESTs
2600	AATATGTGTAC	1,00	0,19	Hs.279671	katanin p60 (ATPase-containing) subunit

					A 1
2601	TGACCAGGCC	1,00	0,19	Hs.27536	ESTs, Weakly similar to unnamed protein product [H.s
2602	AAATGGATGCA	1,00	0,19	Hs.271943	tetraspanin TM4-B
2603	GTGAACCCACG	1,00	0,19	Hs.270791	ESTs
2604	TCCTATCCAGG	1,00	0,19	Hs.26045	protein tyrosine phosphatase, receptor type, A
2605	TATATATGGGG	1,00	0,19	Hs.25426	ESTs
2606	GCAGGTACTGA	1,00	0,19	Hs.24030	solute carrier family 31 (copper transporters), memb
2607	GCGGCGTGTGC	1,00	0,19	Hs.237040	ESTs, Weakly similar to AF119917_17 PRO1847 [H.sapie
2608	TTATTTCTTCT	1,00	0,19	Hs.22246	ESTs
2609	GTGGCGCACAT	1,00	0,19	Hs.210979	EST
2610	TGTTTCATTCT	1,00	0,19	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T and BN75 tempe
2611	TTTAAATAGCC	1,00	0,19	Hs.182965	Kruppel-like factor 4 (gut)
2612	AGAAATAAATG	1,00	0,19	Hs.178356	EST
2613	TAAAGCACTTA	1,00	0,19	Hs.172806	ESTs
2614	GAAATAGGAAG	1,00	0,19	Hs.172180	KIAA0440 protein
2615	GATCATACTCC	1,00	0,19	Hs.169487	Kreisler (mouse) maf-related leucine zipper homolog
2616	CATAATGTCAT	1,00	0,19	Hs.169152	ESTs
2617	GTGTTTTTGTT	1,00	0,19	Hs.169081	ets variant gene 6 (TEL oncogene)
2618	AGAATTTAAAA	1,00	0,19	Hs.158867	ESTs
2619	CAACATTCAA	1,00	0,19	Hs.14368	SH3 domain binding glutamic acid-rich protein like
2620	TCCTTTGGATT	1,00	0,19	Hs.128659	ESTs
2621	TTCTTTCCTGA	1,00	0,19	Hs.127453	ESTs
2622	AAAAAGGTGGA	1,00	0,19	Hs.12348	ESTs, Moderately similar to B43284 zinc finger prote
2623	GGTATGGCAGG	1,00	0,19	Hs.116998	ESTs
2624	AATGGAAGGTG	1,00	0,19	Hs.11260	hypothetical protein FLJ11264
2625	GGGGCTTTCTG	1,00	0,19	Hs.110480	DC12 protein
2626	AAAATAAACTT	1,00	0,19	Hs.10712	phosphatase and tensin homolog (mutated in multiple
2627	TAATATGAGCA	1,00	0,19	Hs.105642	ESTs
2628	ATATACTGTAG	1,00	0,19	Hs.104557	hypothetical protein FLJ10697
2629	CGCACCGGGTA	1,00	0,19	Hs.104433	Homo sapiens napsin 2 precursor, mRNA, partial seque
2630	GGAGGTGGGGC	23,00	2,13	Hs.180577	granulin
2631	GGAAATGTCAA	17,00	1,70	Hs.111301	matrix metalloproteinase 2 (gelatinase A, 72kD gelat
2632	TGTTCTGGAGA	22,00	2,05	Hs.74471	gap junction protein, alpha 1, 43kD (connexin 43)
2633	TACTTGGGAGG	5,00	0,75	Hs.154103	LIM protein (similar to rat protein kinase C-binding
2634	GCTGTTCAGAA	4,00	0,64	Hs.6975	PRO1073 protein
2635	CTGTCTGTGGC	4,00	0,64	Hs.260150	hypothetical protein FLJ10209
2636	GCACCTAGTGC	4,00	0,64	Hs.1287	zinc finger protein 173

2637	GAGCCTGTAAA	3,00	0,52	Hs.25866	ESTs
2638	AGCGAGAGAGG	3,00	0,52	Hs.232146	ESTs, Weakly similar to bromodomain containing prote
2639	AGTAGCTTGAA	3,00	0,52	Hs.154248	KIAA0549 protein
2640	CTGTCAGCGGC	7,00	0,92	Hs.7247	ESTs, Weakly similar to TIE1_HUMAN TYROSINE-PROTEIN
2641	GCCCAGCGGCC	7,00	0,92	Hs.194385	hypothetical protein FLJ20234
2642	ATGGTGACAC	2,00	0,38	Hs.87521	ESTs, Weakly similar to ORF2 consensus sequence enco
2643	ATGTCGTGGTC	2,00	0,38	Hs.6900	ring finger protein 13
2644	GCCCTTCCCT	2,00	0,38	Hs.63667	transcriptional adaptor 3 (ADA3, yeast homolog)-like
2645	TGAGTTTTACA	2,00	0,38	Hs.58373	ESTs
2646	CGGGGCGCGCA	2,00	0,38	Hs.4299	ESTs
2647	AGGAAGCTGAG	2,00	0,38	Hs.3041	uracil-DNA glycosylase 2
2648	CACCTGTAGTT	2,00	0,38	Hs.271053	ESTs, Weakly similar to A46010 X-linked retinopathy
2649	CCCTGGGCTTC	2,00	0,38	Hs.226770	DKFZP566C0424 protein
2650	TAAGGCCTTTC	2,00	0,38	Hs.20149	leukemia associated gene 1, candidate tumor suppress
2651	AAATCAGGAAC	2,00	0,38	Hs.180549	ESTs, Highly similar to R26660_1, partial CDS [H.sap
2652	GGAAACCCAG	2,00	0,38	Hs.174044	dishevelled 3 (homologous to Drosophila dsh)
2653	ACGCACATTAT	2,00	0,38	Hs.156007	Down syndrome critical region gene 1-like 1
2654	CTTCTCTTGAG	2,00	0,38	Hs.150557	basic transcription element binding protein 1
2655	TTCCTCCAAA	2,00	0,38	Hs.125743	ESTs
2656	GATGAGGAGAC	46,00	3,46	Hs.179573	collagen, type I, alpha 2
2657	CTGTGAGACCT	11,00	1,22	Hs.160741	Fc fragment of IgG, receptor, transporter, alpha
2658	CCACACAAGCA	7,00	0,91	Hs.102737	goliath protein
2659	TTGGCCAGGAT	31,00	2,52	Hs.161785	Homo sapiens cDNA FLJ10952 fis, clone PLACE1000374
2660	CTCCCTCTGCC	11,00	1,21	Hs.194534	vesicle-associated membrane protein 2 (synaptobrevin
2661	GAATAAATGTT	6,00	0,82	Hs.8762	FK506-binding protein 9 (63 kD)
2662	ACCAGCTGTCC	3,00	0,51	Hs.84153	dynamitin (dynactin complex 50 kD subunit)
2663	CTTCTATGTAG	3,00	0,51	Hs.77225	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) poly
2664	GTTTCAGTTAC	3,00	0,51	Hs.7016	RAB7, member RAS oncogene family
2665	GGCCAGTAACA	3,00	0,51	Hs.69559	KIAA1096 protein
2666	GGAGGTGGGAG	3,00	0,51	Hs.105097	thymidine kinase 1, soluble
2667	TGCAATATTTTC	4,00	0,62	Hs.94970	KIAA0306 protein
2668	CAGACTTTTGG	5,00	0,72	Hs.63348	DKFZP586M121 protein
2669	GTGGTGACGC	28,00	2,27	Hs.181318	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY
2670	GACCAGGCCCT	22,00	1,90	Hs.180266	tropomyosin 2 (beta)

2671	CGGCAGAGCTG	4,00	0,61	Hs.9610	purinergic receptor P2X, ligand-gated ion channel, 4	
2672	AACCCAAAAAG	2,00	0,37	Hs.92323	FXFD domain-containing ion transport regulator 3	5
2673	TTGCCTTGCTT	2,00	0,37	Hs.91684	Homo sapiens cDNA FLJ20148 fis, clone COL08032, high	
2674	GTAAATCCTG	2,00	0,37	Hs.8881	ESTs, Weakly similar to RMS1_HUMAN REGULATOR OF MITO	10
2675	TAAGTAAAGTG	2,00	0,37	Hs.36529	ESTs	
2676	ATCAAAAAAAA	2,00	0,37	Hs.271699	polymerase (DNA directed) iota	
2677	ACCTATTTGTG	2,00	0,37	Hs.252229	v-maf musculoaponeurotic fibrosarcoma (avian) oncogene	15
2678	GAATGTTTTTT	2,00	0,37	Hs.21432	SEX gene	
2679	GTTGTGCCACT	2,00	0,37	Hs.196978	EST	
2680	CACTTTAAAGT	2,00	0,37	Hs.194669	enhancer of zeste (Drosophila) homolog 1	20
2681	AAATAAAAAAT	2,00	0,37	Hs.151696	DKFZP727G051 protein	
2682	AAGGTGAAGTA	2,00	0,37	Hs.146861	hypothetical protein FLJ20580	
2683	CTTTAAGAAAG	2,00	0,37	Hs.13456	Homo sapiens clone 24747 mRNA sequence	25
2684	GTGGCTCTTGC	2,00	0,37	Hs.12243	hypothetical protein	
2685	TCTCTACTAAA	16,00	1,51	Hs.249613	PRO0365 protein	
2686	CCCTTCCCCGG	6,00	0,80	Hs.112028	Missshapen/NIK-related kinase	30
2687	ACCTATAAGTA	6,00	0,80	Hs.111029	putative heme-binding protein	
2688	TTATACAAAAA	3,00	0,50	Hs.88558	ESTs	
2689	CTCACTAGTGG	3,00	0,50	Hs.78683	ubiquitin specific protease 7 (herpes virus-associated)	35
2690	GCGAAACCCCT	3,00	0,50	Hs.46468	chemokine (C-C motif) receptor 6	
2691	GACTGTTGCTG	3,00	0,50	Hs.179902	Homo sapiens CTL1 gene	
2692	CCACTGCAGTC	7,00	0,87	Hs.161554	hypothetical protein FLJ20159	
2693	TCAACAAATTT	1,00	0,19	Hs.9315	HNOEL-iso protein	40
2694	GGACCTTTAAT	1,00	0,19	Hs.90011	adenylosuccinate synthase	
2695	GATACTTTGCA	1,00	0,19	Hs.89695	insulin receptor	
2696	TATTGAACACG	1,00	0,19	Hs.8867	cysteine-rich, angiogenic inducer, 61	
2697	ATGCAACTGGG	1,00	0,19	Hs.8617	ESTs	45
2698	TTGCCTTCTCT	1,00	0,19	Hs.82906	CDC20 (cell division cycle 20, S. cerevisiae, homolog)	
2699	TTTTGTATGTC	1,00	0,19	Hs.79025	KIAA0096 protein	
2700	GAAATGCAGCC	1,00	0,19	Hs.78546	ATPase, Ca++ transporting, plasma membrane 1	50
2701	TGGTAGGTTCT	1,00	0,19	Hs.76136	thioredoxin	
2702	ACAAGATATTT	1,00	0,19	Hs.74122	caspase 4, apoptosis-related cysteine protease	55
2703	ACCAGCATCCT	1,00	0,19	Hs.70202	hypothetical protein FLJ10897	
2704	CCTGTCACGAT	1,00	0,19	Hs.6786	ESTs	
2705	GTGCAGAGAGC	1,00	0,19	Hs.66392	intersectin 1 (SH3 domain protein)	
2706	ATGTTACCTAA	1,00	0,19	Hs.62711	ESTs	
2707	CTATTTAGTTA	1,00	0,19	Hs.576	fucosidase, alpha-L-1, tissue	60
2708	CAAGTAGCAAA	1,00	0,19	Hs.4924	DKFZP434N061 protein	
2709	TTTAAGGGAAT	1,00	0,19	Hs.31463	KIAA0281 gene product	65

2710	TGCACTGTGGT	1,00	0,19	Hs.30524	ring finger protein 24
2711	CCATTTCACTC	1,00	0,19	Hs.284467	EST
2712	TTTTTCTCCCC	1,00	0,19	Hs.279583	CGI-81 protein
2713	CTGAACCTGAC	1,00	0,19	Hs.255372	hypothetical protein DKFZp564O1278
2714	TCTACAAAAAA	1,00	0,19	Hs.255298	ESTs
2715	GATTAAATAAT	1,00	0,19	Hs.25485	ESTs
2716	CTTTGTTAGAA	1,00	0,19	Hs.250691	ESTs
2717	TGAAGCCTTGC	1,00	0,19	Hs.246885	hypothetical protein FLJ20783
2718	TAGCCAATGTT	1,00	0,19	Hs.24427	DKFZP566O1646 protein
2719	GCCTCCATAAA	1,00	0,19	Hs.23395	myosin IXA
2720	AATTTGAGTGT	1,00	0,19	Hs.22883	ESTs
2721	TTTTAAAGAGG	1,00	0,19	Hs.22744	Homo sapiens mRNA full length insert cDNA clone EURO
2722	AGCCATTGCAC	1,00	0,19	Hs.223171	EST
2723	TTTAAAAATTA	1,00	0,19	Hs.21537	protein phosphatase 1, catalytic subunit, beta isofo
2724	TATTCAGGGGC	1,00	0,19	Hs.21256	ESTs
2725	TATTCTGAACA	1,00	0,19	Hs.20021	vesicle-associated membrane protein 1 (synaptobrevin
2726	CTTACAGCCAA	1,00	0,19	Hs.195969	ESTs
2727	AGTGACAAACT	1,00	0,19	Hs.18987	Homo sapiens BAC clone RP11-505D17 from 7p22-p21
2728	TTGGCAAAAAA	1,00	0,19	Hs.18136	nicotinamide nucleotide transhydrogenase
2729	GCTGACACTGA	1,00	0,19	Hs.174139	chloride channel 3
2730	AATCAGAATTT	1,00	0,19	Hs.173656	KIAA0941 protein
2731	TGACCATTCT	1,00	0,19	Hs.171952	occludin
2732	CCAAAGCTTCC	1,00	0,19	Hs.171637	ESTs, Weakly similar to KIAA1317 protein [H.sapiens]
2733	ATGTTCAATTT	1,00	0,19	Hs.1710	ATP-binding cassette, sub-family B (MDR/TAP), member
2734	CCACACAAAAA	1,00	0,19	Hs.161554	hypothetical protein FLJ20159
2735	GCCGGGCGCAG	1,00	0,19	Hs.160821	ESTs
2736	TCATCACATTA	1,00	0,19	Hs.155566	CASP2 and RIPK1 domain containing adaptor with death
2737	TTACCCAGGCT	1,00	0,19	Hs.151046	hypothetical protein FLJ11193
2738	CCTCAGTTTGG	1,00	0,19	Hs.140944	DNA segment on chromosome X (unique) 2654 expressed
2739	CACCTATAGTC	1,00	0,19	Hs.138860	Rho GTPase activating protein 1
2740	GGTGCTTCTTT	1,00	0,19	Hs.129692	ESTs
2741	GAGTCCATAAA	1,00	0,19	Hs.126266	ESTs
2742	CTAACAGGATT	1,00	0,19	Hs.125031	choline/ethanolaminephosphotransferase
2743	TCGAAACCCCA	1,00	0,19	Hs.117582	CGI-43 protein
2744	AAGGAGTGAAA	1,00	0,19	Hs.111092	ESTs, Weakly similar to gonadotropin inducible trans
2745	ATCCCTGTGAG	1,00	0,19	Hs.105820	ESTs
2746	CTCCATCGGCT	5,00	0,70	Hs.65238	95 kDa retinoblastoma protein, binding protein; KIAA0
2747	GTGGAACCCCG	5,00	0,70	Hs.270796	ESTs
2748	GACCACGAATA	4,00	0,60	Hs.76476	cathepsin H

2749	CCCTTGTGACT	4,00	0,60	Hs.74649	cytochrome c oxidase subunit VIc	
2750	GACCGCGGCTT	4,00	0,60	Hs.110903	claudin 5 (transmembrane protein deleted in velocard	
2751	CTACCAGGCCT	6,00	0,78	Hs.54457	CD81 antigen (target of antiproliferative antibody 1	5
2752	TTCCGGTTCCA	18,00	1,59	Hs.172609	nucleobindin 1	
2753	GATAGCACAGT	27,00	2,10	Hs.103391	Human insulin-like growth factor binding protein 5 (	10
2754	TACTGTATGTC	3,00	0,49	Hs.5867	KIAA0851 protein	
2755	TAATTTCTCAA	3,00	0,49	Hs.5306	Homo sapiens mRNA; cDNA DKFZp586F1122 (from clone DK	
2756	GCAAAACCCCC	3,00	0,49	Hs.277209	EST, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ S	15
2757	GTGCGGTACCT	3,00	0,49	Hs.25313	microspherule protein 1	
2758	TACTGCAAAAA	3,00	0,49	Hs.24557	DKFZP434H018 protein	
2759	TGCCTTAGTAA	3,00	0,49	Hs.13015	ESTs, Highly similar to MTJ1_MOUSE DNAJ PROTEIN HOMO	20
2760	TACTGTGATGT	3,00	0,49	Hs.121619	chromosome 11 open reading frame 15	
2761	GGGGCTGGAGG	5,00	0,69	Hs.105958	KIAA0620 protein	
2762	AACGCTGCGAA	4,00	0,60	Hs.24174	KIAA0876 protein	25
2763	ATGGTGGGCAC	4,00	0,60	Hs.132390	zinc finger protein 36 (KOX 18)	
2764	TTGACTTTTGC	2,00	0,36	Hs.61441	KIAA1311 protein	
2765	CCTGTAATCCG	2,00	0,36	Hs.272798	hypothetical protein FLJ20413	
2766	CTGTGAAAAAA	2,00	0,36	Hs.181350	kallikrein 2, prostatic	30
2767	CAGTGCAGTAT	2,00	0,36	Hs.168640	Ank, mouse, homolog of	
2768	AGCCATTGTGC	2,00	0,36	Hs.163860	ESTs	
2769	GGCAGGGTCGA	2,00	0,36	Hs.104627	Homo sapiens cDNA FLJ10158 fis, clone HEMBA1003463	35
2770	TAATTTTGAAA	12,00	1,19	Hs.117582	CGI-43 protein	
2771	TCTGGCATAGC	6,00	0,77	Hs.168232	ESTs, Weakly similar to I59365 ubiquitin conjugating	
2772	TTTTATGGAAT	12,00	1,18	Hs.77269	guanine nucleotide binding protein (G protein), alph	40
2773	GATTTTAAAA	3,00	0,49	Hs.75447	ralA binding protein 1	
2774	GACGGCCAGAG	3,00	0,49	Hs.74649	cytochrome c oxidase subunit VIc	
2775	TTCTCTGCTCA	3,00	0,49	Hs.21907	histone acetyltransferase	45
2776	TGGAAGGACCG	7,00	0,84	Hs.5086	Human DNA from overlapping chromosome 19 cosmids R31	
2777	TGGGACTCCAG	4,00	0,59	Hs.59384	Homo sapiens mRNA; cDNA DKFZp586E2023 (from clone DK	50
2778	TGGAATTCCCT	4,00	0,59	Hs.154846	phosphatidylinositol 4-kinase, catalytic, beta polyp	
2779	GCTCTCCCCC	6,00	0,76	Hs.100221	nuclear receptor subfamily 1, group H, member 2	55
2780	AGTGGAGGGAA	5,00	0,68	Hs.43509	ataxin 2 related protein	
2781	AGCCACCGCAC	13,00	1,23	Hs.42612	ESTs	
2782	TCTGAAGTCAA	8,00	0,90	Hs.180919	inhibitor of DNA binding 2, dominant negative helix-	60
2783	AACGCGAACAC	7,00	0,83	Hs.18946	squamous cell carcinoma antigen recognised by T cell	

2784	GTGGCGCACAC	15,00	1,33	Hs.246717	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ
2785	ATGGTGCCACT	8,00	0,90	Hs.107479	KIAA0738 gene product
2786	TCAGAAAAAAA	2,00	0,35	Hs.8118	KIAA0650 protein
2787	TCCCCGTGGCT	2,00	0,35	Hs.75616	KIAA0018 gene product
2788	AATAGGGGAAA	2,00	0,35	Hs.6147	KIAA1075 protein
2789	AGTCCTTATGC	2,00	0,35	Hs.39140	Homo sapiens cDNA FLJ10092 fis, clone HEMBA1002349
2790	TCCTTGGACCT	2,00	0,35	Hs.274550	proline oxidase homolog
2791	ATTTTGCTTGG	2,00	0,35	Hs.249495	heterogeneous nuclear ribonucleoprotein A1
2792	CTTGTGTTATA	2,00	0,35	Hs.155024	B-cell CLL/lymphoma 6 (zinc finger protein 51)
2793	CAGCTTAATTA	2,00	0,35	Hs.13996	ESTs
2794	TTGGTCAGGTT	2,00	0,35	Hs.113111	Homo sapiens familial Mediterranean fever locus regi
2795	GTAATTCTCAA	2,00	0,35	Hs.107001	ESTs, Highly similar to 45kDa splicing factor [H.sap
2796	GCCCCACAGCC	5,00	0,67	Hs.40342	putative nuclear protein
2797	GTATACAACAA	3,00	0,48	Hs.279617	steroid dehydrogenase homolog
2798	AGCTAGGGAAG	3,00	0,48	Hs.172180	KIAA0440 protein
2799	TAATTGAAATA	3,00	0,48	Hs.146668	KIAA1253 protein
2800	TGATGTGATCA	3,00	0,48	Hs.12272	beclin 1 (coiled-coil, myosin-like BCL2- interacting
2801	TGTGAGCCCCT	9,00	0,96	Hs.102948	enigma (LIM domain protein)
2802	TACAAGTTTTG	1,00	0,18	Hs.94554	ESTs
2803	GGTACCAAAAA	1,00	0,18	Hs.9450	zinc finger protein 84 (HPF2)
2804	CCTGGCTCAAA	1,00	0,18	Hs.93127	Homo sapiens mRNA; cDNA DKFZp586I0523 (from clone DK
2805	TAAGCCCTTTT	1,00	0,18	Hs.90606	15 kDa selenoprotein
2806	AGACCAATGAA	1,00	0,18	Hs.9029	DKFZP434G032 protein
2807	TGTTTGACTGT	1,00	0,18	Hs.8834	ring finger protein 3
2808	GACCAGCTGCC	1,00	0,18	Hs.84728	Kruppel-like factor 5 (intestinal)
2809	AGTTGAAGAAG	1,00	0,18	Hs.82120	nuclear receptor subfamily 4, group A, member 2
2810	AGTAGAAGAAT	1,00	0,18	Hs.74561	alpha-2-macroglobulin
2811	GAGCCCAGCCC	1,00	0,18	Hs.72885	azurocidin 1 (cationic antimicrobial pro- tein 37)
2812	CACATTTAATT	1,00	0,18	Hs.67619	Homo sapiens cDNA FLJ10533 fis, clone NT2RP2001056
2813	ACATATTGAGC	1,00	0,18	Hs.41086	hypothetical protein FLJ20067
2814	TTTGACTGATA	1,00	0,18	Hs.41086	hypothetical protein FLJ20067
2815	ACCAATACACT	1,00	0,18	Hs.29488	ESTs
2816	GTGAGACCCTA	1,00	0,18	Hs.280237	EST
2817	AAGATATTCTC	1,00	0,18	Hs.279934	Homo sapiens mRNA; cDNA DKFZp434I0835 (from clone DK
2818	GTGGTGCACCC	1,00	0,18	Hs.278709	EST, Weakly similar to A46010 X-linked retinopathy p
2819	TTCTTGCAGCA	1,00	0,18	Hs.273234	Human DNA sequence from clone 223H9 on chromosome 22



2820	CTTAATATATT	1,00	0,18	Hs.272168	tumor differentially expressed 1
2821	GTGATACCCCA	1,00	0,18	Hs.270302	ESTs
2822	GAAAATATTCC	1,00	0,18	Hs.267811	KIAA1099 protein
2823	ATGAAACCTTG	1,00	0,18	Hs.253488	EST
2824	CAAGATGAACC	1,00	0,18	Hs.25272	E1A binding protein p300
2825	ACAAGAAAAAA	1,00	0,18	Hs.234279	microtubule-associated protein, RP/EB family, member
2826	TTTCGATTTTT	1,00	0,18	Hs.225951	topoisomerase-related function protein 4
2827	ATAAAACCCTG	1,00	0,18	Hs.223317	EST, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C W
2828	GTGGCACGCAT	1,00	0,18	Hs.207823	Human EST clone 53125 mariner transposon Hsmar1 sequ
2829	AGGTGTTTCTT	1,00	0,18	Hs.19978	arylsulfatase D
2830	CTTTCTGTTAT	1,00	0,18	Hs.197335	plasma glutamate carboxypeptidase
2831	CTCCAAATCCC	1,00	0,18	Hs.197289	rab3 GTPase-activating protein, non-catalytic subunit
2832	GGGGGCTCCTT	1,00	0,18	Hs.19718	protein tyrosine phosphatase, receptor type, U
2833	CTTGAAAAAAA	1,00	0,18	Hs.184325	CGI-76 protein
2834	AAGGTGAGGAC	1,00	0,18	Hs.184216	DKFZP564C152 protein
2835	CAGGGGGTTCA	1,00	0,18	Hs.183639	hypothetical protein FLJ10210
2836	CCATTATTCTT	1,00	0,18	Hs.182225	RNA binding motif protein 3
2837	TGTTTTTTGTG	1,00	0,18	Hs.180638	Homo sapiens cDNA FLJ11066 fis, clone PLACE1004885
2838	TGATCCATCCT	1,00	0,18	Hs.178121	KIAA0626 gene product
2839	ATTAGTGTTGG	1,00	0,18	Hs.177781	superoxide dismutase 2, mitochondrial
2840	GCTATATTTCA	1,00	0,18	Hs.173571	KIAA1053 protein
2841	GTGCTATCCTG	1,00	0,18	Hs.172330	ESTs, Weakly similar to Wiskott-Aldrich Syndrome pro
2842	GGGAGACCCTG	1,00	0,18	Hs.169401	apolipoprotein E
2843	CTTTCAATGTT	1,00	0,18	Hs.164170	vascular Rab-GAP/TBC-containing
2844	CCATTCTTTTC	1,00	0,18	Hs.162685	ESTs, Moderately similar to similar to KIAA0855 [H.s
2845	CCTCTTTAAAG	1,00	0,18	Hs.156016	KIAA0140 gene product
2846	AAGAAGGGATC	1,00	0,18	Hs.15536	ESTs, Weakly similar to CNBP_HUMAN CELLULAR NUCLEIC
2847	AACCGCACCCA	1,00	0,18	Hs.142003	ESTs, Weakly similar to The KIAA0149 gene product is
2848	GTAAATGAGTA	1,00	0,18	Hs.138717	ESTs
2849	TAAACAAGCAA	1,00	0,18	Hs.135917	hypothetical protein DKFZp761D1823
2850	TGTATGTGGTA	1,00	0,18	Hs.13299	Homo sapiens mRNA; cDNA DKFZp761M0111 (from clone DK
2851	AGCCAGGGTAA	1,00	0,18	Hs.131525	KIAA0998 protein
2852	TTTTGATCACT	1,00	0,18	Hs.129952	KIAA0560 gene product
2853	CAGCTGGCACT	1,00	0,18	Hs.124418	ESTs
2854	TTAAGGGATGA	1,00	0,18	Hs.111177	ESTs
2855	CAGAATGAGCC	1,00	0,18	Hs.111138	KIAA0712 gene product
2856	TGACCACCTAC	1,00	0,18	Hs.108110	DKFZP547E2110 protein
2857	GTGGCAGCCGG	1,00	0,18	Hs.107054	KIAA0821 protein
2858	GAAGCCATTGT	1,00	0,18	Hs.106778	ATPase, Ca++ transporting, type 2C,

					member 1
2859	TATATGGATGG	1,00	0,18	Hs.106309	Friend of GATA2
2860	GTGCCCCGGCAC	1,00	0,18	Hs.104885	ESTs, Weakly similar to zinc finger protein zfp6 [H.
2861	GACCTTATTTT	1,00	0,18	Hs.100217	chromosome 17 open reading frame 1B
2862	CTGGGCCAGCC	4,00	0,57	Hs.74669	vesicle-associated membrane protein 5 (myobrevin)
2863	GCCAAGGGGCC	7,00	0,81	Hs.168669	oxoglutarate dehydrogenase (lipoamide)
2864	TCCTACAATCT	3,00	0,47	Hs.219614	f-box and leucine-rich repeat protein 11
2865	TAACCTAAGCA	3,00	0,47	Hs.184542	CGI-127 protein
2866	TGTAAAAAAA	3,00	0,47	Hs.112743	synaptonemal complex protein 1
2867	TACCCTAGAAC	27,00	1,88	Hs.252588	Homo sapiens mRNA; cDNA DKFZp564F172 (from clone DKF
2868	TCAGCAATAAA	5,00	0,65	Hs.21396	Homo sapiens cDNA FLJ20801 fis, clone ADSU01303
2869	CCTGTAATCCA	10,00	0,99	Hs.253369	EST
2870	TTGTGGAAATC	2,00	0,35	Hs.7807	ESTs, Weakly similar to predicted using Genefinder [
2871	ATGGGCACTGA	2,00	0,35	Hs.274201	60S acidic ribosomal protein PO
2872	GCTGACGAAA	2,00	0,35	Hs.226377	phosphate cytidylyltransferase 2, ethanolamine
2873	GTGCCTCGGAG	2,00	0,35	Hs.143046	Homo sapiens cDNA FLJ20418 fis, clone KAT02427
2874	ATGCTAAAAAA	5,00	0,65	Hs.116455	EST
2875	CTGCTGCCCA	3,00	0,46	Hs.82407	Homo sapiens HSPC296 mRNA, partial cds
2876	TGAGTGGTAGC	3,00	0,46	Hs.77886	lamin A/C
2877	GTGAGACCTTG	3,00	0,46	Hs.246469	EST
2878	GTAGCAGGTGT	11,00	1,04	Hs.140452	cargo selection protein (mannose 6 phosphate recepto
2879	GTCTGGGGGAT	6,00	0,72	Hs.6721	lysophospholipase-like
2880	TTCCACTAACC	13,00	1,15	Hs.79706	plectin 1, intermediate filament binding protein, 50
2881	TGAAGCAGTAA	8,00	0,85	Hs.100407	Homo sapiens mRNA; cDNA DKFZp564H2416 (from clone DK
2882	ACCGCTTGTTT	4,00	0,56	Hs.77515	inositol 1,4,5-triphosphate receptor, type 3
2883	CTGGCCAGGCT	4,00	0,56	Hs.182611	solute carrier family 11 (proton-coupled divalent me
2884	AGATTCAAAC	11,00	1,03	Hs.14368	SH3 domain binding glutamic acid-rich protein like
2885	AGTTGTCCCGG	6,00	0,71	Hs.239686	KIAA0462 protein
2886	CTGACTGTCCT	1,00	0,17	Hs.84298	CD74 antigen (invariant polypeptide of major histoco
2887	ACTGTATTGGA	1,00	0,17	Hs.83114	crystallin, zeta (quinone reductase)
2888	CAAATAACAAG	1,00	0,17	Hs.8262	lysosomal-associated membrane protein 2
2889	ACTTGTAATTA	1,00	0,17	Hs.80624	ESTs
2890	GACGACATTCG	1,00	0,17	Hs.79709	phosphatidylinositol transfer protein
2891	TACAAAGATGT	1,00	0,17	Hs.7890	ESTs

2892	TTTTCCCCTGA	1,00	0,17	Hs.7822	Homo sapiens mRNA; cDNA DKFZp564C1216 (from clone DK
2893	CTTGGATGGCT	1,00	0,17	Hs.7314	KIAA0614 protein
2894	GTAAATGCAA	1,00	0,17	Hs.66744	twist (Drosophila) homolog (acrocephalo- syndactily 3;
2895	CGATCACTGAC	1,00	0,17	Hs.6434	hypothetical protein DKFZp761F2014
2896	ATTGAGTCCAG	1,00	0,17	Hs.58609	ESTs
2897	GGGCTTACTGT	1,00	0,17	Hs.5472	hypothetical protein FLJ20173
2898	TACCTATTGTG	1,00	0,17	Hs.48958	ESTs
2899	CTTTAAGGTTT	1,00	0,17	Hs.48827	Homo sapiens mRNA; cDNA DKFZp761D0223 (from clone DK
2900	ATGCTCTATTT	1,00	0,17	Hs.42179	KIAA1286 protein
2901	GCAGGGAAATA	1,00	0,17	Hs.29263	ESTs
2902	AAAATGACAGA	1,00	0,17	Hs.28707	signal sequence receptor, gamma (trans- locon-associat
2903	AGCCCACTGCT	1,00	0,17	Hs.284251	KIAA0544 protein
2904	GGCCAGTGAGG	1,00	0,17	Hs.279899	tumor necrosis factor receptor super- family, member 1
2905	CCTTGCCTGAA	1,00	0,17	Hs.278431	SCO (cytochrome oxidase deficient, yeast) homolog 2
2906	AAAGTGTATTT	1,00	0,17	Hs.274396	KIAA1423 protein
2907	CAGCTTTGCTG	1,00	0,17	Hs.25248	ESTs
2908	TGAGCACTCGA	1,00	0,17	Hs.25005	ESTs
2909	CCTGTAATTTC	1,00	0,17	Hs.249622	EST
2910	AGTCACCAGCA	1,00	0,17	Hs.23598	CREB binding protein (Rubinstein-Taybi syndrome)
2911	GGTACACATAC	1,00	0,17	Hs.225568	ESTs
2912	TGAAAGTGATT	1,00	0,17	Hs.20695	KIAA0294 gene product
2913	CAGAGGCGTCC	1,00	0,17	Hs.193053	eukaryotic translation initiation factor 2C, 2
2914	TTTGTTGTTGA	1,00	0,17	Hs.18571	protein kinase, interferon-inducible dou- ble stranded
2915	TGCCCAACTTC	1,00	0,17	Hs.18376	KIAA1319 protein
2916	TAGTATGGCTA	1,00	0,17	Hs.173001	hypothetical protein
2917	CTATGTCTTTA	1,00	0,17	Hs.172280	SWI/SNF related, matrix associated, actin dependent
2918	CAAGTAACTAG	1,00	0,17	Hs.172199	adenylate cyclase 7
2919	CTTCCTTG TAG	1,00	0,17	Hs.171917	hypothetical protein FLJ11085
2920	GAAGATTGAGA	1,00	0,17	Hs.167503	signal transducer and activator of tran- scription 5A
2921	CCGTGAAGTTT	1,00	0,17	Hs.159448	surfeit 2
2922	GTGATGTGCGC	1,00	0,17	Hs.158455	ESTs
2923	TGATTACAATC	1,00	0,17	Hs.149155	voltage-dependent anion channel 1
2924	TTTCAATACCA	1,00	0,17	Hs.127006	ESTs
2925	GCAACCGTACT	1,00	0,17	Hs.126388	ESTs
2926	CTATGTTCTGT	1,00	0,17	Hs.11494	fibulin 5
2927	CCTAACGATAC	1,00	0,17	Hs.11317	ESTs
2928	TAAAGGCTTTT	1,00	0,17	Hs.109045	hypothetical protein FLJ10498
2929	GACACAGTTAT	1,00	0,17	Hs.108396	ALR-like protein
2930	TGTAGAAAAAA	10,00	0,96	Hs.179661	tubulin, beta polypeptide

2931	CTCATATGTTA	3,00	0,46	Hs.8939	yes-associated protein 65 kDa
2932	GGAGCCAGGCC	3,00	0,46	Hs.77490	glutathion S-transferase theta 1
2933	GTGAAACACCA	3,00	0,46	Hs.231777	EST
2934	GCTCTCGGCGG	3,00	0,46	Hs.183994	protein phosphatase 1, catalytic subunit, alpha isof
2935	CAGATTGCTGA	5,00	0,63	Hs.21537	protein phosphatase 1, catalytic subunit, beta isofo
2936	TCCACTACCAA	4,00	0,55	Hs.18885	CGI-116 protein
2937	TATCCTGGCTC	4,00	0,55	Hs.160483	erythrocyte membrane protein band 7.2 (stomatin)
2938	CCCAGCCTGAA	2,00	0,34	Hs.95783	ESTs
2939	TCTTTTAAAA	2,00	0,34	Hs.748	fibroblast growth factor receptor 1 (fms-related tyr
2940	AGGAGATGGAG	2,00	0,34	Hs.73987	CDC-like kinase 3
2941	CTGCAGAATAT	2,00	0,34	Hs.4310	eukaryotic translation initiation factor 1A
2942	ATTTTCCTTAG	2,00	0,34	Hs.279819	APR-1 protein
2943	TATTTATTCAA	2,00	0,34	Hs.267690	KIAA1228 protein
2944	CCGATTTTAC	2,00	0,34	Hs.26570	hypothetical protein FLJ20422
2945	AGCCTCGGCCA	2,00	0,34	Hs.252280	Rho guanine nucleotide exchange factor (GEF) 1
2946	GGACCACCCAA	2,00	0,34	Hs.239298	microtubule-associated protein 4
2947	CGAGTGAGAGG	2,00	0,34	Hs.206259	Homo sapiens mRNA for KIAA1190 protein, partial cds
2948	GTGAACCCTGT	2,00	0,34	Hs.204169	ESTs
2949	TGTGCATCTTG	2,00	0,34	Hs.18878	ESTs, Weakly similar to dJ876B10.4 [H.sapiens]
2950	TGTAGTATTTG	2,00	0,34	Hs.18842	protein kinase C and casein kinase substrate in neur
2951	TCTATCTCAGG	2,00	0,34	Hs.181406	endothelin converting enzyme 1
2952	CGGGGTGGCCG	2,00	0,34	Hs.1584	cartilage oligomeric matrix protein (pseudoachondrop
2953	CAGTGTATATA	2,00	0,34	Hs.108725	HSPC040 protein
2954	ACTTTAGATGG	8,00	0,83	Hs.80988	collagen, type VI, alpha 3
2955	GCCCAAGGACC	31,00	1,90	Hs.195464	filamin A, alpha (actin-binding protein-280)
2956	TGCACGTTTTTC	189,00	7,65	Hs.169793	ribosomal protein L32
2957	CATTATAACTT	5,00	0,63	Hs.84359	hypothetical protein
2958	GACCCTAGCTC	5,00	0,63	Hs.30570	polyglutamine binding protein 1
2959	AGCCACTGCAC	23,00	1,56	Hs.122126	ESTs
2960	AGGGGCCCGGGG	4,00	0,55	Hs.77448	aldehyde dehydrogenase 4 (glutamate gamma-semialdehy
2961	AGGAAGGAACA	4,00	0,55	Hs.173664	v-erb-b2 avian erythroblastic leukemia viral oncogen
2962	CCTAAACTCAA	3,00	0,45	Hs.16187	uncharacterized hematopoietic stem/progenitor cells
2963	TGTTCCCTTTG	3,00	0,45	Hs.118630	MAX-interacting protein 1
2964	GTTCATAGTAT	3,00	0,45	Hs.109253	N-terminal acetyltransferase complex ard1subunit
2965	AACTAACAAAA	59,00	2,94	Hs.3297	ribosomal protein S27a
2966	AAGGTGCCTCC	6,00	0,69	Hs.75410	heat shock 70kD protein 5 (glucose-

					regulated protein
2967	GGGGCTTCTGT	5,00	0,62	Hs.18069	protease, cysteine, 1 (legumain)
2968	GTGGTGGACAC	13,00	1,08	Hs.285196	hypothetical protein PRO1847
2969	CCGTGACTCTG	19,00	1,35	Hs.155712	Homo sapiens mRNA; cDNA DKFZp586O2223 (from clone DK
2970	TGCAGATGGTT	6,00	0,69	Hs.3628	mitogen-activated protein kinase kinase kinase
2971	AAAGGAATGAG	2,00	0,33	Hs.79672	KIAA0652 gene product
2972	ATAATAAAGCT	2,00	0,33	Hs.37682	retinoic acid receptor responder (tazaro- tene induced
2973	CTGCAGAAATT	2,00	0,33	Hs.286205	Homo sapiens clone 23938 mRNA se- quence
2974	ATCGATCGCCT	2,00	0,33	Hs.285211	KIAA1067 protein
2975	CCAGTAACCCC	2,00	0,33	Hs.238442	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY
2976	CACTTTTCTGT	2,00	0,33	Hs.23786	ESTs
2977	GTGGCATACAC	2,00	0,33	Hs.223603	Homo sapiens mRNA; cDNA DKFZp761D09121 (from clone D
2978	GTCCCAGGATT	2,00	0,33	Hs.158084	peroxisome receptor 1
2979	ATGTCTTCGTT	2,00	0,33	Hs.144926	ESTs
2980	AAAAGGAGATC	2,00	0,33	Hs.144904	nuclear receptor co-repressor 1
2981	GCGACCAACAT	5,00	0,61	Hs.4055	chromosome 21 open reading frame 50
2982	ATCCGCCTGCT	5,00	0,61	Hs.279904	ESTs
2983	GTGAAACCCAT	5,00	0,61	Hs.17311	hypothetical protein FLJ20004
2984	GACCACCTTTA	3,00	0,44	Hs.83551	microfibrillar-associated protein 2
2985	GAGCTTACATT	3,00	0,44	Hs.285706	ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C
2986	GTGAGACCTCA	3,00	0,44	Hs.268541	novel SH2-containing protein 1
2987	GAAACAAAATG	3,00	0,44	Hs.14896	DHHC1 protein
2988	GGTGAAGACAA	10,00	0,91	Hs.26951	KIAA0375 gene product
2989	TTGCTGTGTGA	4,00	0,53	Hs.108258	actin binding protein; macrophin (micro- filament and
2990	GTCTAGAATCT	5,00	0,61	Hs.92384	vitamin A responsive; cytoskeleton re- lated
2991	GCGAAACCCTG	62,00	2,85	Hs.199067	v-erb-b2 avian erythroblastic leukemia viral oncogen
2992	CTTCCTGTACA	7,00	0,74	Hs.273237	postmeiotic segregation increased 2-like 8
2993	GCTATGGTTTC	1,00	0,17	Hs.93560	ESTs, Weakly similar to unnamed pro- tein product [H.s
2994	GTGCAGTTAGC	1,00	0,17	Hs.8836	CGI-56 protein
2995	GTGCTATTATT	1,00	0,17	Hs.86386	myeloid cell leukemia sequence 1 (BCL2-related)
2996	GACCTTAAGGC	1,00	0,17	Hs.8562	hypothetical protein FLJ20374
2997	AGCAGTCCAAC	1,00	0,17	Hs.84264	acidic protein rich in leucines
2998	CCACTCCAAAA	1,00	0,17	Hs.82890	defender against cell death 1
2999	TTGTACAACCTG	1,00	0,17	Hs.79019	baculoviral IAP repeat-containing 1
3000	TCTTTTTTCAG	1,00	0,17	Hs.75209	protein kinase (cAMP-dependent, cata- lytic) inhibitor
3001	ACGCCGCCCAA	1,00	0,17	Hs.7306	secreted frizzled-related protein 1

3002	TGGTTTAAAAA	1,00	0,17	Hs.6298	KIAA1151 protein
3003	TAATTAATAAA	1,00	0,17	Hs.60293	ESTs
3004	CTTCATAACCA	1,00	0,17	Hs.55896	ESTs
3005	AGAAGCAAGAG	1,00	0,17	Hs.5470	IL-17B receptor
3006	TGTGGCCTCCA	1,00	0,17	Hs.5258	chromosome 11 open reading frame2
3007	GGCAGAAGATA	1,00	0,17	Hs.49349	beta-site APP-cleaving enzyme
3008	AGATAATCTGT	1,00	0,17	Hs.46571	SH3 domain protein 1B
3009	CATTTTGGATG	1,00	0,17	Hs.3994	ESTs
3010	GTGAAGAGTAA	1,00	0,17	Hs.38750	ESTs, Weakly similar to mSin3A associated polypeptid
3011	ATCAGTATGTG	1,00	0,17	Hs.278554	heterochromatin-like protein 1
3012	AGAATCCCTTG	1,00	0,17	Hs.277073	EST
3013	GAAGAAAAAAA	1,00	0,17	Hs.274429	Homo sapiens cDNA FLJ11192 fis, clone PLACE1007618.
3014	ACTGATCTTGA	1,00	0,17	Hs.27268	Homo sapiens mRNA; cDNA DKFZp564N196 (from clone DKF
3015	ACCCTTTTTTT	1,00	0,17	Hs.257486	hypothetical protein FLJ20062
3016	TTGTAAAAAAA	1,00	0,17	Hs.251377	taxol resistance associated gene 3
3017	GGGGAAAGCAG	1,00	0,17	Hs.242262	ESTs
3018	TAAGTGTCAA	1,00	0,17	Hs.238205	hypothetical protein PRO2013
3019	GTGGCTGATGC	1,00	0,17	Hs.238118	EST
3020	AAATTTGTATG	1,00	0,17	Hs.235445	Homo sapiens mRNA; cDNA DKFZp761G2312 (from clone DK
3021	AGCCACCAGGC	1,00	0,17	Hs.230396	EST
3022	AAGGACATTGG	1,00	0,17	Hs.214982	laminin, gamma 1 (formerly LAMB2)
3023	CCATAGATTTC	1,00	0,17	Hs.194035	KIAA0737 gene product
3024	TTCTCAATACA	1,00	0,17	Hs.193164	ESTs
3025	GCTTGTATGAG	1,00	0,17	Hs.186655	Homo sapiens mRNA; cDNA DKFZp434M0223 (from clone DK
3026	CCTGTCAATGT	1,00	0,17	Hs.18387	transcription factor AP-2 alpha (activating enhancer
3027	GGAATTTGCTT	1,00	0,17	Hs.183745	ESTs
3028	GGGCTAGTGGG	1,00	0,17	Hs.182591	RAS guanyl releasing protein 1 (calcium and DAG-regu
3029	GTGACGCCCCG	1,00	0,17	Hs.179661	tubulin, beta polypeptide
3030	CAATGAGCATC	1,00	0,17	Hs.173993	RNA binding motif protein 6
3031	AATGTACCTGG	1,00	0,17	Hs.173422	cAMP responsive element binding protein 3 (luman)
3032	GCCCTCATTA	1,00	0,17	Hs.169370	FYN oncogene related to SRC, FGR, YES
3033	ATACAAATATG	1,00	0,17	Hs.16533	myosin phosphatase, target subunit 1
3034	TTGCACTTAAT	1,00	0,17	Hs.16206	uncharacterized hypothalamus protein HT008
3035	AAAGCTGTGTT	1,00	0,17	Hs.155485	huntingtin interacting protein 2
3036	AGAATAAATCT	1,00	0,17	Hs.154437	phosphodiesterase 2A, cGMP-stimulated
3037	GAAACTACCC	1,00	0,17	Hs.150741	2',3'-cyclic nucleotide 3' phosphodiesterase
3038	TGGCCTAATAA	1,00	0,17	Hs.1501	syndecan 2 (heparan sulfate proteoglycan 1, cell sur
3039	GTATCAAGCAG	1,00	0,17	Hs.149436	kinesin family member 5B

3040	CCTGAGTGCCT	1,00	0,17	Hs.14595	hypothetical protein FLJ20615
3041	TAACACTGACT	1,00	0,17	Hs.13809	hypothetical protein FLJ10648
3042	TAATTCTTTTA	1,00	0,17	Hs.13572	calcium modulating ligand
3043	GCTCAAAACCT	1,00	0,17	Hs.123210	ESTs
3044	GCACGGAAAAA	1,00	0,17	Hs.118397	AE-binding protein 1
3045	CCTCTCCAACA	1,00	0,17	Hs.1162	major histocompatibility complex, class II, DM beta
3046	AGGGATATGGG	1,00	0,17	Hs.114434	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
3047	GATCAAAATTT	1,00	0,17	Hs.109805	Homo sapiens cDNA FLJ20153 fis, clone COL08656, high
3048	AGAGGGACAAC	1,00	0,17	Hs.10647	FLJ00005 protein
3049	CCATCCAGGCA	1,00	0,17	Hs.106260	sorting nexin 10
3050	TGTAACGTGGG	3,00	0,44	Hs.66762	Homo sapiens mRNA; cDNA DKFZp564A026 (from clone DKF
3051	CACCTTCTGCC	3,00	0,44	Hs.25511	transforming growth factor beta 1 induced transcript
3052	CTGTACAGACA	35,00	1,88	Hs.251653	tubulin, beta, 2
3053	AAAGTTTGAGA	4,00	0,53	Hs.23581	leptin receptor gene-related protein
3054	GGCTTCCTAAT	2,00	0,33	Hs.284146	hypothetical protein DKFZp762N0610
3055	CGAGGGGGGCG	2,00	0,33	Hs.169875	thrombospondin 3
3056	CCCAAGCTAGC	67,00	2,89	Hs.76067	heat shock 27kD protein 1
3057	CATATCATTA	28,00	1,60	Hs.119206	insulin-like growth factor binding protein 7
3058	CTCGGAGGCCT	4,00	0,52	Hs.279623	selenoprotein X
3059	GTAGACTTGTC	4,00	0,52	Hs.25213	hypothetical protein
3060	TCTGCAAGCAG	3,00	0,43	Hs.105598	ESTs, Weakly similar to neural variant mena++ protei
3061	ACCCCCCGGCC	22,00	1,36	Hs.277167	EST
3062	TGCAGTGACTG	4,00	0,52	Hs.79691	LIM domain protein
3063	TGGCTCCTCCC	4,00	0,52	Hs.76506	lymphocyte cytosolic protein 1 (L-plastin)
3064	CACTGTGTTGA	4,00	0,52	Hs.42362	hypothetical protein FLJ10330
3065	TATTTACCGT	6,00	0,65	Hs.138860	Rho GTPase activating protein 1
3066	TCCAGGAAACT	6,00	0,65	Hs.11590	cathepsin F
3067	CTGGGGGGAAG	2,00	0,32	Hs.77864	KIAA0638 protein
3068	GCTTTTGGAGG	2,00	0,32	Hs.35096	KIAA1538 protein
3069	TGCCTTAAACA	2,00	0,32	Hs.151518	TAR (HIV) RNA-binding protein 1
3070	AACATAGGAAA	2,00	0,32	Hs.119663	CD59 antigen p18-20 (antigen identified by monoclonal
3071	TAAGAGTGCTG	2,00	0,32	Hs.117582	CGI-43 protein
3072	GCTGTAGACAA	2,00	0,32	Hs.10362	ESTs
3073	GCGAAACCCTA	3,00	0,43	Hs.270249	ESTs
3074	GCTCAGATCGG	3,00	0,43	Hs.158286	KIAA0446 gene product
3075	TGGCCTCTCTG	4,00	0,51	Hs.75437	peroxisomal long-chain acyl-coA thio-esterase ; putat
3076	TTCTTGAACAA	11,00	0,90	Hs.76228	amplified in osteosarcoma
3077	GTGGCACACGC	33,00	1,67	Hs.192023	eukaryotic translation initiation factor 3, subunit
3078	TGTGGCCTCCT	10,00	0,85	Hs.5258	chromosome 11 open reading frame2
3079	GTTGTGATGTT	5,00	0,58	Hs.129953	Ewing sarcoma breakpoint region 1

3080	GTAGCAGGTGC	6,00	0,64	Hs.8728	hypothetical protein DKFZp434G171
3081	ACATCCCAGAA	6,00	0,64	Hs.17377	coronin, actin-binding protein, 1C
3082	TAATTTTGGAA	6,00	0,64	Hs.117582	CGI-43 protein
3083	GAAATTTTGA	1,00	0,16	Hs.98069	Sec23-interacting protein p125
3084	TTCTTTGAATA	1,00	0,16	Hs.979	pyruvate dehydrogenase (lipoamide) beta
3085	ACACTAAAATG	1,00	0,16	Hs.91640	nuclear factor of kappa light polypeptide gene enhan
3086	CAACCCAGATT	1,00	0,16	Hs.9096	hypothetical protein FLJ20473
3087	TCTTTCGTCTG	1,00	0,16	Hs.87138	ESTs
3088	ACTATCTCTAG	1,00	0,16	Hs.86347	hypothetical protein
3089	TTTGCTTGCAA	1,00	0,16	Hs.83938	ESTs, Moderately similar to MASP-2 [H.sapiens]
3090	TTTTGTACGCA	1,00	0,16	Hs.82116	myeloid differentiation primary response gene (88)
3091	AAGGAGATTAT	1,00	0,16	Hs.79402	polymerase (RNA) II (DNA directed) polypeptide C (33)
3092	AGGCTATTGGA	1,00	0,16	Hs.76507	LPS-induced TNF-alpha factor
3093	CATAAATATGC	1,00	0,16	Hs.75598	heterogeneous nuclear ribonucleoprotein A2/B1
3094	TTTATAACTAT	1,00	0,16	Hs.75066	translin
3095	GAAAATAAACT	1,00	0,16	Hs.71252	Homo sapiens mRNA; cDNA DKFZp761C169 (from clone DKF
3096	TAAGGCTTAAC	1,00	0,16	Hs.69423	kallikrein 10
3097	TGGTTAGATAA	1,00	0,16	Hs.6179	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17 (72k
3098	CAGGCTGCTGG	1,00	0,16	Hs.60440	ESTs, Weakly similar to serin protease with IGF-bind
3099	GCCTGGAGTTG	1,00	0,16	Hs.57877	ESTs
3100	ACCCACTTTCT	1,00	0,16	Hs.5716	KIAA0310 gene product
3101	ACGATGGCCGA	1,00	0,16	Hs.5210	glia maturation factor, gamma
3102	TAAATTGGATA	1,00	0,16	Hs.5151	RAN binding protein 7
3103	AACTGTATACA	1,00	0,16	Hs.502	ATP-binding cassette, sub-family B (MDR/TAP), member
3104	GATTCTGAGTT	1,00	0,16	Hs.47679	Homo sapiens mRNA; cDNA DKFZp564I112 (from clone DKF
3105	TTGAGTGCAGT	1,00	0,16	Hs.44754	ESTs
3106	AGTTGCAGATA	1,00	0,16	Hs.30258	ESTs
3107	GCGCACCCTG	1,00	0,16	Hs.29385	AFG3 (ATPase family gene 3, yeast)-like 2
3108	GCTTCACACCA	1,00	0,16	Hs.284932	Homo sapiens clone 24650 ubiquitin hydrolase mRNA, p
3109	GTGGGCCAGGA	1,00	0,16	Hs.284380	gamma-glutamyltransferase 1
3110	CCAGAAAAGAG	1,00	0,16	Hs.279914	zinc finger protein 232
3111	CCCAACTAATT	1,00	0,16	Hs.279893	hypothetical protein FLJ20342
3112	AATCCCCATCC	1,00	0,16	Hs.262292	ESTs
3113	GTGCTCATTCT	1,00	0,16	Hs.25945	ESTs
3114	CTCTGCTGTCT	1,00	0,16	Hs.257135	EST
3115	TCTAAATAAAA	1,00	0,16	Hs.238814	EST
3116	ACCAACTAGAA	1,00	0,16	Hs.23853	ESTs



3117	GGAGGTTGAGG	1,00	0,16	Hs.228827	EST
3118	GAGAAGAAATG	1,00	0,16	Hs.211773	checkpoint suppressor 1
3119	CCTACTAAATG	1,00	0,16	Hs.21016	coagulation factor C (Limulus polyphemus) homology (
3120	AGCTACCACGC	1,00	0,16	Hs.193965	ESTs
3121	CTAAATCACTG	1,00	0,16	Hs.19180	Homo sapiens mRNA; cDNA DKFZp564E122 (from clone DKF
3122	TGGAAGGTAAT	1,00	0,16	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (from clone DKF
3123	ATTGCTAAAAA	1,00	0,16	Hs.182470	PTD010 protein
3124	GCCAAGGGGTT	1,00	0,16	Hs.180832	arginyl-tRNA synthetase
3125	TTTTTTAAAAA	1,00	0,16	Hs.177559	interferon gamma receptor 2 (interferon gamma transd
3126	GAGAGATGACG	1,00	0,16	Hs.17240	ESTs
3127	AATAAGCCAAT	1,00	0,16	Hs.169963	butyrophilin, subfamily 2, member A1
3128	CTGTGCTCTAC	1,00	0,16	Hs.169501	ESTs
3129	GCTGCCAGCAC	1,00	0,16	Hs.1578	baculoviral IAP repeat-containing 5 (survivin)
3130	CCAACAGTCTT	1,00	0,16	Hs.154429	KIAA0693 protein
3131	CCTCCTCTGCT	1,00	0,16	Hs.153503	ESTs
3132	TGAAACCCTGT	1,00	0,16	Hs.142067	ESTs
3133	AATTGAATAAT	1,00	0,16	Hs.132415	prefoldin 2
3134	AGAAAATGTGA	1,00	0,16	Hs.127842	CGI-142
3135	CCCTCTCTGTA	1,00	0,16	Hs.126783	ESTs
3136	GGATTCTGACT	1,00	0,16	Hs.12150	retinal short-chain dehydrogenase/reductase retSDR2
3137	TTCTAAGTGTG	1,00	0,16	Hs.119488	cystein-rich hydrophobic domain 2
3138	GCATTGTTTTA	1,00	0,16	Hs.118722	fucosyltransferase 8 (alpha (1,6) fucosyltransferase
3139	GAGAAGACTGT	1,00	0,16	Hs.118281	zinc finger protein 266
3140	TTACAACAGCA	1,00	0,16	Hs.118174	tetratricopeptide repeat domain 3
3141	GTAGAGTAGGA	1,00	0,16	Hs.106826	hypothetical protein
3142	CTAATTTTACA	1,00	0,16	Hs.10283	ESTs
3143	CTGAGGGTGGT	4,00	0,50	Hs.279761	HSPC134 protein
3144	CCACTCTGGCT	3,00	0,42	Hs.83919	glucosidase I
3145	GTGAGCAAGAC	3,00	0,42	Hs.78040	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein
3146	CACTGTGTGTA	3,00	0,42	Hs.164207	ESTs
3147	TAGCAATCAGA	2,00	0,32	Hs.83795	interferon regulatory factor 2
3148	GATGGAATGTT	2,00	0,32	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (from clone DK
3149	ACTGGGTGGAA	2,00	0,32	Hs.59622	ESTs, Weakly similar to unknown [H.sapiens]
3150	CACCTAATTGA	2,00	0,32	Hs.282283	baculoviral IAP repeat-containing 2
3151	TTCACAGTGCA	2,00	0,32	Hs.25129	hypothetical protein FLJ10420
3152	GTGGACTTTTG	2,00	0,32	Hs.226372	DKFZP434J154 protein
3153	CCTTACCTACA	2,00	0,32	Hs.184542	CGI-127 protein
3154	CATAACCTTCC	2,00	0,32	Hs.167460	splicing factor, arginine/serine-rich 3
3155	GCTAGGTATTT	2,00	0,32	Hs.165986	testin
3156	TTGTAAAGTAA	2,00	0,32	Hs.158688	translation initiation factor IF2

3157	CCCTTGACCCT	2,00	0,32	Hs.124009	Human DNA sequence from clone RP5-860F19 on chromoso
3158	CCACTAATGGA	4,00	0,50	Hs.180139	SMT3 (suppressor of mif two 3, yeast) homolog 2
3159	AGCTCTGCTGC	4,00	0,50	Hs.102402	Mad4 homolog
3160	TTTGCACCTTT	21,00	1,22	Hs.75511	connective tissue growth factor
3161	GCTTTGATGAT	9,00	0,78	Hs.89649	epoxide hydrolase 1, microsomal (xeno-biotic)
3162	TGTGGCCTGCA	3,00	0,42	Hs.76480	ubiquitin-like 4
3163	CGGAACACCGT	3,00	0,42	Hs.155191	villin 2 (ezrin)
3164	CTAACCAGACA	10,00	0,82	Hs.76368	capping protein (actin filament) muscle Z-line, beta
3165	CTTAATCCTGA	22,00	1,23	Hs.234433	amino acid transporter 2
3166	GTCACCTGCCTC	5,00	0,56	Hs.105584	ribosomal protein S6 kinase, 90kD, polypeptide 4
3167	AGAGGGTGGGA	2,00	0,31	Hs.82646	heat shock 40kD protein 1
3168	TTGTTTAATTT	2,00	0,31	Hs.75546	capping protein (actin filament) muscle Z-line, alph
3169	CTTGTAACCTG	2,00	0,31	Hs.57209	ESTs
3170	GTCAAAAAAAA	2,00	0,31	Hs.271699	polymerase (DNA directed) iota
3171	GGGGTACCCCT	2,00	0,31	Hs.187520	ESTs, Weakly similar to dJ353E16.2 [H.sapiens]
3172	GTGGCATTTC	2,00	0,31	Hs.1244	CD9 antigen (p24)
3173	ATTGATCAATA	2,00	0,31	Hs.122489	ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C
3174	TGGCTAAAAAA	11,00	0,85	Hs.110048	ESTs
3175	TGCCAGAAATG	3,00	0,41	Hs.63510	KIAA0141 gene product
3176	GCTCTGGTTCT	3,00	0,41	Hs.6127	ESTs, Weakly similar to A46010 X-linked retinopathy
3177	GCTCCTTTTAC	3,00	0,41	Hs.13233	ESTs
3178	CTCTGGGATAG	4,00	0,49	Hs.285254	ESTs
3179	AAGAAAGGAGT	5,00	0,56	Hs.202097	procollagen C-endopeptidase enhancer
3180	ATGAACCGCAG	7,00	0,66	Hs.252259	ribosomal protein S3
3181	GTTACATTAG	62,00	2,18	Hs.84298	CD74 antigen (invariant polypeptide of major histoco
3182	GATGCTTTCTC	2,00	0,31	Hs.75852	casein kinase 1, delta
3183	ATGACCTGAAG	2,00	0,31	Hs.74050	follicular lymphoma variant translocation 1
3184	GGAACCAGGTC	2,00	0,31	Hs.7404	ESTs
3185	TCCTCTACCTG	2,00	0,31	Hs.32018	SNARE associated protein snapin
3186	TGAAGAGACTT	2,00	0,31	Hs.240767	Human DNA sequence from clone RP1-12G14 on chromosom
3187	GCACCAAAAAA	2,00	0,31	Hs.23585	KIAA1078 protein
3188	TAACCAAATAC	2,00	0,31	Hs.201623	ESTs
3189	TATTCCCCACC	2,00	0,31	Hs.199316	ESTs
3190	TTCCAGCTGCT	2,00	0,31	Hs.19121	adaptor-related protein complex 2, alpha 2 subunit
3191	GTAGACTCTTT	2,00	0,31	Hs.181300	sel-1 (suppressor of lin-12, C.elegans)-like
3192	CTTCAATTCTG	2,00	0,31	Hs.167700	Homo sapiens cDNA FLJ10174 fis, clone

					HEMBA1003959
3193	ACAGCTAACAG	2,00	0,31	Hs.12183	KIAA0935 protein
3194	CTCGCTTCTCC	2,00	0,31	Hs.110953	Homo sapiens mRNA; cDNA DKFZp434A139 (from clone DKF
3195	TCATTCCACTG	1,00	0,16	Hs.99804	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
3196	TACTGATTACT	1,00	0,16	Hs.9599	solute carrier family 25, member 13 (citrin)
3197	TCAGGTACTGA	1,00	0,16	Hs.83951	Hermansky-Pudlak syndrome
3198	AAACTGTGAAT	1,00	0,16	Hs.83623	nuclear receptor subfamily 1, group I, member 3
3199	ACTGACTGACT	1,00	0,16	Hs.83050	phosphoinositide-3-kinase, regulatory subunit 4, p15
3200	TACTTGAAGGA	1,00	0,16	Hs.79067	MAD (mothers against decapentaplegic, Drosophila) ho
3201	TTTAACAGAAA	1,00	0,16	Hs.77617	nuclear antigen Sp100
3202	TATCAAAACAC	1,00	0,16	Hs.74420	origin recognition complex, subunit 3 (yeast homolog
3203	GTTATATCCAA	1,00	0,16	Hs.71475	hypothetical protein
3204	ATGAACTGATT	1,00	0,16	Hs.6630	ESTs
3205	CTGACGGGTAT	1,00	0,16	Hs.63795	Homo sapiens mRNA; cDNA DKFZp434P232 (from clone DKF
3206	GAATATGGCTA	1,00	0,16	Hs.59594	ESTs, Weakly similar to F33G12.3 gene product [C.ele
3207	CTTGGGTCCTA	1,00	0,16	Hs.5288	Homo sapiens mRNA; cDNA DKFZp434M245 (from clone DKF
3208	GGTGGGAAGTC	1,00	0,16	Hs.40834	transitional epithelia response protein
3209	GAATGGGCTGG	1,00	0,16	Hs.32988	ESTs, Weakly similar to KIAA0412 [H.sapiens]
3210	CAGTTTGCATC	1,00	0,16	Hs.31547	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex,
3211	TAGTCATTGAG	1,00	0,16	Hs.28020	KIAA0766 gene product
3212	ACAATAATAGA	1,00	0,16	Hs.27258	calcyclin binding protein
3213	CCTTTCCTACC	1,00	0,16	Hs.26731	ESTs
3214	TTGAGCTTATG	1,00	0,16	Hs.26129	ESTs
3215	AGCCACTGCAT	1,00	0,16	Hs.258916	ESTs
3216	GAGCAAATGTT	1,00	0,16	Hs.24724	MFH-amplified sequences with leucine-rich tandem rep
3217	TTGGTATGAAG	1,00	0,16	Hs.2471	KIAA0020 gene product
3218	TGTAAAATGGG	1,00	0,16	Hs.247099	hypothetical protein from EUROIMAGE 2260343
3219	ATTAATAAAAA	1,00	0,16	Hs.24594	ubiquitination factor E4B (homologous to yeast UFD2)
3220	AGAATCATTTG	1,00	0,16	Hs.236651	EST, Moderately similar to ALU7_HUMAN ALU SUBFAMILY
3221	GAATTCCAGTT	1,00	0,16	Hs.235709	ESTs
3222	TCTCCATCACT	1,00	0,16	Hs.226770	DKFZP566C0424 protein
3223	AGTATGAGGAA	1,00	0,16	Hs.211600	tumor necrosis factor, alpha-induced protein 3
3224	GTAAGTGCCCA	1,00	0,16	Hs.198491	ESTs
3225	TGGGAAACAAG	1,00	0,16	Hs.184668	SBBI31 protein

3226	AAAACCTGCCTG	1,00	0,16	Hs.180338	tumor necrosis factor receptor super-family, member 1
3227	CTAAATAAAGT	1,00	0,16	Hs.172649	ESTs
3228	GCCATACAGCC	1,00	0,16	Hs.17110	Homo sapiens mRNA; cDNA DKFZp434C2016 (from clone DK
3229	GTCTGATATCT	1,00	0,16	Hs.14920	Homo sapiens mRNA; cDNA DKFZp564I1916 (from clone DK
3230	GGCAACAAAGC	1,00	0,16	Hs.14434	ESTs
3231	AATGGGAGTTT	1,00	0,16	Hs.128355	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY
3232	GAAACCCAAAA	1,00	0,16	Hs.125522	ESTs
3233	GAAAAACCCCTG	1,00	0,16	Hs.124946	ESTs
3234	AGGCCCTTAT	1,00	0,16	Hs.124740	ESTs, Moderately similar to ALU4_HUMAN ALU SUBFAMILY
3235	AATAAATTTGC	1,00	0,16	Hs.1117	tripeptidyl peptidase II
3236	TCATACCATTG	1,00	0,16	Hs.111138	KIAA0712 gene product
3237	CCAAGGATTGG	6,00	0,61	Hs.9003	Homo sapiens cDNA FLJ20672 fis, clone KAIA4492, high
3238	AAAAGATACTA	4,00	0,49	Hs.82071	Cbp/p300-interacting transactivator, with Glu/Asp-ri
3239	GGGCCAGGGG	4,00	0,49	Hs.3803	reticulon 2
3240	GGCAAGCCCCA	110,00	3,14	Hs.252574	ribosomal protein L10a
3241	GAGCCTGGATA	3,00	0,41	Hs.9004	chondroitin sulfate proteoglycan 4 (melanoma-associ
3242	GAGGGTTCCAG	3,00	0,41	Hs.167835	acyl-Coenzyme A oxidase 1, palmitoyl
3243	TAGACCAGATA	3,00	0,41	Hs.108945	KIAA0515 protein
3244	CTGCCAAGTTG	27,00	1,31	Hs.75873	zyxin
3245	CCTGCCACCC	5,00	0,55	Hs.4909	dickkopf (Xenopus laevis) homolog 3
3246	AACACATCAGC	3,00	0,40	Hs.76253	spinocerebellar ataxia 2 (olivopontocerebellar ataxi
3247	AGCTATTCCTC	3,00	0,40	Hs.75334	exostoses (multiple) 2
3248	ACCAGCTCCCC	3,00	0,40	Hs.22546	ESTs, Weakly similar to C561_HUMAN CYTOCHROME B561 [
3249	AAGACCGAGGG	3,00	0,40	Hs.116754	ESTs, Highly similar to MPP8_HUMAN M-PHASE PHOSPHOPR
3250	TGTTTGTGTGT	5,00	0,54	Hs.85015	ESTs, Weakly similar to A4P_HUMAN INTESTINAL MEMBRAN
3251	GGGGCTTCCAG	2,00	0,30	Hs.9729	KIAA0239 protein
3252	ATGATCTGCCT	2,00	0,30	Hs.9460	ESTs
3253	TTGAATTTGTT	2,00	0,30	Hs.80248	RNA-binding protein gene with multiple splicing
3254	TATTTTCTAG	2,00	0,30	Hs.7579	hypothetical protein FLJ10402
3255	TTATATTGCCA	2,00	0,30	Hs.74569	KIAA0842 protein
3256	TAGCTGTCTTT	2,00	0,30	Hs.43141	DKFZP727C091 protein
3257	TGGCTTCCCCA	2,00	0,30	Hs.279851	hypothetical protein FLJ10241
3258	GTTCCAACAAA	2,00	0,30	Hs.15430	neuroblastoma-amplified protein
3259	CGAATGTCCTT	2,00	0,30	Hs.111758	keratin 6B
3260	TGTAGCTGCAA	2,00	0,30	Hs.107882	hypothetical protein FLJ10659
3261	GAGCAGGAGCC	4,00	0,48	Hs.9028	histone deacetylase 5
3262	AAACCAAAAAA	4,00	0,48	Hs.76753	endoglin (Osler-Rendu-Weber syndrome

					1)
3263	GCTTTTATTCA	4,00	0,48	Hs.31819	HT014
3264	AGGAACACAAA	4,00	0,48	Hs.211539	eukaryotic translation initiation factor 2, subunit
3265	TCTCTTTTCT	7,00	0,64	Hs.119529	epididymal secretory protein (19.5kD)
3266	CCCCAGCCAGT	75,00	2,20	Hs.252259	ribosomal protein S3
3267	AGTCGCCTTCA	3,00	0,40	Hs.7811	eukaryotic translation initiation factor 3, subunit
3268	GAGGGTCTTGT	3,00	0,40	Hs.256310	SH3 domain-containing protein 6511
3269	GCGGCTGACAG	3,00	0,40	Hs.236511	ESTs, Moderately similar to RNA splicing-related pro
3270	ATGTGTAACGA	10,00	0,76	Hs.81256	S100 calcium-binding protein A4 (calcium protein, ca
3271	GGGTTTGTTTC	5,00	0,53	Hs.75969	proline-rich protein with nuclear targeting signal
3272	GCAACTTGGAG	5,00	0,53	Hs.33787	vinexin beta (SH3-containing adaptor molecule-1)
3273	TTGCCAACACC	2,00	0,30	Hs.80919	synaptophysin-like protein
3274	AATGTGAAATG	2,00	0,30	Hs.61164	ESTs, Weakly similar to unknown [D.melanogaster]
3275	GGAATGCCTCT	2,00	0,30	Hs.43125	ESTs
3276	TTCTAGTCTGC	2,00	0,30	Hs.282283	baculoviral IAP repeat-containing 2
3277	GTTATAATACG	2,00	0,30	Hs.159640	serum/glucocorticoid regulated kinase
3278	CCAAGGGTCCA	2,00	0,30	Hs.13494	ESTs
3279	GGAGTCCTAGC	2,00	0,30	Hs.108894	hypothetical protein FLJ20411
3280	GAAGTAAAAA	1,00	0,15	Hs.92381	nudix (nucleoside diphosphate linked moiety X)-type
3281	CTTCAAGAGTT	1,00	0,15	Hs.90093	heat shock 70kD protein 4
3282	TTCTGTCCCTT	1,00	0,15	Hs.89781	upstream binding transcription factor, RNA polymeras
3283	CCTACAGACAC	1,00	0,15	Hs.8904	Ig superfamily protein
3284	CTTACATTTTA	1,00	0,15	Hs.82128	5T4 oncofetal trophoblast glycoprotein
3285	TTCTGAAGACA	1,00	0,15	Hs.76901	for protein disulfide isomerase-related
3286	ATTCTTAAACA	1,00	0,15	Hs.75544	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase
3287	TCCTGAATGAA	1,00	0,15	Hs.72085	hypothetical protein FLJ10853
3288	TGTGTTTATTG	1,00	0,15	Hs.6809	RAP2A, member of RAS oncogene family
3289	GCAACGTAATA	1,00	0,15	Hs.65329	kraken-like
3290	CAGTAAAGGTT	1,00	0,15	Hs.6163	ESTs, Weakly similar to myotonic dystrophy kinase [H
3291	AAATCCTCAAA	1,00	0,15	Hs.55024	hypothetical protein FLJ10307
3292	GAGCCTCACAC	1,00	0,15	Hs.51039	KIAA0076 gene product
3293	CCTTTCTTTAT	1,00	0,15	Hs.50535	ESTs
3294	GAAGTTCTCTG	1,00	0,15	Hs.47438	SH3 domain binding glutamic acid-rich protein
3295	AGGGCACAGGG	1,00	0,15	Hs.32112	ESTs
3296	TCAATATCACT	1,00	0,15	Hs.29276	hypothetical protein FLJ20457
3297	TTTTTATTTAG	1,00	0,15	Hs.284169	Homo sapiens mRNA full length insert cDNA clone EURO

3298	CACAGTATTTG	1,00	0,15	Hs.279009	seven in absentia (Drosophila) homolog 1
3299	TGAGAGTATTT	1,00	0,15	Hs.273391	Homo sapiens mRNA; cDNA DKFZp761N05121 (from clone D
3300	CAATAAACTG	1,00	0,15	Hs.267905	hypothetical protein FLJ10422
3301	GTGGCCGCGCAC	1,00	0,15	Hs.258519	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC
3302	AGGATCGCTTG	1,00	0,15	Hs.255687	ESTs
3303	TTCCAGTAAAC	1,00	0,15	Hs.241543	DKFZP586F1524 protein
3304	TTTTCCACATC	1,00	0,15	Hs.21291	ESTs
3305	GTGACAGAGTG	1,00	0,15	Hs.210496	hypothetical protein PRO2738
3306	TCACACTGGCT	1,00	0,15	Hs.1975	TAL1 (SCL) interrupting locus
3307	GGA CTGGGTCG	1,00	0,15	Hs.194714	synaptosomal-associated protein, 29kD
3308	GTGAACCCCAT	1,00	0,15	Hs.185973	membrane fatty acid (lipid) desaturase
3309	TGGCTGCATAG	1,00	0,15	Hs.164478	ESTs, Weakly similar to AF161483_1 HSPC134 [H.sapien
3310	AACTCAGCTCC	1,00	0,15	Hs.156044	ESTs
3311	GAATAAACCAT	1,00	0,15	Hs.155894	protein tyrosine phosphatase, non-receptor type 1
3312	CCTGCCGCCTA	1,00	0,15	Hs.147176	epidermal growth factor receptor substrate EPS15R
3313	CACACCATTGT	1,00	0,15	Hs.136644	CS box-containing WD protein
3314	GTTCTGTAAA	1,00	0,15	Hs.13525	hypothetical protein
3315	TTGACAAATTG	1,00	0,15	Hs.130824	ESTs
3316	ATATACTGTAC	1,00	0,15	Hs.126857	ESTs
3317	CGCCGAGCACG	1,00	0,15	Hs.123426	ESTs, Weakly similar to putative serine/threonine pr
3318	ACATTTTAAAG	1,00	0,15	Hs.117582	CGI-43 protein
3319	GACGGTATCAC	1,00	0,15	Hs.112110	PTD007 protein
3320	GAAATATTGCT	1,00	0,15	Hs.11123	ESTs, Weakly similar to B38919 hypothetical protein
3321	AAACTACCCTT	1,00	0,15	Hs.101282	Homo sapiens mRNA; cDNA DKFZp434B102 (from clone DKF
3322	CAGCAGTAGCG	5,00	0,53	Hs.74441	chromodomain helicase DNA binding protein 4
3323	GTGGAATAAAG	3,00	0,40	Hs.83337	latent transforming growth factor beta binding prote
3324	AAGGTGGAGGA	148,00	3,27	Hs.163593	ribosomal protein L18a
3325	GGTGGCACTCA	25,00	1,14	Hs.77273	ras homolog gene family, member A
3326	AATCTTGCAA	5,00	0,53	Hs.109201	CGI-86 protein
3327	TCAACTGAAGT	4,00	0,47	Hs.74170	metallothionein 1E (functional)
3328	GTGGCGCGCAC	4,00	0,47	Hs.261403	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX
3329	CTCACC GCCCT	4,00	0,47	Hs.183650	cellular retinoic acid-binding protein 2
3330	AGATAACACAG	3,00	0,39	Hs.194369	arginine-glutamic acid dipeptide (RE) repeats
3331	CCTTGCTTTT	3,00	0,39	Hs.183438	DKFZP566J153 protein
3332	GAGTAAAAAAA	3,00	0,39	Hs.17752	phosphatidylserine-specific phospholipase A1alpha
3333	GCGGCTTCCG	6,00	0,58	Hs.278431	SCO (cytochrome oxidase deficient,

					yeast) homolog 2
3334	GTGGTGCGCAC	6,00	0,58	Hs.11090	high affinity immunoglobulin epsilon receptor beta s
3335	AAATAAAAGCT	8,00	0,66	Hs.155191	villin 2 (ezrin)
3336	TCACCTTAGGT	11,00	0,77	Hs.239625	integral membrane protein 2B
3337	CTTCTAGCAAA	2,00	0,30	Hs.9042	Homo sapiens EST from clone 491476, full insert
3338	GCAAATGCCGT	2,00	0,30	Hs.8551	PRP4/STK/WD splicing factor
3339	TGTCCTCCCCA	2,00	0,30	Hs.62119	Homo sapiens clone 25020 mRNA sequence
3340	CCGCTTCTGCT	2,00	0,30	Hs.5245	hypothetical protein FLJ20643
3341	TACCCTGGAAC	2,00	0,30	Hs.283048	hypothetical protein PRO0128
3342	GTCGGACACTG	2,00	0,30	Hs.278559	tailin
3343	TCCTGTAAAGG	11,00	0,76	Hs.74034	Homo sapiens clone 24651 mRNA sequence
3344	AGGATGACCAG	4,00	0,46	Hs.69554	hypothetical protein FLJ20552
3345	TTGCAACCAAA	4,00	0,46	Hs.10101	ESTs, Weakly similar to coded for by C. elegans cDNA
3346	TGAGGGTTAGA	3,00	0,39	Hs.6603	hypothetical protein FLJ20296
3347	CTCCCCATCAG	3,00	0,39	Hs.238030	secretory carrier membrane protein 2
3348	CTGGGATCATC	5,00	0,52	Hs.12623	ESTs
3349	CCTAAGGCTAA	5,00	0,52	Hs.108371	E2F transcription factor 4, p107/p130-binding
3350	GATTAAACCAG	6,00	0,57	Hs.90375	hypothetical protein FLJ10597
3351	GTTGTGGTTAA	115,00	2,41	Hs.75415	beta-2-microglobulin
3352	GCTGGCAGGCC	4,00	0,46	Hs.154886	choline kinase-like
3353	TAGGAAAGTAA	3,00	0,39	Hs.62192	coagulation factor III (thromboplastin, tissue facto
3354	AGGCCCTGCTC	3,00	0,39	Hs.6193	Homo sapiens mRNA; cDNA DKFZp434C1717 (from clone DK
3355	ACAGAGCACAG	2,00	0,29	Hs.78672	laminin, alpha 4
3356	GCACTTCAAAC	2,00	0,29	Hs.66191	Homo sapiens clone 24675 mRNA sequence
3357	CCTGCCTCGTA	2,00	0,29	Hs.61490	schwannomin interacting protein 1
3358	AGCCAGCCATT	2,00	0,29	Hs.33287	nuclear factor I/B
3359	CTTTATGTGTA	2,00	0,29	Hs.284136	PRO2047 protein
3360	CATTAAAGGGT	2,00	0,29	Hs.105509	CTL2 gene
3361	GTGGCGCGTGT	2,00	0,29	Hs.102483	KIAA1002 protein
3362	GAATAACAACC	1,00	0,15	Hs.99603	ESTs, Moderately similar to ALU8 HUMAN ALU SUBFAMILY
3363	TTTGTGAATAT	1,00	0,15	Hs.91393	Homo sapiens clone HQ0189 PRO0189 mRNA, complete cds
3364	AGAAAGGGAGA	1,00	0,15	Hs.819	homeo box B7
3365	CTTAATGGTGT	1,00	0,15	Hs.8026	ESTs, Moderately similar to p53 regulated PA26-T2 nu
3366	TTTGTCAATTT	1,00	0,15	Hs.7918	uncharacterized hypothalamus protein HSMNP1
3367	AAAGAATATGA	1,00	0,15	Hs.79162	structure specific recognition protein 1
3368	TAATGCTAAAA	1,00	0,15	Hs.78944	regulator of G-protein signalling 2, 24kD
3369	AATTAATTAAA	1,00	0,15	Hs.74050	follicular lymphoma variant translocation

					1
	3370	AGAAGACTGGT	1,00	0,15	Hs.71523 ESTs
5	3371	ATTCAACAATT	1,00	0,15	Hs.7120 cytokine receptor-like molecule 9
	3372	CTTAAAGTCTG	1,00	0,15	Hs.7099 hypothetical protein FLJ20265
	3373	GGCCCTTGCCT	1,00	0,15	Hs.6259 ESTs
	3374	TTGGAGCAAAG	1,00	0,15	Hs.55346 ESTs, Weakly similar to Z141_HUMAN ZINC FINGER PROTE
10	3375	CAGAAGAGAAG	1,00	0,15	Hs.5003 KIAA0456 protein
	3376	GTATTTATCTT	1,00	0,15	Hs.34804 ESTs
	3377	GACTCTGGAAA	1,00	0,15	Hs.2953 ribosomal protein S15a
	3378	GGGTGGGCAGT	1,00	0,15	Hs.284226 F-box only protein 6
15	3379	AAATATAATGA	1,00	0,15	Hs.279586 adrenal gland protein AD-004
	3380	AAGCAAGTTCC	1,00	0,15	Hs.277076 EST
	3381	CTCACAAAAAA	1,00	0,15	Hs.27356 ESTs
20	3382	TATATAGGTCC	1,00	0,15	Hs.272814 Homo sapiens mRNA; cDNA DKFZp434E1723 (from clone DK
	3383	AAATCAATAAA	1,00	0,15	Hs.270552 ESTs
	3384	TTTTATTATTT	1,00	0,15	Hs.23703 ESTs
25	3385	GGCCGTTGACC	1,00	0,15	Hs.22653 KIAA0844 protein
	3386	TGTTAATTTAT	1,00	0,15	Hs.216958 KIAA0194 protein
	3387	AAGCTGGCCCA	1,00	0,15	Hs.20594 hypothetical protein FLJ20203
	3388	ACAGCTACAGT	1,00	0,15	Hs.19631 ESTs
30	3389	GTGATGCACGC	1,00	0,15	Hs.193396 ESTs, Weakly similar to alternatively spliced produc
	3390	AAGTTCCCATT	1,00	0,15	Hs.189886 ESTs
	3391	ACCAGAGAGCA	1,00	0,15	Hs.181185 DKFZP564D116 protein
35	3392	GAAGATGAAGG	1,00	0,15	Hs.178452 catenin (cadherin-associated protein), alpha 1 (102k
	3393	TAAATTCAAGC	1,00	0,15	Hs.174905 KIAA0033 protein
	3394	AAATGTAACAT	1,00	0,15	Hs.164649 hypothetical protein DKFZp434H247
40	3395	AAACAGAGCTG	1,00	0,15	Hs.161554 hypothetical protein FLJ20159
	3396	GGAGCTGTCTG	1,00	0,15	Hs.15476 Human DNA sequence from clone RP3-329A5 on chromosom
	3397	ACAAAGTTGTG	1,00	0,15	Hs.154510 carbonyl reductase 3
45	3398	AGTATGCAGAG	1,00	0,15	Hs.144407 hypothetical protein FLJ10956
	3399	GATGGATGGAA	1,00	0,15	Hs.137516 ESTs
	3400	TGGTATTTCCG	1,00	0,15	Hs.133494 ESTs, Weakly similar to SP49_HUMAN SPLICEOSOME ASSOC
50	3401	TCTAAAAGAAA	1,00	0,15	Hs.13328 ESTs
	3402	GGAGAGGCCCC	1,00	0,15	Hs.129928 KIAA0454 protein
	3403	AAATAAAAAGAT	1,00	0,15	Hs.129778 gastrointestinal peptide
	3404	AACTAAAAAAC	1,00	0,15	Hs.11866 hypothetical protein PRO1197
55	3405	GGTCAAGCCAG	1,00	0,15	Hs.115222 ESTs
	3406	ACTCAGATGCC	1,00	0,15	Hs.11367 hypothetical protein RP1-317E23
	3407	AAGTTGTGAAG	1,00	0,15	Hs.104788 hypothetical protein LOC55565
	3408	CCTGTATTTGC	1,00	0,15	Hs.103158 ESTs
	3409	CCTTCGAGATC	52,00	1,52	Hs.76194 ribosomal protein S5
60	3410	TGGTGTTGAGG	147,00	2,68	Hs.275865 ribosomal protein S18
	3411	AGAACCTTCCA	17,00	0,89	Hs.181244 major histocompatibility complex, class I, A



3412	ACCTGTATCCC	34,00	1,21	Hs.182241	interferon induced transmembrane protein 3 (1-8U)
3413	GGGAGGTAGCA	3,00	0,38	Hs.171825	basic helix-loop-helix domain containing, class B, 2
3414	AGCAGATCAGG	67,00	1,66	Hs.119301	S100 calcium-binding protein A10 (annexin II ligand,
3415	AGTCTGATGTT	14,00	0,81	Hs.173255	small nuclear ribonucleoprotein polypeptide A
3416	GATACACTGGC	4,00	0,45	Hs.25797	splicing factor 3b, subunit 4, 49kD
3417	GGCCCCTCCCT	4,00	0,45	Hs.107374	chromobox homolog 6
3418	GCCAGGGCCAC	2,00	0,29	Hs.7647	MYC-associated zinc finger protein (purine-binding t
3419	GCTTAATGTTT	2,00	0,29	Hs.76359	catalase
3420	ACAGTGTGAGA	2,00	0,29	Hs.173824	thymine-DNA glycosylase
3421	GGAGAGGAAGT	2,00	0,29	Hs.16313	ESTs
3422	ACAACATAGAA	2,00	0,29	Hs.12436	ESTs
3423	TTAAAAGTCAC	2,00	0,29	Hs.12210	Homo sapiens cDNA FLJ11289 fis, clone PLACE1009621
3424	GAGTTTGGCCC	2,00	0,29	Hs.102402	Mad4 homolog
3425	CGACGAGGAGG	12,00	0,75	Hs.9999	epithelial membrane protein 3
3426	GCTCACTGCAG	11,00	0,72	Hs.128605	EST
3427	ATTCTGACCC	3,00	0,38	Hs.166204	PHD finger protein 1
3428	CCCTGATTTTA	13,00	0,77	Hs.183684	eukaryotic translation initiation factor 4 gamma, 2
3429	CCAGAGAACTT	12,00	0,74	Hs.243886	nuclear autoantigenic sperm protein (histone-binding
3430	CTATGGCTTCA	5,00	0,50	Hs.75618	RAB11A, member RAS oncogene family
3431	AGTTGTCACTT	3,00	0,38	Hs.74649	cytochrome c oxidase subunit VIc
3432	TGGGGGCCGAT	3,00	0,38	Hs.285340	transducin-like enhancer of split 2, homolog of Dros
3433	TGCAAAAAAAA	3,00	0,38	Hs.181624	ESTs
3434	TGGAGATGTGA	3,00	0,38	Hs.16130	Homo sapiens cDNA FLJ10064 fis, clone HEMBA1001450
3435	GCGGCAGTTAC	2,00	0,29	Hs.82201	casein kinase 2, alpha prime polypeptide
3436	GCCCTGTAGTT	2,00	0,29	Hs.76578	protein inhibitor of activated STAT3
3437	TCACAAGCCAC	2,00	0,29	Hs.34953	ESTs
3438	TATGAAAACAT	2,00	0,29	Hs.3337	transmembrane 4 superfamily member 1
3439	GGAGAAACAGC	2,00	0,29	Hs.286035	ESTs
3440	GGGGCCTGAGT	2,00	0,29	Hs.284280	hypothetical protein DKFZp547H236
3441	AGGCCAGGAGT	2,00	0,29	Hs.22237	lethal (3) malignant brain tumor l(3)mbt protein (Dr
3442	AGGTCTGGGAGA	2,00	0,29	Hs.193292	ESTs
3443	AAATGCAATAA	2,00	0,29	Hs.168157	nuclear transcription factor Y, gamma
3444	CGCCTGTGGTC	2,00	0,29	Hs.138263	Homo sapiens clone 24528 mRNA sequence
3445	ACTTTTGCCCC	2,00	0,29	Hs.10117	CGI-15 protein
3446	ACCTAACCGTC	1,00	0,15	Hs.9965	ESTs
3447	TCAGTGTATTA	1,00	0,15	Hs.9853	ESTs
3448	CCTCTGTTTCT	1,00	0,15	Hs.91684	Homo sapiens cDNA FLJ20148 fis, clone COL08032, high

	3449	TCCGTGTGTCA	1,00	0,15	Hs.83869	hypothetical protein
	3450	TATTTAAATAG	1,00	0,15	Hs.82028	transforming growth factor, beta receptor II (70-80k
5	3451	AGGGCCGACTG	1,00	0,15	Hs.80976	antigen identified by monoclonal anti-body Ki-67
	3452	ATGCTTTCACA	1,00	0,15	Hs.80741	propionyl Coenzyme A carboxylase, alpha polypeptide
10	3453	TAACCTTGCTG	1,00	0,15	Hs.80562	gelsolin (amyloidosis, Finnish type)
	3454	GGAAATAAAAA	1,00	0,15	Hs.79672	KIAA0652 gene product
	3455	CCTTGTTAGCA	1,00	0,15	Hs.788	A kinase (PRKA) anchor protein (gravin) 12
15	3456	CTTTGTACACT	1,00	0,15	Hs.74649	cytochrome c oxidase subunit VIc
	3457	AAATTACATAG	1,00	0,15	Hs.73291	hypothetical protein FLJ10881
	3458	AAGGCCATCTT	1,00	0,15	Hs.65328	Homo sapiens cDNA FLJ10854 fis, clone NT2RP4001507
20	3459	AGTGCTGAGGG	1,00	0,15	Hs.6241	phosphoinositide-3-kinase, regulatory subunit, polyp
	3460	GATGGGACCAT	1,00	0,15	Hs.46829	Homo sapiens mRNA full length insert cDNA clone EURO
25	3461	ATTTTGGGCAA	1,00	0,15	Hs.28827	mitogen-activated protein kinase kinase kinase 2
	3462	TAATTTAAAAA	1,00	0,15	Hs.283682	hypothetical protein PRO0992
	3463	GTGAGAAGAGA	1,00	0,15	Hs.274318	ESTs
30	3464	GGCAAGCCCCC	1,00	0,15	Hs.252574	ribosomal protein L10a
	3465	TGATGTCTGCC	1,00	0,15	Hs.252514	ESTs
	3466	TTCTTGTTTGT	1,00	0,15	Hs.250824	ESTs
	3467	GACCTTGATCG	1,00	0,15	Hs.227730	integrin, alpha 6
35	3468	TTGAAATTGTA	1,00	0,15	Hs.21857	ESTs
	3469	TATTATTTTCA	1,00	0,15	Hs.21255	ESTs
	3470	GAGTAATGGAT	1,00	0,15	Hs.204501	hypothetical protein FLJ10534
	3471	GCAACAAATCC	1,00	0,15	Hs.19192	cyclin-dependent kinase 2
40	3472	ACTACAGCCAT	1,00	0,15	Hs.186961	ubiquitin specific protease 25
	3473	CCTGATCTGTA	1,00	0,15	Hs.181357	laminin receptor 1 (67kD, ribosomal protein SA)
	3474	CTAAAGTACTT	1,00	0,15	Hs.171553	ESTs
45	3475	TTCAAGTGAAA	1,00	0,15	Hs.169681	death effector domain-containing
	3476	AACTGGAGTCT	1,00	0,15	Hs.169600	KIAA0826 protein
	3477	ACCTGCTTAAC	1,00	0,15	Hs.169149	karyopherin alpha 1 (importin alpha 5)
	3478	AAAATTGTAAC	1,00	0,15	Hs.166982	phosphatidylinositol glycan, class F
50	3479	GCCGGCTGTCT	1,00	0,15	Hs.16561	HSPC141 protein
	3480	CCAGCCAGGTG	1,00	0,15	Hs.154978	KIAA0261 protein
	3481	AACTAGAAAT	1,00	0,15	Hs.153260	Homo sapiens c-Cbl-interacting protein (CIN85) mRNA,
55	3482	GGGGGTCGGGG	1,00	0,15	Hs.147996	protein kinase, X-linked
	3483	AATGTTTAACG	1,00	0,15	Hs.13366	ESTs
	3484	TGGTGTTTGG	1,00	0,15	Hs.13234	ESTs
	3485	CATCTTATGAA	1,00	0,15	Hs.12891	ESTs
60	3486	AGAGCACACCT	1,00	0,15	Hs.118162	fibronectin 1
	3487	AACAGGGACAG	1,00	0,15	Hs.115284	zinc finger protein 213
	3488	TTAAAATACAG	1,00	0,15	Hs.11356	ESTs

3489	AGGGCTTGGAG	1,00	0,15	Hs.112278	arrestin, beta 1
3490	GCCTGGACCAT	1,00	0,15	Hs.10964	Homo sapiens mRNA; cDNA DKFZp434L0816 (from clone DK
3491	TAGCAGCAACC	1,00	0,15	Hs.106070	cyclin-dependent kinase inhibitor 1C (p57, Kip2)
3492	CCTTTCACACA	16,00	0,82	Hs.278589	general transcription factor II, i
3493	CAGAGACGTGG	5,00	0,50	Hs.76111	dystroglycan 1 (dystrophin-associated glycoprotein 1
3494	TTTTCAAGAAG	4,00	0,44	Hs.75447	ralA binding protein 1
3495	TCTACTTTTGT	4,00	0,44	Hs.74598	polymerase (DNA directed), delta 2, regulatory subun
3496	TAACAGCCAGG	11,00	0,70	Hs.81328	nuclear factor of kappa light polypeptide gene enhan
3497	TCAGATCTTTG	117,00	1,95	Hs.75344	ribosomal protein S4, X-linked
3498	CACCAGCATTG	9,00	0,65	Hs.75847	chromosome 15 open reading frame 3
3499	GCATACCTGCA	3,00	0,37	Hs.8258	DKFZP434D1335 protein
3500	CTGCCCCCACC	3,00	0,37	Hs.164410	chromosome 16 open reading frame 7
3501	GTGCAGGCTCC	3,00	0,37	Hs.158164	ATP-binding cassette, sub-family B (MDR/TAP), member
3502	TCAGTGAACGC	5,00	0,49	Hs.78504	inner membrane protein, mitochondrial (mitofilin)
3503	GCCCCTGCGCA	4,00	0,44	Hs.267200	ESTs, Moderately similar to T20D3.3 [C.elegans]
3504	AAGAGGCTTCG	2,00	0,28	Hs.90017	ESTs, Weakly similar to Ig-like mem- brane protein [H.
3505	ATTTAGCAAGC	2,00	0,28	Hs.83213	fatty acid binding protein 4, adipocyte
3506	CACTGAGCCAA	2,00	0,28	Hs.7960	hypothetical protein FLJ20027
3507	GGATGATGTCT	2,00	0,28	Hs.74861	activated RNA polymerase II transcrip- tion cofactor 4
3508	TGTTTCAGGAT	2,00	0,28	Hs.6216	tumorous imaginal discs (Drosophila) homolog
3509	TCTGTGCTGTC	2,00	0,28	Hs.231301	ESTs
3510	AAGAACTAAAA	2,00	0,28	Hs.18778	hypothetical protein
3511	CCCTGCTTCCA	2,00	0,28	Hs.181077	KIAA1306 protein
3512	GCTACTCTTTG	2,00	0,28	Hs.171807	Human clone 23652 mRNA sequence
3513	CATTGAGCTCC	2,00	0,28	Hs.12820	SnRNP assembly defective 1 homolog
3514	GCACTTACAAA	2,00	0,28	Hs.100407	Homo sapiens mRNA; cDNA DKFZp564H2416 (from clone DK
3515	TTCTGCTCTTG	5,00	0,49	Hs.110802	von Willebrand factor
3516	GCTGAACGCGT	6,00	0,53	Hs.99029	CCAAT/enhancer binding protein (C/EBP), beta
3517	GGGAAACCCCG	6,00	0,53	Hs.254283	EST
3518	CCACTTCCTCT	3,00	0,37	Hs.77495	KIAA0242 protein
3519	TTCAGCGTTCT	3,00	0,37	Hs.109929	hypothetical protein MPMGp800B12492Q3
3520	AGCCAAAAAAA	11,00	0,69	Hs.63525	poly(rC)-binding protein 2
3521	ATGGCCTCCTC	4,00	0,44	Hs.83734	syntaxin 4A (placental)
3522	ATTTCAGATG	4,00	0,44	Hs.155097	carbonic anhydrase II
3523	GTGATGGATGG	5,00	0,49	Hs.181046	Homo sapiens mRNA; cDNA DKFZp586O1919 (from clone DK

3524	GATTTGTGTTTC	6,00	0,53	Hs.173125	peptidylprolyl isomerase F (cyclophilin F)
3525	TTAAAAA	9,00	0,63	Hs.70266	yeast Sec31p homolog
3526	AAGAAAACCTGT	6,00	0,53	Hs.179294	KIAA1522 protein
3527	TGATCTGCCTG	4,00	0,43	Hs.5723	ESTs, Weakly similar to CA12_HUMAN COLLAGEN ALPHA 1(
3528	TGCTGCATTGA	3,00	0,37	Hs.5344	adaptor-related protein complex 1, gamma 1 subunit
3529	GCAGAGATGGG	3,00	0,37	Hs.39850	hypothetical protein FLJ20517
3530	TTTCTGGAGGT	3,00	0,37	Hs.129943	KIAA0545 protein
3531	GCAGAACCAT	2,00	0,28	Hs.96264	alpha thalassemia/mental retardation syndrome X-link
3532	CCTAGTAAAAA	2,00	0,28	Hs.96247	translin-associated factor X
3533	GCACAATGGGA	2,00	0,28	Hs.85838	solute carrier family 16 (monocarboxylic acid transp
3534	CAGTCCCCCTC	2,00	0,28	Hs.82563	KIAA0153 protein
3535	TAGACTGGCAC	2,00	0,28	Hs.7970	DKFZP434B027 protein
3536	CACTCAATAAA	2,00	0,28	Hs.79361	kallikrein 6 (neurosin, zyme)
3537	TTCAGGAGGGG	2,00	0,28	Hs.5890	ESTs, Weakly similar to A49134 Ig kappa chain V-I re
3538	CCAGTGGCTCA	2,00	0,28	Hs.5753	inositol(myo)-1(or 4)-monophosphatase 2
3539	TGTATTTTGAC	2,00	0,28	Hs.29882	predicted osteoblast protein
3540	CCGATTTTAA	2,00	0,28	Hs.26570	hypothetical protein FLJ20422
3541	GAATTTGGGAT	2,00	0,28	Hs.195729	ESTs, Highly similar to KIAA0780 protein [H.sapiens]
3542	AAAGTGAAAAA	2,00	0,28	Hs.183868	glucuronidase, beta
3543	AAAGTGGGTGG	2,00	0,28	Hs.146409	wingless-type MMTV integration site family, member 4
3544	TGACTGGCAAA	2,00	0,28	Hs.130849	ESTs
3545	TTACAGAGCTT	2,00	0,28	Hs.10590	zinc finger protein 313
3546	GTAACAAAATG	1,00	0,14	Hs.99437	Homo sapiens mRNA; cDNA DKFZp586G1924 (from clone DK
3547	CTACCCAACAG	1,00	0,14	Hs.9292	ESTs
3548	GAAACCCCAGA	1,00	0,14	Hs.84359	hypothetical protein
3549	AACACCCCTTC	1,00	0,14	Hs.82911	protein tyrosine phosphatase type IVA, member 2
3550	TATAAAAGTGG	1,00	0,14	Hs.82084	integrin beta 3 binding protein (beta3-endonexin)
3551	GCACCCACTGG	1,00	0,14	Hs.8184	ESTs
3552	GAAACCTGAAA	1,00	0,14	Hs.75772	nuclear receptor subfamily 3, group C, member 1
3553	TGTGGGAGTAG	1,00	0,14	Hs.6783	ESTs
3554	TGCTCCCTTTA	1,00	0,14	Hs.65450	reticulon 4
3555	CTGGTCGTTGG	1,00	0,14	Hs.5985	Homo sapiens clone 25186 mRNA sequence
3556	AGATTGCTGTT	1,00	0,14	Hs.59838	hypothetical protein FLJ10808
3557	GCCTGGCACCG	1,00	0,14	Hs.58167	zinc finger protein 282
3558	GATCTTTTGTC	1,00	0,14	Hs.5148	FLN29 gene product
3559	CATTTTATTTTC	1,00	0,14	Hs.49136	ESTs
3560	ATGTTTCTTCC	1,00	0,14	Hs.41143	KIAA0581 protein

3561	CCCTTGCACTC	1,00	0,14	Hs.284528	EST
3562	ATGAGTTTCTG	1,00	0,14	Hs.26930	ESTs
3563	TTGCCAGACT	1,00	0,14	Hs.244245	EST
3564	GTTTATGTTCC	1,00	0,14	Hs.24341	DKFZP586I1419 protein
3565	CTGAACCTTC	1,00	0,14	Hs.202737	ESTs
3566	CCATATGATCA	1,00	0,14	Hs.192966	KIAA0265 protein
3567	AGAAAAAATAA	1,00	0,14	Hs.18587	ESTs
3568	AGGTCAATGAA	1,00	0,14	Hs.18376	KIAA1319 protein
3569	AAACAATACAC	1,00	0,14	Hs.181466	Homo sapiens TRAF4 associated factor 1 mRNA, partial
3570	TACAGATCACA	1,00	0,14	Hs.173859	frizzled (Drosophila) homolog 7
3571	CTGTAAAAAAA	1,00	0,14	Hs.17364	zinc finger protein 79 (pT7)
3572	GTGAAGCCCTA	1,00	0,14	Hs.171501	ubiquitin specific protease 11
3573	GTTTGGGATGA	1,00	0,14	Hs.16193	Homo sapiens mRNA; cDNA DKFZp586B211 (from clone DKF
3574	GCCTGTGGATG	1,00	0,14	Hs.150601	chymotrypsin-like
3575	CCTCTGCCGGG	1,00	0,14	Hs.128512	ESTs
3576	TACAGTAAAC	1,00	0,14	Hs.125819	putative dimethyladenosine transferase
3577	TCCATTGCTGG	1,00	0,14	Hs.12303	suppressor of Ty (S.cerevisiae) 6 homolog
3578	ATCGTGCCATT	1,00	0,14	Hs.110630	Human BRCA2 region, mRNA sequence CG006
3579	GCGACAAAAG	1,00	0,14	Hs.110347	REV1 protein
3580	ACGTGACACCT	1,00	0,14	Hs.10881	WD repeat domain 7
3581	GAAAGTGGCTG	1,00	0,14	Hs.108788	ESTs, Weakly similar to zeste [D.melanogaster]
3582	TTTGCTGAACA	1,00	0,14	Hs.108660	ATP-binding cassette, sub-family C (CFTR/MRP), membe
3583	CTGCAAAGGAG	1,00	0,14	Hs.104519	phospholipase D2
3584	ATGGGCTTGAT	5,00	0,48	Hs.8185	CGI-44 protein; sulfide dehydrogenase like (yeast)
3585	TGCTTTGCTC	4,00	0,43	Hs.9589	ubiquilin 1
3586	AGCTACCGGGC	4,00	0,43	Hs.6059	EGF-containing fibulin-like extracellular matrix pro
3587	CCAGGCACGCT	7,00	0,56	Hs.198427	hexokinase 2
3588	TGAGCCCGGCC	9,00	0,63	Hs.238839	latent transforming growth factor beta binding prote
3589	CTCTGTAATTT	3,00	0,37	Hs.75618	RAB11A, member RAS oncogene family
3590	CTCAGCCTGAG	3,00	0,37	Hs.3496	ESTs
3591	AGGGGGGAGGG	3,00	0,37	Hs.284181	hypothetical protein DKFZp434P0531
3592	TGGCAAAAAAA	2,00	0,28	Hs.77783	membrane-associated tyrosine- and threonine-specific
3593	TGTCAAAAAAA	2,00	0,28	Hs.7120	cytokine receptor-like molecule 9
3594	TCAGTGAAC TG	2,00	0,28	Hs.6657	Novel human gene mapping to chromosome 22
3595	GCTCAAAC TAC	2,00	0,28	Hs.284332	ESTs
3596	CCCTCACTCCT	2,00	0,28	Hs.21143	(Manual assignment) MEMOREC PSL4 presenilin-like pro
3597	GGGCTGGACGG	2,00	0,28	Hs.180338	tumor necrosis factor receptor superfamily, member 1

3598	CAGGGCGAGAT	2,00	0,28	Hs.154680	DKFZP434M154 protein
3599	GCTATCTCAGC	2,00	0,28	Hs.153639	hypothetical SBB103 protein
3600	GGAGACAGAGT	2,00	0,28	Hs.141011	calmodulin 3 (phosphorylase kinase, delta)
3601	CAGTTGGTTGT	7,00	0,56	Hs.155218	E1B-55kDa-associated protein 5
3602	TCAGACAAAAG	5,00	0,48	Hs.66881	Homo sapiens mRNA; cDNA DKFZp434A1518 (from clone DK
3603	CTCATTGAGCT	6,00	0,52	Hs.180139	SMT3 (suppressor of mif two 3, yeast) homolog 2
3604	GTGAAACCCCTT	3,00	0,37	Hs.206955	ESTs
3605	TTCTGGACCCA	3,00	0,37	Hs.155543	proteasome (prosome, macropain) 26S subunit, non-ATP
3606	GCTTGGATCTC	12,00	0,69	Hs.250723	FK506 binding protein 12-rapamycin associated protei
3607	CTCAACAGCAA	10,00	0,64	Hs.7811	eukaryotic translation initiation factor 3, subunit
3608	GACTCTGAAAA	6,00	0,52	Hs.2953	ribosomal protein S15a
3609	TTGCCGGTTAA	5,00	0,48	Hs.75925	proteasome (prosome, macropain) inhibitor subunit 1
3610	ACCCTGCCAAA	5,00	0,48	Hs.284546	EST
3611	TACAGAGGGAA	12,00	0,69	Hs.3776	zinc finger protein 216
3612	GGGTGGGGTTG	7,00	0,56	Hs.75216	protein tyrosine phosphatase, receptor type, F
3613	GAAATACAGTT	43,00	1,07	Hs.79572	cathepsin D (lysosomal aspartyl protease)
3614	CAACATTCCTG	11,00	0,67	Hs.180015	D-dopachrome tautomerase
3615	TCCTTGCTTCT	6,00	0,52	Hs.94491	hypothetical protein FLJ20297
3616	CGAGGGGCCAG	33,00	0,97	Hs.182485	actinin, alpha 4
3617	AGAGGTGGTGT	4,00	0,43	Hs.6968	KIAA1460 protein
3618	CCACGTCCATC	2,00	0,28	Hs.9018	exostoses (multiple)-like 3
3619	GCCTTGGGGGC	2,00	0,28	Hs.75658	phosphorylase, glycogen; brain
3620	AGGAGCCGGGG	2,00	0,28	Hs.25700	Homo sapiens mRNA; cDNA DKFZp434M0435 (from clone DK
3621	CGGCAAAAAAA	2,00	0,28	Hs.179747	ecotropic viral integration site 5
3622	CTGGACTCCGC	2,00	0,28	Hs.173159	transforming, acidic coiled-coil containing protein
3623	CCCGCTCTTGA	2,00	0,28	Hs.118282	ESTs
3624	GTGATATCCAA	2,00	0,28	Hs.110950	Homo sapiens clone 25007 mRNA sequence
3625	TCAGTAAAAAT	1,00	0,14	Hs.9805	KIAA1291 protein
3626	GCAGCTATGAG	1,00	0,14	Hs.90960	ESTs
3627	CTCTCTGTGGA	1,00	0,14	Hs.8858	bromodomain adjacent to zinc finger domain, 1A
3628	TCTCAGATGAG	1,00	0,14	Hs.82568	cytochrome P450, subfamily XXVIIA (steroid 27-hydrox
3629	CTGTAGTTGCC	1,00	0,14	Hs.75798	hypothetical protein
3630	ATTTACATTT	1,00	0,14	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (from clone DKF
3631	ACTATTTTACA	1,00	0,14	Hs.72134	KIAA1064 protein
3632	TTGTTGAAAGG	1,00	0,14	Hs.70337	immunoglobulin superfamily, member 4

3633	TGCCCTGTTCC	1,00	0,14	Hs.6651	Homo sapiens clone 23645 mRNA sequence
3634	ATGATTCCCTG	1,00	0,14	Hs.64595	DKFZP566E2346 protein
3635	ATAATTTTTTG	1,00	0,14	Hs.539	ribosomal protein S29
3636	GCCCACTTCCT	1,00	0,14	Hs.32117	ESTs, Weakly similar to unknown [D.melanogaster]
3637	GGACTCATCCC	1,00	0,14	Hs.286102	ESTs
3638	CTGCCTTATTT	1,00	0,14	Hs.28501	ESTs
3639	GACAGTGGAGA	1,00	0,14	Hs.284284	ESTs, Highly similar to beta-1,3-N-acetylglucosaminy
3640	CAGCAATAAAA	1,00	0,14	Hs.284251	KIAA0544 protein
3641	GTGGCTCAAGC	1,00	0,14	Hs.283708	hypothetical protein PRO0758
3642	ACCTTGGATTT	1,00	0,14	Hs.278920	PRO1510 protein
3643	GGGCTGCTGCC	1,00	0,14	Hs.277630	EST
3644	ATGTGGGCTCA	1,00	0,14	Hs.27018	Ris
3645	GGCACCCTGGC	1,00	0,14	Hs.256144	ESTs
3646	GAGAAACCCAG	1,00	0,14	Hs.252895	ESTs
3647	ATTTTGGCCAC	1,00	0,14	Hs.24831	ESTs
3648	TGAAGATAGAC	1,00	0,14	Hs.24809	hypothetical protein FLJ10826
3649	AGCCCTTCCTC	1,00	0,14	Hs.237856	peptide transporter 3
3650	CTTCTCTGTTT	1,00	0,14	Hs.23449	insulin receptor tyrosine kinase substrate
3651	TTTATCCCAA	1,00	0,14	Hs.227391	DKFZP547E1010 protein
3652	CTTGTGGTCCC	1,00	0,14	Hs.193717	interleukin 10
3653	TGCAATTCCTT	1,00	0,14	Hs.177461	ribosomal protein L39
3654	GATATTTTTTC	1,00	0,14	Hs.17667	SH3-domain binding protein 4
3655	CTTTGTGAACA	1,00	0,14	Hs.169946	GATA-binding protein 3
3656	TAGACCCCTTG	1,00	0,14	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase
3657	AGCGTGGCTCT	1,00	0,14	Hs.15589	PPAR binding protein
3658	TTTGACAATAC	1,00	0,14	Hs.155596	BCL2/adenovirus E1B 19kD-interacting protein 2
3659	GTCTAGTCAAT	1,00	0,14	Hs.152629	KIAA0179 protein
3660	CTGGACTTTAT	1,00	0,14	Hs.146861	hypothetical protein FLJ20580
3661	TGTA CTGGCAC	1,00	0,14	Hs.144090	ESTs
3662	TGAAAACCTGA	1,00	0,14	Hs.143460	protein kinase C, nu
3663	GTTATATGCCC	1,00	0,14	Hs.13350	Homo sapiens mRNA; cDNA DKFZp586D0918 (from clone DK
3664	TTAATAAATGT	1,00	0,14	Hs.13313	cAMP responsive element binding protein-like 2
3665	GACCAGCGGCT	1,00	0,14	Hs.127401	DKFZP434A163 protein; selective LIM binding factor,
3666	AGCCAAATAAA	1,00	0,14	Hs.123652	ESTs
3667	CCAACCCATTT	1,00	0,14	Hs.121076	ESTs, Weakly similar to S64705 cyclophilin-like prot
3668	TTGGGGACGGG	1,00	0,14	Hs.118400	singed (Drosophila)-like (sea urchin fascin homolog
3669	TATTGACAACA	3,00	0,36	Hs.75608	tight junction protein 2 (zona occludens 2)
3670	CAGATTAGTTA	3,00	0,36	Hs.286195	Homo sapiens clone 25244 DEAD-box protein p72 mRNA s

3671	AGGAGTCGACA	3,00	0,36	Hs.181369	ubiquitin fusion degradation 1-like
3672	CAAAATCAGGA	14,00	0,72	Hs.79933	cyclin I
3673	CTCTAAGAAGC	8,00	0,58	Hs.9641	complement component 1, q subcomponent, alpha polype
3674	AAACCAGGGCC	4,00	0,43	Hs.279836	HSPC166 protein
3675	ATGGCGCAGTC	4,00	0,43	Hs.239509	ESTs
3676	GGATTTGGCCT	168,00	1,70	Hs.251247	(Manual assignment) Acidic ribosomal phosphoprotein
3677	CCCCCAGATGA	6,00	0,52	Hs.25817	hypothetical protein FLJ20386
3678	TGAAAAAAAAA	15,00	0,74	Hs.57904	mago-nashi (Drosophila) homolog, proliferation-assoc
3679	AAGGTGGAGTG	3,00	0,36	Hs.9573	ATP-binding cassette, sub-family F (GCN20), member 1
3680	TTGTTGGATAT	3,00	0,36	Hs.4099	nardilysin (N-arginine dibasic convertase)
3681	AAGTTTGCCTG	3,00	0,36	Hs.28988	glutaredoxin (thioltransferase)
3682	CCATTGCATTC	3,00	0,36	Hs.185156	ESTs
3683	TGCTGCTGCTT	5,00	0,47	Hs.283685	hypothetical protein FLJ20396
3684	GACCCCAAGGC	14,00	0,72	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatosis 1)
3685	TGGTTTTGGCA	4,00	0,42	Hs.75721	profilin 1
3686	GTGTCGGCTGT	4,00	0,42	Hs.275959	eukaryotic translation elongation factor 1 beta 2
3687	GGCTGTACCCA	21,00	0,82	Hs.108080	cysteine and glycine-rich protein 1
3688	GTTTTTCATTG	15,00	0,73	Hs.119502	ubiquitin A-52 residue ribosomal protein fusion prod
3689	CGACCCTCTCC	2,00	0,28	Hs.74649	cytochrome c oxidase subunit VIc
3690	GCCACGTTGTC	2,00	0,28	Hs.32352	hypothetical protein DKFZp434K1210
3691	ATGTATGGGGA	2,00	0,28	Hs.283429	SMC (mouse) homolog, X chromosome
3692	TGCCACCACGC	2,00	0,28	Hs.233480	EST
3693	CGAAAAAAAAA	2,00	0,28	Hs.20815	erythroblast macrophage protein
3694	GTCTTCAAAGA	2,00	0,28	Hs.184227	F-box only protein 21
3695	AAGTAGAGCAG	2,00	0,28	Hs.144645	POM (POM121 rat homolog) and ZP3 fusion protein
3696	TAGAAAGGCAG	9,00	0,61	Hs.78909	butyrate response factor 2 (EGF-response factor 2)
3697	CAGGCCCCACC	16,00	0,75	Hs.256290	S100 calcium-binding protein A11 (calgizzarin)
3698	ATTCTGTTGTA	5,00	0,47	Hs.150580	putative translation initiation factor
3699	CGCTGGTTCCA	83,00	1,25	Hs.179943	ribosomal protein L11
3700	TACCCACCTT	4,00	0,42	Hs.75258	H2A histone family, member Y
3701	TGATGTTCCAC	4,00	0,42	Hs.277401	bromodomain adjacent to zinc finger domain, 2A
3702	GAGTCTGTTCG	3,00	0,36	Hs.283636	Homo sapiens HSPC253 mRNA, partial cds
3703	TTGCGGAGCCC	3,00	0,36	Hs.199695	hypothetical protein
3704	AGTCTCCCCTA	3,00	0,36	Hs.12303	suppressor of Ty (S.cerevisiae) 6 homolog
3705	GTTGGGAGTCC	3,00	0,36	Hs.108504	hypothetical protein FLJ20113
3706	CCAGAACAGAC	119,00	1,41	Hs.111222	ribosomal protein L30



3707	TAGGGCAATCT	17,00	0,76	Hs.180139	SMT3 (suppressor of mif two 3, yeast) homolog 2
3708	GACTTCACTTT	5,00	0,47	Hs.77356	transferrin receptor (p90, CD71)
3709	GTGGACCCTGT	5,00	0,47	Hs.7236	CGI-25 protein
3710	CACGCAATGCT	22,00	0,82	Hs.244	amino-terminal enhancer of split
3711	GCCTATGGTCC	8,00	0,58	Hs.16561	HSPC141 protein
3712	TGGAAGTGTAA	5,00	0,47	Hs.234839	vacuolar sorting protein 4
3713	AACCAAAAAA	5,00	0,47	Hs.155410	isocitrate dehydrogenase 3 (NAD+) beta
3714	TTGTAAATGCG	6,00	0,51	Hs.149436	kinesin family member 5B
3715	ACCAGGCAAGG	2,00	0,28	Hs.93871	hypothetical protein FLJ10783
3716	AGTGCCCCTCT	2,00	0,28	Hs.90232	KIAA0552 gene product
3717	TGTGGCAAAGT	2,00	0,28	Hs.7243	ubiquitin specific protease 24
3718	TACCAGGAACC	2,00	0,28	Hs.7010	NPD002 protein
3719	ATTTTTTCAAG	2,00	0,28	Hs.3833	3-prime-phosphoadenosine 5-prime-phosphosulfate synt
3720	AGGCGCTTAGA	2,00	0,28	Hs.276	ESTs
3721	GGGATGGAAGG	2,00	0,28	Hs.272972	hypothetical protein FLJ20185
3722	TCAAGGCCCCC	2,00	0,28	Hs.193065	hypothetical protein DKFZp547M136 similar to widely-
3723	AGACGCACTCT	2,00	0,28	Hs.139929	ESTs
3724	CTGAACTGTGA	2,00	0,28	Hs.121031	ESTs
3725	TCTGTAAAAA	1,00	0,14	Hs.94842	ESTs
3726	AAGTCATCTAT	1,00	0,14	Hs.8769	Homo sapiens mRNA; cDNA DKFZp564E153 (from clone DKF
3727	TATTTTGAATA	1,00	0,14	Hs.8146	translocation protein 1
3728	GGATCAAGTCC	1,00	0,14	Hs.77602	damage-specific DNA binding protein 2 (48kD)
3729	AAACTATGCAC	1,00	0,14	Hs.76930	synuclein, alpha (non A4 component of amyloid precur
3730	AAGTCCTGCAC	1,00	0,14	Hs.75871	protein kinase C binding protein 1
3731	ACGGTCCAGGA	1,00	0,14	Hs.72924	cytidine deaminase
3732	TTTTAAAAAA	1,00	0,14	Hs.72865	ESTs
3733	GGACACTCCTT	1,00	0,14	Hs.69360	kinesin-like 6 (mitotic centromere-associated kinesi
3734	GATTGCGGATA	1,00	0,14	Hs.61472	ESTs, Weakly similar to unknown [S.cerevisiae]
3735	GTGTTGGGGTG	1,00	0,14	Hs.52763	anaphase-promoting complex subunit 7
3736	TTGCTAAAGGC	1,00	0,14	Hs.5216	HSPC028 protein
3737	TATACAGATTG	1,00	0,14	Hs.4996	DKFZP564D166 protein
3738	CTGCAGAAAAA	1,00	0,14	Hs.4310	eukaryotic translation initiation factor 1A
3739	CAGTGTATTCTG	1,00	0,14	Hs.42733	CHMP1.5 protein
3740	CAGGGCTCACC	1,00	0,14	Hs.40411	ESTs
3741	GTGGGTCAGCT	1,00	0,14	Hs.38592	ESTs
3742	TAATGAATGAG	1,00	0,14	Hs.3164	nucleobindin 2
3743	AATTACTTCCT	1,00	0,14	Hs.285449	ESTs
3744	GAGGGGTTTGC	1,00	0,14	Hs.285112	ESTs
3745	CCCTCCATTG	1,00	0,14	Hs.279891	truncated calcium binding protein
3746	CCCTTCAAAAA	1,00	0,14	Hs.272897	Tubulin, alpha, brain-specific
3747	CTGGTTTAAAT	1,00	0,14	Hs.267690	KIAA1228 protein
3748	TTTGTTTTAAG	1,00	0,14	Hs.25732	eukaryotic translation initiation factor 4

					gamma, 3
3749	GACAATGTATG	1,00	0,14	Hs.23767	guanine nucleotide binding protein (G protein), gamm
3750	CCACTGCCCTT	1,00	0,14	Hs.199695	hypothetical protein
3751	ATCCTCTGCGT	1,00	0,14	Hs.184402	calcium/calmodulin-dependent protein kinase I
3752	GGAAATTGTCT	1,00	0,14	Hs.181112	HSPC126 protein
3753	CATTCAACATA	1,00	0,14	Hs.16552	Homo sapiens clone TCBA00758 mRNA sequence
3754	TTCAACAGGAA	1,00	0,14	Hs.158195	heat shock transcription factor 2
3755	ACTTCTGGAAC	1,00	0,14	Hs.155623	KIAA0171 gene product
3756	GAAAATGCATC	1,00	0,14	Hs.154919	KIAA0625 protein
3757	TGAATAAAATG	1,00	0,14	Hs.154057	matrix metalloproteinase 19
3758	GAGAACTAGA	1,00	0,14	Hs.139120	ribonuclease P (30kD)
3759	GAGTGCAGGAC	1,00	0,14	Hs.129836	KIAA1028 protein
3760	GATTGGACTTG	1,00	0,14	Hs.129228	galactokinase 2
3761	TGCCCTGAGAG	1,00	0,14	Hs.11127	PET112 (yeast homolog)-like
3762	CTTTTCTATGT	1,00	0,14	Hs.10711	ESTs
3763	TGAAGTGTATA	1,00	0,14	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) transferase (U
3764	AGACCAAAGTG	10,00	0,63	Hs.82646	heat shock 40kD protein 1
3765	AAACTCGAGCA	5,00	0,47	Hs.161554	hypothetical protein FLJ20159
3766	TTACAGTCTTA	4,00	0,42	Hs.194110	Homo sapiens mRNA; cDNA DKFZp434C0814 (from clone DK
3767	AGCTTGCGCTC	4,00	0,42	Hs.161554	hypothetical protein FLJ20159
3768	TTAAACTCTAA	3,00	0,36	Hs.226213	cytochrome P450, 51 (lanosterol 14-alpha-demethylase
3769	CCACCTTTCCC	3,00	0,36	Hs.19597	ESTs
3770	TAATAAAGGTG	76,00	1,16	Hs.151604	ribosomal protein S8
3771	GTGGGTTGGCT	7,00	0,54	Hs.195432	aldehyde dehydrogenase 2, mitochondrial
3772	CAGTTACAAAG	4,00	0,42	Hs.77508	glutamate dehydrogenase 1
3773	ATGTGAAGAGT	59,00	1,07	Hs.111779	secreted protein, acidic, cysteine-rich (osteonectin
3774	TGTATGCCGTC	2,00	0,27	Hs.83469	nuclear factor (erythroid-derived 2)-like 1
3775	TATGAATGCTG	2,00	0,27	Hs.81800	chondroitin sulfate proteoglycan 2 (versican)
3776	ATATGAATGTG	2,00	0,27	Hs.7862	hypothetical protein FLJ20312
3777	CACTTCCTCCT	2,00	0,27	Hs.6375	uncharacterized hypothalamus protein HT010
3778	TTGTTATATTG	2,00	0,27	Hs.5862	hypothetical protein
3779	GATGTCTTGTT	2,00	0,27	Hs.5637	ESTs
3780	GAGGAGGAGGT	2,00	0,27	Hs.29956	KIAA0460 protein
3781	GAGCCAACAAT	2,00	0,27	Hs.283680	hypothetical protein
3782	TGAGATTCTT	2,00	0,27	Hs.279061	CGI-150 protein
3783	GAGCTGCATCA	2,00	0,27	Hs.112722	step II splicing factor SLU7
3784	GTGCTCTGTAC	5,00	0,47	Hs.177556	melanoma antigen, family D, 1
3785	TTCTTGTGGCG	45,00	0,99	Hs.182740	ribosomal protein S11
3786	GTGATGTACGG	3,00	0,36	Hs.6639	Homo sapiens cDNA FLJ20818 fis, clone ADSE00627

3787	AAAGCATTTTC	3,00	0,36	Hs.6406	MO25 protein	5
3788	CGGCTGCCCCAC	3,00	0,36	Hs.63236	synuclein, gamma (breast cancer-specific protein 1)	
3789	ACCAGGCCACC	3,00	0,36	Hs.12068	carnitine acetyltransferase	
3790	TTGCCCAGCAC	7,00	0,54	Hs.23954	cerebral cell adhesion molecule	
3791	TGCTGAATCAG	8,00	0,57	Hs.2853	poly(rC)-binding protein 1	
3792	GCCTTGATCTC	3,00	0,36	Hs.91146	DKFZP586E0820 protein	10
3793	ACAAAGGGCCC	3,00	0,36	Hs.7416	KIAA0397 gene product	
3794	CCTCTGCACTC	3,00	0,36	Hs.265124	ESTs	
3795	AGCCACTGCGC	9,00	0,59	Hs.236506	EST, Moderately similar to ALU7_HUMAN ALU SUBFAMILY	15
3796	ATTATCCAGGG	9,00	0,59	Hs.182225	RNA binding motif protein 3	
3797	TACCAAGACCC	6,00	0,50	Hs.3059	coatome protein complex, subunit beta	
3798	GGCCGCGTTCG	36,00	0,91	Hs.5174	ribosomal protein S17	
3799	ATCCTCCCTAT	2,00	0,27	Hs.865	RAP1A, member of RAS oncogene family	20
3800	GCAGCTCAAAG	2,00	0,27	Hs.74561	alpha-2-macroglobulin	
3801	CTCAAGCGGCT	2,00	0,27	Hs.6364	HIV-1 Tat interactive protein, 60 kDa	
3802	GTCCGAGTCT	2,00	0,27	Hs.63304	protein phosphatase methylesterase-1	25
3803	AGCCACCACAG	2,00	0,27	Hs.245474	ESTs, Moderately similar to ALU5_HUMAN ALU SUBFAMILY	
3804	AGCCAATTAAA	2,00	0,27	Hs.207625	EST	
3805	GTGTAGTTGAG	2,00	0,27	Hs.171811	adenylate kinase 2	30
3806	ACCCAGCAAC	2,00	0,27	Hs.164036	Homo sapiens cDNA FLJ20263 fis, clone COLF7804, high	
3807	GCGATTAATTA	2,00	0,27	Hs.149436	kinesin family member 5B	
3808	TCAAATGCAAA	2,00	0,27	Hs.116875	KIAA0156 gene product	35
3809	GGCAGAGACCC	1,00	0,14	Hs.9877	hypothetical protein	
3810	CTTCAAAAAA	1,00	0,14	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate dioxygenase (g)	
3811	CCGACGTCTCC	1,00	0,14	Hs.94943	ESTs	40
3812	CTGTGTTTGT	1,00	0,14	Hs.9460	ESTs	
3813	GGAGCTTAGAA	1,00	0,14	Hs.9194	putative glioblastoma cell differentiation-related	
3814	GAAGATCCAGC	1,00	0,14	Hs.81875	growth factor receptor-bound protein 10	45
3815	AGGAAAAAAC	1,00	0,14	Hs.79306	eukaryotic translation initiation factor 4E	
3816	AACCAAAGGAA	1,00	0,14	Hs.78524	TcD37 homolog	
3817	GAGCCAAGTGA	1,00	0,14	Hs.76536	transducin (beta)-like 1	
3818	TCAAATCTTTG	1,00	0,14	Hs.75344	ribosomal protein S4, X-linked	50
3819	GCTTCCAGCTT	1,00	0,14	Hs.7407	KIAA1065 protein	
3820	AAGGACACATC	1,00	0,14	Hs.6217	ESTs, Weakly similar to ALU2_HUMAN ALU SUBFAMILY SB	
3821	AGTAGTATGAA	1,00	0,14	Hs.56066	fibroblast growth factor 2 (basic)	55
3822	TTCTCTTTCAA	1,00	0,14	Hs.5354	Homo sapiens mRNA; cDNA DKFZp434N0317 (from clone DK	
3823	CTGTTTATCTA	1,00	0,14	Hs.51043	hexosaminidase B (beta polypeptide)	
3824	CCTGGAACCCC	1,00	0,14	Hs.4076	CTD (carboxy-terminal domain, RNA polymerase II, pol	60
3825	GCTGGAGAGTT	1,00	0,14	Hs.3447	DKFZP564K1964 protein	
3826	TTTTAGACAGC	1,00	0,14	Hs.31720	hephaestin	65

3827	TGTTGGTAAGT	1,00	0,14	Hs.283779	hypothetical protein DKFZp434J1015
3828	ATAGCCTCTTA	1,00	0,14	Hs.279799	putative zinc finger protein NY-REN-34 antigen
3829	TTGGGATGGGA	1,00	0,14	Hs.278568	H factor (complement)-like 1
3830	AGGTCAGGGGA	1,00	0,14	Hs.277328	EST, Moderately similar to ALU2_HUMAN ALU SUBFAMILY
3831	TTGGCTGGGCT	1,00	0,14	Hs.274511	Homo sapiens mRNA; cDNA DKFZp586E121 (from clone DKF
3832	TGGGGAGCTCG	1,00	0,14	Hs.26333	JM1 protein
3833	TCATTTTTTTG	1,00	0,14	Hs.261643	ESTs
3834	GGGGGGGGGTT	1,00	0,14	Hs.251664	insulin-like growth factor 2 (somatomedin A)
3835	CATTTTTATAT	1,00	0,14	Hs.236030	SWI/SNF related, matrix associated, actin dependent
3836	GCTCACTGTAG	1,00	0,14	Hs.235183	EST
3837	TTAAACCCACC	1,00	0,14	Hs.226799	HSPC039 protein
3838	TTCCCAAGGCC	1,00	0,14	Hs.197366	smoothened (Drosophila) homolog
3839	AGGCTTTAGCT	1,00	0,14	Hs.193082	ESTs
3840	GTAGCGCACAC	1,00	0,14	Hs.18759	KIAA0539 gene product
3841	GCGACAGTAAT	1,00	0,14	Hs.170853	ESTs
3842	AAGTGTGTTTT	1,00	0,14	Hs.169387	KIAA0036 gene product
3843	CCAGTAGAAGG	1,00	0,14	Hs.165986	testin
3844	TTTATTGCACA	1,00	0,14	Hs.155829	KIAA0676 protein
3845	GAGATTGAGGC	1,00	0,14	Hs.152372	ESTs
3846	GAGCACTTCCT	1,00	0,14	Hs.15144	hypothetical protein DKFZp564O043
3847	CCCACCGGTGC	1,00	0,14	Hs.134901	ESTs
3848	CAGGAGCCCCT	1,00	0,14	Hs.12785	KIAA0939 protein
3849	TAGCAATTGCA	1,00	0,14	Hs.126557	ESTs
3850	GATGCAGCAGC	1,00	0,14	Hs.117582	CGI-43 protein
3851	TTGGCCTTTTA	1,00	0,14	Hs.10554	ESTs, Weakly similar to unknown [D.melanogaster]
3852	GGGTCTGCTGT	1,00	0,14	Hs.105280	ESTs, Weakly similar to dJ963K23.2 [H.sapiens]
3853	TTGTTCTGCTA	7,00	0,54	Hs.237225	ribosomal protein S5 pseudogene 1
3854	TTGGTCCTCTG	241,00	1,46	Hs.108124	ribosomal protein L41
3855	AGGATGTGGGC	9,00	0,59	Hs.139648	KIAA0706 gene product
3856	CCCTTAGCTTT	11,00	0,64	Hs.233936	myosin, light polypeptide, regulatory, non-sarcomeri
3857	TTTCAGTGGGT	3,00	0,36	Hs.31218	secretory carrier membrane protein 1
3858	GCCCAGCCCTG	3,00	0,36	Hs.180903	hypothetical protein
3859	GTTTGGAGCTG	3,00	0,36	Hs.180533	mitogen-activated protein kinase kinase 3
3860	AACTAAAAAAA	47,00	0,97	Hs.55921	glutamyl-prolyl-tRNA synthetase
3861	GACACCTCCTG	7,00	0,54	Hs.6455	RuvB (E coli homolog)-like 2
3862	CCTCCCTGATG	5,00	0,46	Hs.167013	dynammin 2
3863	AGGAATGGTAG	2,00	0,27	Hs.7911	KIAA0323 protein
3864	TGGTCCAGCGC	2,00	0,27	Hs.75627	CD14 antigen
3865	TGACTTATTAA	2,00	0,27	Hs.74649	cytochrome c oxidase subunit VIc
3866	TGTGTGTGACA	2,00	0,27	Hs.55148	ESTs
3867	CCAAAGAGTAT	2,00	0,27	Hs.41007	HSPC158 protein

3868	TTTCTTAATGT	2,00	0,27	Hs.233650	ESTs, Weakly similar to H beta 58 homolog (H.sapiens)
3869	TAAAACAAGAA	2,00	0,27	Hs.1369	decay accelerating factor for complement (CD55, Crom
3870	GACAAAAA	20,00	0,77	Hs.2953	ribosomal protein S15a
3871	AGGTCAAGAGA	5,00	0,46	Hs.268488	KIAA1185 protein
3872	TCAATAAAGAA	8,00	0,56	Hs.79322	glutamyl-tRNA synthetase
3873	TGCTGGTGTGG	3,00	0,36	Hs.84883	KIAA0864 protein
3874	CCAATTTACAA	3,00	0,36	Hs.274472	high-mobility group (nonhistone chromosomal) protein
3875	CTGTAGAAATG	3,00	0,36	Hs.215595	guanine nucleotide binding protein (G protein), beta
3876	AATGAATAAAA	3,00	0,36	Hs.118797	ubiquitin-conjugating enzyme E2D 3 (homologous to ye
3877	GCGAGTCTCCG	3,00	0,36	Hs.10632	hypothetical protein DKFZp762M136
3878	GGGAAGTCACC	4,00	0,42	Hs.264428	tissue specific transplantation antigen P35B
3879	GTGGCACCTGC	4,00	0,42	Hs.1244	CD9 antigen (p24)
3880	CTGACTTGTGT	9,00	0,59	Hs.77961	major histocompatibility complex, class I, B
3881	AGGCTACGGAA	135,00	1,21	Hs.119122	ribosomal protein L13a
3882	AAGAGGTTTGC	6,00	0,50	Hs.74368	transmembrane protein (63kD), endoplasmic reticulum/
3883	TGGCTAGTGTT	11,00	0,63	Hs.118065	proteasome (prosome, macropain) subunit, beta type,
3884	TTTTGTTTTGT	2,00	0,27	Hs.95583	transmembrane 4 superfamily member (tetraspan NET-7)
3885	GGGTAATGTGA	2,00	0,27	Hs.76907	HSPC002 protein
3886	ATCCGGACCCT	2,00	0,27	Hs.76556	growth arrest and DNA-damage-inducible 34
3887	TGCCTGGAAC	2,00	0,27	Hs.6820	ESTs, Weakly similar to putative [C.elegans]
3888	GGCTGCAGTCT	2,00	0,27	Hs.48320	DKFZP566B1346 protein
3889	CTCTGATAACT	2,00	0,27	Hs.25846	zinc metalloproteinase, STE24 (yeast, homolog)
3890	GTGTCTCCCGC	2,00	0,27	Hs.219614	f-box and leucine-rich repeat protein 11
3891	GCGAACCCCCC	2,00	0,27	Hs.211862	EST
3892	TTTTTCTTAAA	2,00	0,27	Hs.197955	KIAA0704 protein
3893	AAGAATCAAAA	2,00	0,27	Hs.183435	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1
3894	GTGCTGATTCT	2,00	0,27	Hs.1640	collagen, type VII, alpha 1 (epidermolysis bullosa,
3895	AACCAATCTGG	2,00	0,27	Hs.154654	cytochrome P450, subfamily I (dioxin-inducible), pol
3896	AGGGAAAAA	5,00	0,46	Hs.215595	guanine nucleotide binding protein (G protein), beta
3897	AATTTGCAACA	6,00	0,50	Hs.75258	H2A histone family, member Y
3898	TCAAATGTCAG	3,00	0,36	Hs.89474	ADP-ribosylation factor 6
3899	ATTTTGTGCAA	3,00	0,36	Hs.8750	uncharacterized bone marrow protein BM045
3900	TTCTTGTTTTG	8,00	0,56	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob

					disease, Ge
3901	GCCACTACCCC	4,00	0,42	Hs.71475	hypothetical protein
3902	GAGCAAACGGA	4,00	0,42	Hs.108847	Homo sapiens chromosome 19, cosmid R26445
3903	TCATACAGTTT	1,00	0,14	Hs.94986	ribonuclease P (38kD)
3904	GAGGGAAAAAG	1,00	0,14	Hs.9082	nucleoporin p54
3905	CTGATGAATTC	1,00	0,14	Hs.86386	myeloid cell leukemia sequence 1 (BCL2-related)
3906	AAGCGCTACCT	1,00	0,14	Hs.83848	triosephosphate isomerase 1
3907	GAAGGCTTTAT	1,00	0,14	Hs.8182	KIAA0796 protein
3908	ACTTGATTCAA	1,00	0,14	Hs.80905	Ras association (RalGDS/AF-6) domain family 2
3909	CATTGTAATTC	1,00	0,14	Hs.80338	KIAA0164 gene product
3910	ATTTTGTAAACC	1,00	0,14	Hs.79362	retinoblastoma-like 2 (p130)
3911	CATTCTCCTAG	1,00	0,14	Hs.79008	SKI-INTERACTING PROTEIN
3912	TCCTGCTCATT	1,00	0,14	Hs.7844	golgi autoantigen, golgin subfamily b, macrogolgin (
3913	TGGCCTTTTTG	1,00	0,14	Hs.75761	SFRS protein kinase 1
3914	TTTTACATCTT	1,00	0,14	Hs.73999	thyroid hormone receptor interactor 10
3915	CTGTGTAAAGG	1,00	0,14	Hs.7314	KIAA0614 protein
3916	CAGGGAATGCC	1,00	0,14	Hs.58598	KIAA1266 protein
3917	GCAGAGCAGTC	1,00	0,14	Hs.46446	lymphoblastic leukemia derived sequence 1
3918	TTCACTAATTG	1,00	0,14	Hs.44787	Homo sapiens mRNA; cDNA DKFZp434O0227 (from clone DK
3919	CTATTCCATTT	1,00	0,14	Hs.43505	inhibitor of kappa light polypeptide gene enhancer i
3920	TTTGTATGGGA	1,00	0,14	Hs.431	murine leukemia viral (bmi-1) oncogene homolog
3921	ATGTGGGTCTA	1,00	0,14	Hs.42392	ESTs
3922	GAACTAGATC	1,00	0,14	Hs.37883	ESTs
3923	TTGTAACGTGT	1,00	0,14	Hs.3610	KIAA0205 gene product
3924	CTATGCATCAG	1,00	0,14	Hs.30670	hepatocellular carcinoma-associated antigen 66
3925	TTTGAGTTCTG	1,00	0,14	Hs.29494	PRO1912 protein
3926	CTACTGCAGTC	1,00	0,14	Hs.281680	peroxisomal trans 2-enoyl CoA reductase; putative sh
3927	CTCCTCAGGGC	1,00	0,14	Hs.28088	SGC32445 protein
3928	GACTCTGGCCC	1,00	0,14	Hs.274307	KIAA1442 protein
3929	TAATGGGAGTC	1,00	0,14	Hs.264330	N-acylsphingosine amidohydrolase (acid ceramidase)-I
3930	CCTGTGATCTC	1,00	0,14	Hs.254176	EST
3931	ATTAGCAGAGT	1,00	0,14	Hs.249982	cathepsin B
3932	GTGGTACATAC	1,00	0,14	Hs.232120	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
3933	CCCATCAATAA	1,00	0,14	Hs.220689	Ras-GTPase-activating protein SH3-domain-binding pro
3934	CTATCAGTCTC	1,00	0,14	Hs.211601	mitogen-activated protein kinase kinase kinase 12
3935	TGTTCCAAGGC	1,00	0,14	Hs.211569	G protein-coupled receptor kinase 5

3936	ATTAATGAATC	1,00	0,14	Hs.18259	putative ATP(GTP)-binding protein
3937	AGAGGTTGATG	1,00	0,14	Hs.181244	major histocompatibility complex, class I, A
3938	TCAACATCTAG	1,00	0,14	Hs.171734	protein phosphatase 2, regulatory subunit B (B56), g
3939	AAACTAGTTGC	1,00	0,14	Hs.16533	myosin phosphatase, target subunit 1
3940	CCAGCTCCTTG	1,00	0,14	Hs.16520	hypothetical protein DKFZp762L0311
3941	ATTCTCTCAGG	1,00	0,14	Hs.161554	hypothetical protein FLJ20159
3942	AGAACAGACCA	1,00	0,14	Hs.153961	ARP1 (actin-related protein 1, yeast) homolog A (cen
3943	TAGTCTGGAGT	1,00	0,14	Hs.152981	CDP-diacylglycerol synthase (phosphatidate cytidyl)
3944	TGAAAGTCCTG	1,00	0,14	Hs.152707	glioblastoma amplified sequence
3945	CTACTGAAAAA	1,00	0,14	Hs.15248	ESTs
3946	AATGTTTGTGA	1,00	0,14	Hs.135835	ESTs
3947	TTTGATTCTGT	1,00	0,14	Hs.12245	ESTs
3948	TCTCTAAGCCA	1,00	0,14	Hs.11899	3-hydroxy-3-methylglutaryl-Coenzyme A reductase
3949	GGAGCTTGAGG	1,00	0,14	Hs.11689	Notch (Drosophila) homolog 4
3950	TGAGTGAATTC	1,00	0,14	Hs.10119	Homo sapiens mRNA; cDNA DKFZp586O2124 (from clone DK
3951	TGCTAATTGTA	4,00	0,41	Hs.71968	Homo sapiens mRNA; cDNA DKFZp564F053 (from clone DKF
3952	TCCAGCCCCTG	5,00	0,46	Hs.24956	ESTs, Weakly similar to AF118023_1 SH3 domain-bindin
3953	TATTTATTCCT	5,00	0,46	Hs.239934	CGI-96 protein
3954	GAGAAGACTTC	2,00	0,27	Hs.86978	prolyl endopeptidase
3955	AGTAAACCATC	2,00	0,27	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (from clone DK
3956	TCTTTGCAAAG	2,00	0,27	Hs.42458	Homo sapiens mRNA; cDNA DKFZp586C1817 (from clone DK
3957	ACACTTCTTGG	2,00	0,27	Hs.41066	ESTs, Moderately similar to EFGM_RAT ELONGATION FACT
3958	AAAACAAAAAA	2,00	0,27	Hs.10315	solute carrier family 7 (cationic amino acid transpo
3959	CATCTTCACCA	19,00	0,75	Hs.113029	ribosomal protein S25
3960	AGGCTGGATGC	4,00	0,41	Hs.5898	KIAA0668 protein
3961	TTGGCCAGGGT	4,00	0,41	Hs.209396	ESTs, Weakly similar to plakophilin 2b [H.sapiens]
3962	ATAGACGCAAT	11,00	0,63	Hs.6353	MORF-related gene 15
3963	TATCACTCTGT	5,00	0,46	Hs.278362	male-enhanced antigen
3964	CAAGAGGCAAA	7,00	0,53	Hs.5734	KIAA0679 protein
3965	ATGTACTCTGG	8,00	0,56	Hs.75432	IMP (inosine monophosphate) dehydrogenase 2
3966	GTGGTGCGCGC	3,00	0,35	Hs.252075	Homo sapiens mRNA; cDNA DKFZp434D179 (from clone DKF
3967	TCCTGCCCAT	22,00	0,78	Hs.171814	parathymosin
3968	TTGTTATTGCC	4,00	0,41	Hs.78637	annexin A7
3969	GGGCCCCCTGG	2,00	0,27	Hs.81994	glycophorin C (Gerbich blood group)
3970	TTATGTTTAAT	2,00	0,27	Hs.79914	lumican

3971	AGTAGGAGGGA	2,00	0,27	Hs.274422	hypothetical protein FLJ20550
3972	TTGTATCAGAA	2,00	0,27	Hs.250723	FK506 binding protein 12-rapamycin associated protei
3973	GTGCAGTCCTC	2,00	0,27	Hs.19223	ESTs, Weakly similar to R26660_1, partial CDS [H.sap
3974	TTTTGCTACAG	2,00	0,27	Hs.171545	HIV-1 Rev binding protein
3975	TGAAACTTTTC	2,00	0,27	Hs.107528	androgen induced protein
3976	CTGGCCGCAAG	5,00	0,46	Hs.74649	cytochrome c oxidase subunit VIc
3977	GACTCTCTCAG	3,00	0,35	Hs.178576	similar to Bos taurus P14 protein
3978	AGCTGGGTTGG	3,00	0,35	Hs.131731	hypothetical protein FLJ11099
3979	TCTTCTAAAAA	3,00	0,35	Hs.108112	histone fold protein CHRAC17; DNA polymerase epsilon
3980	GTGGGGTCTCT	1,00	1,26	Hs.99672	ESTs, Weakly similar to predicted using Genefinder [
3981	AATTTGAAAAA	1,00	1,26	Hs.99664	ESTs, Highly similar to CMP-N-acetylneuraminic acid
3982	AGTGCATTGTA	1,00	1,26	Hs.99597	ESTs
3983	CACTGTAGTCC	1,00	1,26	Hs.98952	Human DNA sequence from clone RP1-39G22 on chromosom
3984	GGTAGGCAGGG	1,00	1,26	Hs.97439	ESTs
3985	GTAAATGACT	1,00	1,26	Hs.97258	ESTs
3986	TAACCTTTTTTC	1,00	1,26	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate dioxygenase (g
3987	CCAGTGACACT	1,00	1,26	Hs.96023	CD19 antigen
3988	CAGATGCATCA	1,00	1,26	Hs.94695	ESTs, Moderately similar to AF238978_1 pIFI27-like p
3989	GGATGTCCTAT	1,00	1,26	Hs.94479	transmembrane protein 1
3990	TTGGGCAGGAA	1,00	1,26	Hs.92254	hypothetical protein FLJ20163
3991	TGGCAAATGA	1,00	1,26	Hs.91728	polymyositis/scleroderma autoantigen 1 (75kD)
3992	TTTTAACTTTG	1,00	1,26	Hs.90753	Tat-interacting protein (30kD)
3993	TGTGAATATGC	1,00	1,26	Hs.89679	interleukin 2
3994	TGCAAGGCTTT	1,00	1,26	Hs.89418	prostaglandin F receptor (FP)
3995	TGGGAGCTCAG	1,00	1,26	Hs.88411	DNA segment on chromosome 6 (unique) 49 expressed se
3996	ATAAAGTCTAT	1,00	1,26	Hs.87745	ESTs, Weakly similar to Unknown [H.sapiens]
3997	GCCACTGAACC	1,00	1,26	Hs.87125	EH-domain containing 3
3998	TATATACACAT	1,00	1,26	Hs.857	retinol-binding protein 3, interstitial
3999	GTGTGCATCTT	1,00	1,26	Hs.85112	insulin-like growth factor 1 (somatomedia C)
4000	GCACTCTATGT	1,00	1,26	Hs.846	interleukin 8 receptor, beta
4001	GGAAACCTTTT	1,00	1,26	Hs.8373	ESTs
4002	ATGTTAACATC	1,00	1,26	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (from clone DK
4003	TGTTTAAAAAT	1,00	1,26	Hs.82689	tumor rejection antigen (gp96) 1
4004	CATATTCACAT	1,00	1,26	Hs.82582	integrin, beta-like 1 (with EGF-like repeat domains)
4005	TGGAGACTTGC	1,00	1,26	Hs.82283	5-methyltetrahydrofolate-homocysteine methyltransfer



4006	TACCTAATTAT	1,00	1,26	Hs.82223	chordin-like
4007	CTTGTAACAGA	1,00	1,26	Hs.82124	laminin, beta 1
4008	TATAAGAAAAA	1,00	1,26	Hs.80306	Homo sapiens mRNA, clone:RES4-4
4009	CTACTGTACCC	1,00	1,26	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-ace
4010	ATCTACCTTGG	1,00	1,26	Hs.79093	EBNA-2 co-activator (100kD)
4011	GTGAAACTGTT	1,00	1,26	Hs.79090	exportin 1 (CRM1, yeast, homolog)
4012	GTAGAAAAAAG	1,00	1,26	Hs.78890	numb (Drosophila) homolog
4013	TTTGCACACAC	1,00	1,26	Hs.78518	natriuretic peptide receptor B/guanylate cyclase B (
4014	ACAATCTGTAG	1,00	1,26	Hs.77899	tropomyosin 1 (alpha)
4015	GTGCTATTTTG	1,00	1,26	Hs.77873	Homo sapiens mRNA full length insert cDNA clone EURO
4016	CTGAACGCCAT	1,00	1,26	Hs.77694	KIAA0429 gene product
4017	GAGGTGATGGT	1,00	1,26	Hs.76807	major histocompatibility complex, class II, DR alpha
4018	GGCACAGAGAG	1,00	1,26	Hs.76716	pre-alpha (globulin) inhibitor, H3 polypeptide
4019	TCCCTGAAAAG	1,00	1,26	Hs.76364	allograft inflammatory factor 1
4020	ATCTCAACTCA	1,00	1,26	Hs.75813	polycystic kidney disease 1 (autosomal dominant)
4021	GGTGTCTCCAG	1,00	1,26	Hs.75510	annexin A11
4022	GTGGGTGCTTT	1,00	1,26	Hs.75104	RNA-binding protein S1, serine-rich domain
4023	GAGCCAGAGCG	1,00	1,26	Hs.75080	LIM and SH3 protein 1
4024	AGGGGGGCTGAA	1,00	1,26	Hs.74649	cytochrome c oxidase subunit VIc
4025	GTGACCCCAAA	1,00	1,26	Hs.74649	cytochrome c oxidase subunit VIc
4026	TTCAGCAGCAG	1,00	1,26	Hs.7239	SEC24 (S. cerevisiae) related gene family, member B
4027	TTTTGAACAGC	1,00	1,26	Hs.72249	protease-activated receptor 3
4028	GAACCTGAAGT	1,00	1,26	Hs.7165	zinc finger protein 259
4029	GTAAGCGCTGT	1,00	1,26	Hs.70725	gamma-aminobutyric acid (GABA) A receptor, pi
4030	AGTTGACTCCC	1,00	1,26	Hs.69606	ESTs
4031	GCGTTTCTCCA	1,00	1,26	Hs.6853	carbohydrate (N-acetylglucosamine 6-O) sulfotransfer
4032	TGAGCTTGGAA	1,00	1,26	Hs.6820	ESTs, Weakly similar to putative [C.elegans]
4033	TGTGGGAATAG	1,00	1,26	Hs.6783	ESTs
4034	AACTCACAGTT	1,00	1,26	Hs.66072	ESTs
4035	TGCAACATAAA	1,00	1,26	Hs.66020	ESTs
4036	ACTTGAAAAAA	1,00	1,26	Hs.64837	cystinosis, nephropathic
4037	GGAAGCTGGG	1,00	1,26	Hs.6434	hypothetical protein DKFZp761F2014
4038	CCCAGCAGGTT	1,00	1,26	Hs.6351	cleavage and polyadenylation specific factor 4, 30kD
4039	CAAACCTTTGG	1,00	1,26	Hs.63348	DKFZP586M121 protein
4040	AAAAGATCCAG	1,00	1,26	Hs.6318	peroxisomal short-chain alcohol dehydrogenase
4041	ACATTCTACAA	1,00	1,26	Hs.61957	ESTs
4042	ATTTCTTGTTT	1,00	1,26	Hs.61508	Homo sapiens cDNA FLJ10991 fis, clone

					PLACE1002072
5	4043	CACATTTCTGT	1,00	1,26	Hs.6136 KIAA1391 protein
	4044	TAATTGATCAT	1,00	1,26	Hs.606 ATPase, Cu++ transporting, alpha poly-peptide (Menkes
	4045	GCACACTTGCA	1,00	1,26	Hs.60440 ESTs, Weakly similar to serin protease with IGF-bind
10	4046	CGCTCTAGGCT	1,00	1,26	Hs.59970 ESTs
	4047	GAGGAGTGCAT	1,00	1,26	Hs.59395 Homo sapiens clone IMAGE:112574 mRNA sequence
	4048	TTCTTGGA	1,00	1,26	Hs.58882 Microfibril-associated glycoprotein-2
15	4049	AGCCTGACCCC	1,00	1,26	Hs.58611 ESTs
	4050	CAGAGTCCCTG	1,00	1,26	Hs.57922 X-prolyl aminopeptidase (aminopeptidase P) 2, membra
	4051	CTTCCTCTTGC	1,00	1,26	Hs.57836 ESTs
20	4052	TTGACGCTGTA	1,00	1,26	Hs.57697 hyaluronan synthase 1
	4053	GTAATAAGTGT	1,00	1,26	Hs.5476 serine protease inhibitor, Kazal type, 5
	4054	ATGGGCCCTAG	1,00	1,26	Hs.5378 spondin 1, (f-spondin) extracellular matrix protein
25	4055	CCCAATGGCCC	1,00	1,26	Hs.5181 proliferation-associated 2G4, 38kD
	4056	ATAATGCCATT	1,00	1,26	Hs.49927 Homo sapiens mRNA; cDNA DKFZp434H1720 (from clone DK
	4057	GCTTGACAAGT	1,00	1,26	Hs.49599 Homo sapiens mRNA; cDNA DKFZp434G0827 (from clone DK
30	4058	GCTTAACCGCC	1,00	1,26	Hs.48962 ESTs
	4059	TATTTACTTTG	1,00	1,26	Hs.48778 Homo sapiens mRNA; cDNA DKFZp586O0221 (from clone DK
35	4060	ACCCAGGGGAG	1,00	1,26	Hs.46794 ESTs
	4061	TAGAAACTTC	1,00	1,26	Hs.44649 ESTs
	4062	AGAGTGAAAAA	1,00	1,26	Hs.44592 beta-1,4 mannosyltransferase
	4063	CCCTTTACTGC	1,00	1,26	Hs.44441 ESTs
40	4064	CTGACCTTTTA	1,00	1,26	Hs.44296 ESTs, Highly similar to dJ842G6.1 [H.sapiens]
	4065	TCATCTTTGCC	1,00	1,26	Hs.43658 DKFZP586L151 protein
	4066	GGCCCATCCCT	1,00	1,26	Hs.42853 cAMP responsive element binding protein-like 1
45	4067	TGAAATACAAA	1,00	1,26	Hs.42745 ESTs
	4068	AATCCTTACTC	1,00	1,26	Hs.41735 purinergic receptor P2X, ligand-gated ion channel, 1
50	4069	CTGGGCCATTG	1,00	1,26	Hs.4 alcohol dehydrogenase 2 (class I), beta polypeptide
	4070	CTGTAATATTC	1,00	1,26	Hs.38703 ESTs
	4071	CCACAGCCTAT	1,00	1,26	Hs.36131 collagen, type XIV, alpha 1 (undulin)
55	4072	GGTGAGATTGT	1,00	1,26	Hs.33983 ESTs, Weakly similar to ALU6_HUMAN ALU SUBFAMILY SP
	4073	GAATCTCTCCC	1,00	1,26	Hs.32425 ESTs
	4074	ATGGACCAAAG	1,00	1,26	Hs.32345 ESTs
	4075	AATCTTGTTAA	1,00	1,26	Hs.32343 ESTs
60	4076	GCCTCTTTTCT	1,00	1,26	Hs.31439 serine protease inhibitor, Kunitz type, 2
	4077	AATGGCCTTGA	1,00	1,26	Hs.31431 ESTs
	4078	GGCATTGGTCA	1,00	1,26	Hs.3128 polymerase (RNA) II (DNA directed)

					polypeptide H
4079	GTCTTGTAATC	1,00	1,26	Hs.31016	putative DNA binding protein
4080	TAGATAGCACA	1,00	1,26	Hs.31016	putative DNA binding protein
4081	TCTCAAAACAA	1,00	1,26	Hs.30591	ESTs
4082	AAGAACTCTGC	1,00	1,26	Hs.30250	v-maf musculoaponeurotic fibrosarcoma (avian) oncogene
4083	AGTAATTTAAA	1,00	1,26	Hs.30172	ESTs
4084	CATTCTTTCTT	1,00	1,26	Hs.30035	splicing factor, arginine/serine-rich (transformer 2)
4085	GGCAGCAGGAC	1,00	1,26	Hs.29759	RNA POLYMERASE I AND TRANSCRIPT RELEASE FACTOR
4086	CTTGTTATTCA	1,00	1,26	Hs.29664	Human DNA sequence from clone 682J15 on chromosome 6
4087	CACTCTGTTTG	1,00	1,26	Hs.29499	toll-like receptor 3
4088	TTCCCCACCT	1,00	1,26	Hs.286217	KIAA0685 gene product
4089	CCTCAGCCTCT	1,00	1,26	Hs.285657	ESTs
4090	CTTTTTTCATT	1,00	1,26	Hs.285122	ESTs, Weakly similar to S53869 laminin beta-2 chain
4091	TCTCCACCCC	1,00	1,26	Hs.285042	ESTs
4092	CACCTGTAAGC	1,00	1,26	Hs.284664	EST
4093	GCAGCGGGGAT	1,00	1,26	Hs.284422	ESTs
4094	GTTGTTTTTGG	1,00	1,26	Hs.284394	complement component 3
4095	CCAGCCTCTGT	1,00	1,26	Hs.284171	KIAA1535 protein
4096	TGTGGGAGCCA	1,00	1,26	Hs.284145	chromosome 3 open reading frame 4
4097	CTTGTAGCCCT	1,00	1,26	Hs.283607	hypothetical protein PRO3077
4098	TTCCAGAAGCA	1,00	1,26	Hs.283600	ESTs
4099	CATCCACCTGG	1,00	1,26	Hs.283527	ESTs
4100	AAAAGAATACT	1,00	1,26	Hs.282887	ESTs
4101	TATATCTCTCT	1,00	1,26	Hs.28273	ESTs
4102	TTGGCAGCAAT	1,00	1,26	Hs.280531	ESTs
4103	GTAAATTTGA	1,00	1,26	Hs.279939	mitochondrial carrier homolog 1
4104	TATATAATGTG	1,00	1,26	Hs.279840	zinc finger protein 222
4105	GAAACCCAGGG	1,00	1,26	Hs.279813	hypothetical protein
4106	CCACAGCTCTC	1,00	1,26	Hs.279671	katanin p60 (ATPase-containing) subunit A 1
4107	TTTGTTCTGA	1,00	1,26	Hs.279531	ESTs
4108	GCAGAAGCACC	1,00	1,26	Hs.279396	EST, Weakly similar to AF119917_56 PRO2729 [H.sapien]
4109	AGTGGTGAGGG	1,00	1,26	Hs.279298	ESTs
4110	TCAGCCCTGGC	1,00	1,26	Hs.278550	ESTs, Weakly similar to KIAA0940 protein [H.sapiens]
4111	CCTCTCATCCA	1,00	1,26	Hs.278028	ESTs
4112	GTGGTGCGCTT	1,00	1,26	Hs.277808	EST
4113	CACCCTGTAGT	1,00	1,26	Hs.277531	ESTs
4114	GTGAGACCTAA	1,00	1,26	Hs.277186	ESTs, Weakly similar to ALU6_HUMAN ALU SUBFAMILY SP
4115	ACTTTGTAAAA	1,00	1,26	Hs.274976	EST
4116	TGCTGGGAACCT	1,00	1,26	Hs.274667	EST
4117	CACCTATAGTA	1,00	1,26	Hs.274510	Homo sapiens mRNA; cDNA DKFZp564B032 (from clone DKF

4118	GCAGGTACGCT	1,00	1,26	Hs.274429	Homo sapiens cDNA FLJ11192 fis, clone PLACE1007618,
4119	CCAGGGGGGCC	1,00	1,26	Hs.272813	dual oxidase 1
4120	CTGGCCAACGT	1,00	1,26	Hs.272791	hypothetical protein FLJ20306
4121	CCCAAACGCGC	1,00	1,26	Hs.272572	hemoglobin, alpha 2
4122	CCCAACGCGTT	1,00	1,26	Hs.272572	hemoglobin, alpha 2
4123	CCCTTTTAAAA	1,00	1,26	Hs.272325	Homo sapiens mRNA; cDNA DKFZp434A2322 (from clone DK
4124	ATTGCTCCAAT	1,00	1,26	Hs.272146	ESTs, Moderately similar to ALU5_HUMAN ALU SUBFAMILY
4125	AAACAGTGTCT	1,00	1,26	Hs.270618	ESTs, Weakly similar to KIAA0822 protein [H.sapiens]
4126	AGCTACCACCC	1,00	1,26	Hs.269541	ESTs
4127	CCCCTGCACTG	1,00	1,26	Hs.264610	ESTs, Moderately similar to Ibd1 [H.sapiens]
4128	ATCCACAATGG	1,00	1,26	Hs.264428	tissue specific transplantation antigen P35B
4129	AAACACGGCAA	1,00	1,26	Hs.264221	ESTs
4130	TTGCCCAAAAA	1,00	1,26	Hs.26339	ESTs
4131	CCTGTAATTTT	1,00	1,26	Hs.259691	Homo sapiens mRNA; cDNA DKFZp761E0311 (from clone DK
4132	TGAGAAAACAG	1,00	1,26	Hs.259315	ESTs
4133	GGGCCCTGGGC	1,00	1,26	Hs.25895	ESTs, Weakly similar to PI-3 kinase [H.sapiens]
4134	CCTGAAGCCTG	1,00	1,26	Hs.258538	striatin, calmodulin-binding protein
4135	AATATGCATCC	1,00	1,26	Hs.258400	ESTs
4136	GATCAAAGAAG	1,00	1,26	Hs.257620	EST
4137	TATTTTGGTGC	1,00	1,26	Hs.257540	ESTs
4138	TGTTTTAGTTC	1,00	1,26	Hs.257441	EST
4139	AGTTGCTCTGG	1,00	1,26	Hs.257249	ESTs
4140	AGATTAACATT	1,00	1,26	Hs.256132	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
4141	CATTCATTCAT	1,00	1,26	Hs.255906	ESTs
4142	GGTGTTTCAGGG	1,00	1,26	Hs.255530	ESTs
4143	CACTCAAATA	1,00	1,26	Hs.255374	ESTs
4144	GCCTGAGGCTT	1,00	1,26	Hs.255308	EST
4145	TAGCCGCTGGG	1,00	1,26	Hs.255176	ESTs, Moderately similar to CD45_HUMAN LEUKOCYTE COM
4146	TGCTTGCCAG	1,00	1,26	Hs.255170	EST
4147	AATGGGAAGAT	1,00	1,26	Hs.255037	EST
4148	CAATGTAAAAG	1,00	1,26	Hs.254881	ESTs
4149	GCCCTAGAGCA	1,00	1,26	Hs.25475	aquaporin 7
4150	CAACCATTTC	1,00	1,26	Hs.25447	ESTs
4151	GAAGGGGCAAT	1,00	1,26	Hs.253793	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAMILY SB2
4152	ATGTTGGAAAG	1,00	1,26	Hs.253704	ESTs
4153	CAAATAGGCCA	1,00	1,26	Hs.25300	hypothetical protein DKFZp761G1923
4154	GAGATGTATCT	1,00	1,26	Hs.252934	ESTs
4155	GATGACAAAAA	1,00	1,26	Hs.252807	ESTs
4156	CCCCAGCAGTC	1,00	1,26	Hs.252259	ribosomal protein S3

4157	CCACACAATTC	1,00	1,26	Hs.250911	Homo sapiens clone 23967 unknown mRNA, partial cds	
4158	CAACATTTTAA	1,00	1,26	Hs.250158	ESTs	5
4159	TATAAAAAGTA	1,00	1,26	Hs.249759	EST	
4160	GGGGCAGATCC	1,00	1,26	Hs.249669	EST	
4161	AGCCACTGTCC	1,00	1,26	Hs.246187	ESTs, Highly similar to cep250 centrosome associated	10
4162	AGCTTTCTCAA	1,00	1,26	Hs.245297	ESTs	
4163	TTTCTTTGACC	1,00	1,26	Hs.244865	ESTs	
4164	GGCCGGGACCC	1,00	1,26	Hs.244844	EST, Weakly similar to S39803 ribosomal protein L4 -	15
4165	AGAGATACTAG	1,00	1,26	Hs.244473	ESTs	
4166	GAAGCTTGGTC	1,00	1,26	Hs.243582	EST	
4167	GCATCGCTGTT	1,00	1,26	Hs.243570	EST	
4168	GTAAAACCCC	1,00	1,26	Hs.243542	EST, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX S	20
4169	AAGAGATGTGC	1,00	1,26	Hs.242885	EST	
4170	TCTACTAAAGA	1,00	1,26	Hs.242122	EST, Moderately similar to ALU6_HUMAN ALU SUBFAMILY	25
4171	GCCACGCCCAG	1,00	1,26	Hs.241507	ribosomal protein S6	
4172	TATAAACAGA	1,00	1,26	Hs.24078	ESTs	
4173	GACTTTTCTGG	1,00	1,26	Hs.2407	POU domain, class 2, associating factor 1	30
4174	AAAAACTGTCC	1,00	1,26	Hs.239818	phosphoinositide-3-kinase, catalytic, beta polypepti	
4175	ATAGCTTTGAT	1,00	1,26	Hs.23767	guanine nucleotide binding protein (G protein), gamm	35
4176	GAATACTACTC	1,00	1,26	Hs.237097	ESTs	
4177	CCCTTCTTTGT	1,00	1,26	Hs.236545	hydroxyacid oxidase 2 (long chain)	
4178	TTCTATGATCC	1,00	1,26	Hs.235860	ESTs	
4179	GCACACTCATA	1,00	1,26	Hs.235782	organic anion transporter OATP-E	40
4180	GGGACCCTCAG	1,00	1,26	Hs.235604	EST	
4181	GATCCAGTTT	1,00	1,26	Hs.234489	lactate dehydrogenase B	
4182	TCCAACAGCCT	1,00	1,26	Hs.233789	ESTs	
4183	AAGAAAGACTA	1,00	1,26	Hs.233431	ESTs	45
4184	GAAGACAAAAG	1,00	1,26	Hs.233383	ESTs	
4185	TTGCTTCTCAA	1,00	1,26	Hs.233172	EST	
4186	TGTATTTCTTT	1,00	1,26	Hs.233045	EST	
4187	GAATAGCTCTG	1,00	1,26	Hs.233041	EST	50
4188	TGAGCATATTT	1,00	1,26	Hs.232010	ESTs	
4189	ATCTAACTAGA	1,00	1,26	Hs.230905	EST	
4190	GATCAAAAATA	1,00	1,26	Hs.230647	EST	
4191	GGTGCCAGAGT	1,00	1,26	Hs.229501	EST, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C W	55
4192	GGGTGGGTTTT	1,00	1,26	Hs.229064	EST	
4193	CCTTTGAGATC	1,00	1,26	Hs.228944	EST, Weakly similar to RS5_HUMAN 40S RIBOSOMAL PROTE	60
4194	CCTTTCTCTCT	1,00	1,26	Hs.227948	squamous cell carcinoma antigen 1	
4195	TGGCAGCTTTG	1,00	1,26	Hs.22708	ESTs	
4196	TCGACTGAGAA	1,00	1,26	Hs.226133	growth arrest-specific 7	65

5	4197	AATCAGGGGAC	1,00	1,26	Hs.225767	IDN3 protein
	4198	TCTTAGTAGAG	1,00	1,26	Hs.22564	myosin VI
	4199	CTCCCAGAATC	1,00	1,26	Hs.225160	ESTs
	4200	TGGGGATGAAA	1,00	1,26	Hs.225118	ESTs
	4201	TCCAATAAAAT	1,00	1,26	Hs.224808	EST
10	4202	TTCTGAATAA	1,00	1,26	Hs.224235	EST, Moderately similar to nucleolar RNA-helicase [H
	4203	CTGAGACTAAA	1,00	1,26	Hs.224015	ESTs
	4204	AGCTATAATTG	1,00	1,26	Hs.223572	EST, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE
15	4205	AAAGCCAAGAC	1,00	1,26	Hs.222728	ESTs
	4206	GCTTTTAGGTT	1,00	1,26	Hs.221660	blood vessel epicardial substance
	4207	CAGCACTCCTT	1,00	1,26	Hs.217882	ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY
20	4208	CCTCCCTCGGC	1,00	1,26	Hs.21729	splicing factor 3a, subunit 1, 120kD
	4209	CCACTGGAGTC	1,00	1,26	Hs.215893	ESTs, Weakly similar to RMS1_HUMAN REGULATOR OF MITO
	4210	ATCACCAAAGT	1,00	1,26	Hs.214039	ESTs
25	4211	CCTCCGGTACT	1,00	1,26	Hs.214004	EST
	4212	GATTCATTGCA	1,00	1,26	Hs.214	neuro-oncological ventral antigen 1
	4213	AGTCAAGATCA	1,00	1,26	Hs.21321	Homo sapiens mRNA; cDNA DKFZp564E1363 (from clone DK
30	4214	TAAAAAAAGGA	1,00	1,26	Hs.212481	ESTs
	4215	CATTGATACTA	1,00	1,26	Hs.210347	ESTs
	4216	GAGTCCCGGCT	1,00	1,26	Hs.210265	ESTs
	4217	AGGGGAAGGCG	1,00	1,26	Hs.208035	EST
35	4218	TGTGATTGTAA	1,00	1,26	Hs.207915	ESTs
	4219	GTAACCAAAAA	1,00	1,26	Hs.207593	EST
	4220	ACTTTTCCCAC	1,00	1,26	Hs.207345	ESTs
	4221	CACCTGAATA	1,00	1,26	Hs.205769	EST
40	4222	GTGGTTGCCCT	1,00	1,26	Hs.205466	ESTs
	4223	CAAAGTAATCT	1,00	1,26	Hs.203800	ESTs
	4224	CTTCTGTGTGG	1,00	1,26	Hs.202202	EST
	4225	CTGGCAAATTT	1,00	1,26	Hs.202072	ESTs
45	4226	ACATTTAAAAG	1,00	1,26	Hs.20142	ESTs
	4227	CACAGCCTGCC	1,00	1,26	Hs.201377	aprase, lysosomal
	4228	CTCCCCCCCCC	1,00	1,26	Hs.199913	EST
50	4229	GTAAGACTCTG	1,00	1,26	Hs.199827	Homo sapiens mRNA; cDNA DKFZp564P1816 (from clone DK
	4230	ATTCTTAGCT	1,00	1,26	Hs.198253	major histocompatibility complex, class II, DQ alpha
	4231	TATTATGGCCA	1,00	1,26	Hs.197766	Human clone 23932 mRNA sequence
55	4232	GGTCAAGTCTG	1,00	1,26	Hs.197708	ESTs
	4233	TGCAAAAATCT	1,00	1,26	Hs.197671	ESTs
	4234	ATCCATTTTGA	1,00	1,26	Hs.19762	ESTs, Weakly similar to unknown [D.melanogaster]
60	4235	AAGCACCTACG	1,00	1,26	Hs.197143	ESTs
	4236	TTATGCTCTTG	1,00	1,26	Hs.197143	ESTs
	4237	GTGCTCAATTT	1,00	1,26	Hs.196663	ESTs
65	4238	GCGTCTCGATG	1,00	1,26	Hs.196058	ESTs

4239	GTAAACGCTGT	1,00	1,26	Hs.195175	CASP8 and FADD-like apoptosis regula- tor	
4240	CATTCTCATTG	1,00	1,26	Hs.194984	ESTs	5
4241	ACTTGCTGTGT	1,00	1,26	Hs.194031	ESTs	
4242	TCTGTGTCTAA	1,00	1,26	Hs.194024	ESTs	
4243	TAACCTAAAAC	1,00	1,26	Hs.194019	attractin (with dipeptidylpeptidase IV activity)	10
4244	TTGGTGTCAC	1,00	1,26	Hs.193988	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S	
4245	CCTCCATCTTC	1,00	1,26	Hs.193762	ESTs, Weakly similar to Rigui [H.sapiens]	15
4246	AAAAAGAGTTT	1,00	1,26	Hs.193743	ESTs	
4247	TTTAGTGAAAA	1,00	1,26	Hs.193370	ESTs, Highly similar to LIM domains containing prote	20
4248	TGATCTTTATG	1,00	1,26	Hs.192374	ESTs	
4249	CCCTCCCAGCT	1,00	1,26	Hs.191742	ESTs	
4250	TTCCAGCTGC	1,00	1,26	Hs.19121	adaptor-related protein complex 2, alpha 2 subunit	25
4251	CAAAAACAGTA	1,00	1,26	Hs.191077	ESTs	
4252	AGAGCAGGGCA	1,00	1,26	Hs.190874	ESTs	
4253	GTATGGTAGAG	1,00	1,26	Hs.189773	ESTs	
4254	TCACCCCTATG	1,00	1,26	Hs.189583	putative protein similar to nessy (Droso- phila)	30
4255	GAAGCTCCAAA	1,00	1,26	Hs.186711	hypothetical protein FLJ20070	
4256	TATTTTACCGT	1,00	1,26	Hs.184693	transcription elongation factor B (SIII), polypeptid	35
4257	CGGTCCGGGCAG	1,00	1,26	Hs.184634	hypothetical protein FLJ20005	
4258	AGGACATCTAT	1,00	1,26	Hs.184175	chromosome 2 open reading frame 3	
4259	TCCATAAAGAA	1,00	1,26	Hs.183805	ankyrin 1, erythrocytic	
4260	GAGTCATCGGC	1,00	1,26	Hs.183745	ESTs	
4261	GCACTTTTCCT	1,00	1,26	Hs.183704	ubiquitin C	40
4262	TGGCTCCCCTT	1,00	1,26	Hs.183648	protein tyrosine phosphatase, receptor type, f polyp	
4263	GGGCCAGGTGG	1,00	1,26	Hs.183138	procollagen (type III) N-endopeptidase	
4264	TCCTACCCTAT	1,00	1,26	Hs.181781	ESTs, Highly similar to GBG8_HUMAN GUANINE NUCLEOTID	45
4265	AGGTTTTGAGG	1,00	1,26	Hs.181682	ESTs	
4266	AGTGGAGAGTA	1,00	1,26	Hs.180737	Homo sapiens clone 23664 and 23905 mRNA sequence	50
4267	TAAAAGCCTTT	1,00	1,26	Hs.180668	ESTs	
4268	CCCAGGGGAAA	1,00	1,26	Hs.180414	heat shock 70kd protein 10 (HSC71)	
4269	GCAAGTTGCCA	1,00	1,26	Hs.180398	LIM domain-containing preferred translo- cation partne	55
4270	GTTTTGGTATT	1,00	1,26	Hs.179526	upregulated by 1,25-dihydroxyvitamin D- 3	
4271	GAGATTCTCAT	1,00	1,26	Hs.17917	lymphatic vessel endothelial hyaluronan receptor 1	60
4272	AATTAGGATAA	1,00	1,26	Hs.17914	ESTs, Weakly similar to AF201951_1 high affinity imm	
4273	TCTCCAGGGCC	1,00	1,26	Hs.178803	ESTs	

5	4274	AGCTGTCTCTT	1,00	1,26	Hs.177744	ESTs
	4275	AGATTTGGGCG	1,00	1,26	Hs.177655	ESTs
	4276	TTCCCTTTTTC	1,00	1,26	Hs.177486	amyloid beta (A4) precursor protein (protease nexin-
	4277	GGAGTGCAAAT	1,00	1,26	Hs.177162	ESTs
	4278	GTTGTTTTTTA	1,00	1,26	Hs.177096	ESTs
10	4279	TATGTCTTGGA	1,00	1,26	Hs.1765	lymphocyte-specific protein tyrosine kinase
	4280	CAGTAAACCTC	1,00	1,26	Hs.176005	Homo sapiens mRNA full length insert cDNA clone EURO
15	4281	TGGATGAAAAA	1,00	1,26	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (from clone DK
	4282	GGGAAAAAAG	1,00	1,26	Hs.175351	EST
	4283	ATTGTGGGGCC	1,00	1,26	Hs.175350	EST
20	4284	GAAGTTTCTGC	1,00	1,26	Hs.175339	EST
	4285	GGGAAGTTCTT	1,00	1,26	Hs.175218	potassium channel, subfamily K, member 7
	4286	CTACCTGACCT	1,00	1,26	Hs.174044	dishevelled 3 (homologous to Drosophila dsh)
25	4287	GAAAGGGCCCT	1,00	1,26	Hs.173159	transforming, acidic coiled-coil containing protein
	4288	ACCAAAGAGAC	1,00	1,26	Hs.172652	KIAA0013 gene product
30	4289	AAAGGAAGATT	1,00	1,26	Hs.172405	cell division cycle 27
	4290	CTTATAATCTC	1,00	1,26	Hs.172182	poly(A)-binding protein, cytoplasmic 1
	4291	AAGTATCAGCT	1,00	1,26	Hs.171957	triple functional domain (PTPRF interact- ing)
35	4292	GATATGGTTTG	1,00	1,26	Hs.170773	ESTs
	4293	TAACCTCTAGAA	1,00	1,26	Hs.170714	ESTs
	4294	AGAAGATGCCG	1,00	1,26	Hs.169902	solute carrier family 2 (facilitated glucose transpo
40	4295	TTTCGCAGAAA	1,00	1,26	Hs.169395	ESTs
	4296	CTTTTGTAATG	1,00	1,26	Hs.169149	karyopherin alpha 1 (importin alpha 5)
	4297	AAATGATCCCG	1,00	1,26	Hs.168941	ESTs
	4298	TTCAAAGTTGA	1,00	1,26	Hs.168363	ESTs
	4299	TAATTGTTTAT	1,00	1,26	Hs.168241	hypothetical protein FLJ10242
45	4300	GGCAAGTTCCT	1,00	1,26	Hs.166832	ESTs
	4301	GGAGATAGTGC	1,00	1,26	Hs.166369	ESTs, Highly similar to sodium bicarbon- ate cotranspo
50	4302	TTCTGCTTTTCG	1,00	1,26	Hs.1652	chemokine (C-C motif) receptor 7
	4303	TCACGCCGGAC	1,00	1,26	Hs.165003	ESTs
	4304	TTCCCTTTATT	1,00	1,26	Hs.164427	ESTs
	4305	AATATGTACAC	1,00	1,26	Hs.163900	ESTs
	4306	CAAGAACAATC	1,00	1,26	Hs.163724	HSPC019 protein
55	4307	GGCAGCTGGTA	1,00	1,26	Hs.163252	EST
	4308	AGGGATATTGG	1,00	1,26	Hs.163203	ESTs, Weakly similar to B34087 hypo- thetical protein
60	4309	ACACTGTACTC	1,00	1,26	Hs.163189	ESTs
	4310	GAAGCAGAAAA	1,00	1,26	Hs.162852	EST
	4311	GAGCAAACCTT	1,00	1,26	Hs.16249	ESTs
	4312	GACTGGAAGTA	1,00	1,26	Hs.162252	EST



4313	AGGCTGAGGAA	1,00	1,26	Hs.161790	EST
4314	TGGAACTCAG	1,00	1,26	Hs.161719	ESTs
4315	ACAGATTTTGG	1,00	1,26	Hs.161554	hypothetical protein FLJ20159
4316	ATTCTTTAAAA	1,00	1,26	Hs.161554	hypothetical protein FLJ20159
4317	CTAGTGCACAC	1,00	1,26	Hs.161554	hypothetical protein FLJ20159
4318	GGCAACAAGGT	1,00	1,26	Hs.161554	hypothetical protein FLJ20159
4319	TAAACCTTTTG	1,00	1,26	Hs.161554	hypothetical protein FLJ20159
4320	TTGAAATTTGA	1,00	1,26	Hs.161305	tachykinin receptor 2
4321	GTCTGTGCTAT	1,00	1,26	Hs.161277	EST
4322	TTTCTTGGTAA	1,00	1,26	Hs.161065	EST
4323	AAAAATGCTTC	1,00	1,26	Hs.160914	EST
4324	CTAAATTCGGA	1,00	1,26	Hs.160275	EST
4325	CCAGCTAGAAA	1,00	1,26	Hs.160013	ESTs
4326	GAGCAGCTCAC	1,00	1,26	Hs.159553	chemokine-like receptor 1
4327	TAGAGTGATGG	1,00	1,26	Hs.159153	ESTs
4328	TACCCAGACTT	1,00	1,26	Hs.158287	KIAA0468 gene product
4329	CCACCTGAATT	1,00	1,26	Hs.15740	Homo sapiens mRNA; cDNA DKFZp434E033 (from clone DKF
4330	GGGCTGGTGGGA	1,00	1,26	Hs.156836	ESTs
4331	TCACGAGCTAT	1,00	1,26	Hs.155764	ESTs
4332	CCCTTTGAGCA	1,00	1,26	Hs.155381	ESTs, Moderately similar to I38022 hypothetical prot
4333	GAATTTACTTA	1,00	1,26	Hs.155314	KIAA0095 gene product
4334	TCAGGGTGAAG	1,00	1,26	Hs.154156	myosin, light polypeptide 4, alkali; atrial, embryon
4335	GGACTTTCAAA	1,00	1,26	Hs.153739	ESTs
4336	AGAGAAGATGC	1,00	1,26	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3' untranslate
4337	TACTCCCCTGA	1,00	1,26	Hs.152936	adaptor-related protein complex 2, mu 1 subunit
4338	TGACCTACTGG	1,00	1,26	Hs.152666	ESTs
4339	AGTGTAAGTTT	1,00	1,26	Hs.152129	ESTs
4340	CACCGTGTGTC	1,00	1,26	Hs.152016	ESTs
4341	TAACTCCTCCC	1,00	1,26	Hs.150784	ESTs
4342	GGGTAAGGAGG	1,00	1,26	Hs.150423	cyclin-dependent kinase 9 (CDC2-related kinase)
4343	AATTTATATAA	1,00	1,26	Hs.150073	ESTs, Moderately similar to alternatively spliced pr
4344	TGTAATGTAAA	1,00	1,26	Hs.149623	group III secreted phospholipase A2
4345	TGGGTGAAAAA	1,00	1,26	Hs.148725	ESTs
4346	TTGTCTACAAA	1,00	1,26	Hs.148217	ESTs, Moderately similar to AF161544_1 HSPC059 [H.sa
4347	AACTTGATAT	1,00	1,26	Hs.148129	EST
4348	TTAACTTTTTT	1,00	1,26	Hs.148091	ESTs
4349	TTTCTTAGGTT	1,00	1,26	Hs.147317	ESTs
4350	CCTCCCCCATT	1,00	1,26	Hs.146893	EST
4351	TTGTTGCTGGT	1,00	1,26	Hs.146730	ESTs
4352	GTGCTGTTAGT	1,00	1,26	Hs.146712	ESTs
4353	ATGACATTGGA	1,00	1,26	Hs.146335	ESTs
4354	ATTGGTAGACA	1,00	1,26	Hs.146311	ESTs, Moderately similar to

					ALU1_HUMAN ALU SUBFAMILY
5	4355	TTTATCTTTT	1,00	1,26	Hs.145584 ESTs
	4356	TTGTCAAAAA	1,00	1,26	Hs.145279 SET translocation (myeloid leukemia-associated)
	4357	TATATTATAGA	1,00	1,26	Hs.144931 ATPase, aminophospholipid transporter (APLT), Class
10	4358	GGAATTGTTGT	1,00	1,26	Hs.143866 ESTs
	4359	AGCCTTTGCCA	1,00	1,26	Hs.143574 ESTs
	4360	TCTTTATTTTC	1,00	1,26	Hs.14286 flavin containing monooxygenase 5
	4361	TTTCCTATAAA	1,00	1,26	Hs.141939 ESTs
15	4362	TCTAAAGAATT	1,00	1,26	Hs.141055 Homo sapiens clone 23758 mRNA sequence
	4363	TCAGCGGACTG	1,00	1,26	Hs.138280 ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY
20	4364	ACAATGTAGGA	1,00	1,26	Hs.137415 Homo sapiens BAC clone RP11-294L11 from 2
	4365	TGACTTGGCCA	1,00	1,26	Hs.137401 ESTs
	4366	CTCCCCAAAA	1,00	1,26	Hs.13684 hypothetical protein FLJ10761
25	4367	CTCCCTCTTTC	1,00	1,26	Hs.136468 EST
	4368	GAAGCCCAATT	1,00	1,26	Hs.136432 ESTs
	4369	CTCTAGGTAAA	1,00	1,26	Hs.136423 ESTs
	4370	GTGATATGACT	1,00	1,26	Hs.136200 ESTs
30	4371	GAGAGAAATGG	1,00	1,26	Hs.136169 Homo sapiens clone 25215 mRNA sequence, partial cds
	4372	CACATTTTTAA	1,00	1,26	Hs.136008 ESTs
	4373	GTTTTCTCTGT	1,00	1,26	Hs.135503 ESTs
35	4374	TTCATAAGTTT	1,00	1,26	Hs.135473 ESTs
	4375	AGACGGTCCAA	1,00	1,26	Hs.134757 hypothetical protein FLJ20033
	4376	TACCCAGGAA	1,00	1,26	Hs.134350 ESTs
	4377	TTGCTCCTCCT	1,00	1,26	Hs.133521 ESTs
40	4378	CAGGGGAGGAC	1,00	1,26	Hs.133386 ESTs
	4379	AATATGCGGCA	1,00	1,26	Hs.133355 ESTs
	4380	AGTTTGAGATA	1,00	1,26	Hs.133266 ESTs
45	4381	AATCTGGCGTA	1,00	1,26	Hs.132927 ESTs, Moderately similar to p53 regulated PA26-T2 nu
	4382	GTCAGGAGAAG	1,00	1,26	Hs.132278 ESTs
	4383	TCTTTATTTT	1,00	1,26	Hs.131360 ESTs
	4384	GCCTGCAGGAA	1,00	1,26	Hs.131030 ESTs
50	4385	TTGATTCCTAT	1,00	1,26	Hs.130881 hypothetical protein FLJ10173
	4386	TTTAGAGTGGA	1,00	1,26	Hs.130716 ESTs
	4387	TGTCTGGTTTA	1,00	1,26	Hs.130518 ESTs
	4388	TTCAATTCATTC	1,00	1,26	Hs.130253 ESTs
55	4389	GGAGGGCTGTG	1,00	1,26	Hs.129381 ESTs, Moderately similar to melastatin 1 [H.sapiens]
	4390	CTTCCTGCTAC	1,00	1,26	Hs.128018 ESTs
	4391	TCTAAGCTTGT	1,00	1,26	Hs.127780 ESTs
60	4392	TGAGAATTCTG	1,00	1,26	Hs.127378 ESTs
	4393	GTGCCTCAGCC	1,00	1,26	Hs.126943 ESTs
	4394	CCCCAAGGCCT	1,00	1,26	Hs.125359 Thy-1 cell surface antigen
	4395	AGGGAGGCTGA	1,00	1,26	Hs.125246 ESTs

4396	TTTGTCTGTCT	1,00	1,26	Hs.125134	KIAA1172 protein
4397	CACAGCCACTA	1,00	1,26	Hs.125103	ESTs
4398	GATGCTAGAGC	1,00	1,26	Hs.124597	ESTs
4399	ATCTTCAGTAT	1,00	1,26	Hs.1244	CD9 antigen (p24)
4400	GTCTCCAAGCC	1,00	1,26	Hs.124367	ESTs
4401	CATTTCCCTTG	1,00	1,26	Hs.123307	ESTs
4402	ATAAAAGGAAA	1,00	1,26	Hs.122236	EST
4403	ATGAAGTGTTG	1,00	1,26	Hs.121558	fer (fps/fes related) tyrosine kinase (phosphoprotein)
4404	TGTTACTGGGA	1,00	1,26	Hs.120592	ESTs
4405	CCACAGGGATT	1,00	1,26	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danlos syndrome)
4406	TTCCTGGTGCG	1,00	1,26	Hs.119251	ubiquinol-cytochrome c reductase core protein I
4407	CTAGTTTAAAA	1,00	1,26	Hs.11899	3-hydroxy-3-methylglutaryl-Coenzyme A reductase
4408	ATTAAGTACAA	1,00	1,26	Hs.118959	ESTs
4409	CACCTGTTTCT	1,00	1,26	Hs.118796	annexin A6
4410	CCCCGTGGTCA	1,00	1,26	Hs.118795	ESTs, Highly similar to unnamed protein product [H.s]
4411	CTATAATCCCA	1,00	1,26	Hs.117582	CGI-43 protein
4412	GCTAAACTCCG	1,00	1,26	Hs.117582	CGI-43 protein
4413	GGGTCTTGGAG	1,00	1,26	Hs.117582	CGI-43 protein
4414	GTGGCTTTCGC	1,00	1,26	Hs.117582	CGI-43 protein
4415	TTTATTGTAGA	1,00	1,26	Hs.117582	CGI-43 protein
4416	TGGACAGTGAA	1,00	1,26	Hs.116823	EST
4417	TAACCTAGATG	1,00	1,26	Hs.116486	EST
4418	ACTGCCTGCAT	1,00	1,26	Hs.116192	ESTs
4419	GATAAACCCAGA	1,00	1,26	Hs.115580	ESTs
4420	TTTTACAAACC	1,00	1,26	Hs.115175	sterile-alpha motif and leucine zipper containing ki
4421	TGTATTGTAAA	1,00	1,26	Hs.115129	ESTs
4422	AAGGGATGCTG	1,00	1,26	Hs.11383	small inducible cytokine subfamily A (Cys-Cys), memb
4423	GGTAAAAAATG	1,00	1,26	Hs.112264	ESTs
4424	AAAGCCCAAGT	1,00	1,26	Hs.111758	keratin 6B
4425	CAGGGTGTGTG	1,00	1,26	Hs.11032	ESTs, Moderately similar to dJ108K11.3 [H.sapiens]
4426	TTTGGCTTGGC	1,00	1,26	Hs.110028	ESTs
4427	AAACAGTAAAT	1,00	1,26	Hs.109526	zinc finger protein 198
4428	CCTCATTTCCC	1,00	1,26	Hs.109439	DKFZP586P2421 protein
4429	TTGTTGATCCA	1,00	1,26	Hs.107476	ATP synthase, H <sup>+</sup> transporting, mito- chondrial F1F0, s
4430	TTTGAAAACAA	1,00	1,26	Hs.107203	hypothetical protein from EUROIMAGE 1759349
4431	AACCTTCCATA	1,00	1,26	Hs.106833	ESTs
4432	AGGAGCACCGT	1,00	1,26	Hs.106432	ESTs
4433	AGCTCCGGGAC	1,00	1,26	Hs.106019	protein phosphatase 1, regulatory sub- unit 10
4434	ATGTTTACCAG	1,00	1,26	Hs.105965	ESTs

4435	ATACGTTTTTT	1,00	1,26	Hs.105958	KIAA0620 protein
4436	ATGACATCACT	1,00	1,26	Hs.105506	EST
4437	CCCCTGCCCTG	1,00	1,26	Hs.104866	ESTs
4438	ATGTAGTCATT	1,00	1,26	Hs.104219	ESTs
4439	TTTCTGCCTTC	1,00	1,26	Hs.1042	Sjogren syndrome antigen A1 (52kD, ribonucleoprotein)
4440	CAAATGTCCAT	1,00	1,26	Hs.10359	ESTs
4441	GCGGTGTACAC	1,00	1,26	Hs.10306	natural killer cell group 7 sequence
4442	TACAAAAAAA	1,00	0,14	Hs.96560	Human DNA sequence from clone RP11-39402 on chromoso
4443	GGACAAAAAAG	1,00	0,14	Hs.84746	chromosome condensation 1
4444	CGAAGGCTGTA	1,00	0,14	Hs.79334	nuclear factor, interleukin 3 regulated
4445	ATTGTAAGTTT	1,00	0,14	Hs.74649	cytochrome c oxidase subunit VIc
4446	GCCACACTGTC	1,00	0,14	Hs.61763	ESTs
4447	CTTCAAGGCCG	1,00	0,14	Hs.59457	ESTs
4448	CCACACCTCTC	1,00	0,14	Hs.54673	tumor necrosis factor (ligand) super-family, member 1
4449	GACATCTCTTC	1,00	0,14	Hs.43619	ESTs
4450	CCTGGCCCTTA	1,00	0,14	Hs.42287	E2F transcription factor 6
4451	AAGGGCCACAA	1,00	0,14	Hs.37096	zinc finger protein 145 (Kruppel-like, expressed in
4452	TTTATTTTAAT	1,00	0,14	Hs.37040	platelet-derived growth factor alpha polypeptide
4453	GTTTCTCAAAT	1,00	0,14	Hs.32597	ring finger protein (C3H2C3 type) 6
4454	AAATTGCTTAG	1,00	0,14	Hs.30652	KIAA1344 protein
4455	GAAAAAGATGT	1,00	0,14	Hs.283737	AD-017 protein
4456	TTTCAAATAAA	1,00	0,14	Hs.272023	transforming, acidic coiled-coil containing protein
4457	TGGGGAATAGG	1,00	0,14	Hs.23964	sin3-associated polypeptide, 18kD
4458	GTGCAAGCTGT	1,00	0,14	Hs.232068	transcription factor 8 (represses interleukin 2 expr
4459	CCTGGGGTAAG	1,00	0,14	Hs.198253	major histocompatibility complex, class II, DQ alpha
4460	TGTGAGCCTCA	1,00	0,14	Hs.1973	cyclin F
4461	GAGTTGGCACT	1,00	0,14	Hs.194688	bromodomain adjacent to zinc finger domain, 1B
4462	GACTGGAACCTT	1,00	0,14	Hs.186756	KIAA1441 protein
4463	GCGGCAAGCAT	1,00	0,14	Hs.182729	hypothetical protein FLJ10581
4464	TGGATCACCAA	1,00	0,14	Hs.17872	ESTs
4465	GGAGGGGTTCA	1,00	0,14	Hs.173088	ESTs
4466	CCTTATGGAAA	1,00	0,14	Hs.17118	ESTs, Weakly similar to B0025.2 [C.elegans]
4467	GTGGCAGTGGC	1,00	0,14	Hs.16478	ESTs
4468	TGTCCGTCACA	1,00	0,14	Hs.154365	E74-like factor 1 (ets domain transcription factor)
4469	AAATGGCCAAC	1,00	0,14	Hs.12813	DKFZP434J214 protein
4470	TACTGTTTGAT	1,00	0,14	Hs.12313	ESTs
4471	CGTAAGACGTT	1,00	0,14	Hs.122607	B-cell CLL/lymphoma 9
4472	GGCTTTCAGCA	1,00	0,14	Hs.119663	CD59 antigen p18-20 (antigen identified by monoclonal

4473	TAACCCCAAAT	1,00	0,14	Hs.11493	ESTs
4474	GTCAAAATTTTC	1,00	0,14	Hs.108623	thrombospondin 2
4475	CTTTTGTCTG	1,00	0,14	Hs.106823	H.sapiens gene from PAC 42616, similar to syntaxin 7
4476	CTATTCTAAAA	1,00	0,14	Hs.100729	KIAA0692 protein
4477	GTGTCCTCCTC	4,00	0,41	Hs.78979	Golgi apparatus protein 1
4478	TTGGCTTTTCT	13,00	0,66	Hs.218329	hypothetical protein
4479	AAGGGGGCAAG	6,00	0,50	Hs.85266	integrin, beta 4
4480	GTGGCTCATAC	3,00	0,35	Hs.281094	ESTs
4481	GTAACAAGCTC	3,00	0,35	Hs.279849	KIAA0438 gene product
4482	GA CTCAGGGAT	3,00	0,35	Hs.13011	GTP binding protein 2
4483	AGGGACATAAA	3,00	0,35	Hs.101516	BAI1-associated protein 3
4484	CCTGTGTGTGT	5,00	0,46	Hs.5894	hypothetical protein FLJ10305
4485	GGCTGGTCACC	2,00	0,27	Hs.98978	ESTs, Highly similar to WWP2 [H.sapiens]
4486	GACATTTTTCC	2,00	0,27	Hs.8083	hypothetical protein FLJ10769
4487	GGGAGGAGGTT	2,00	0,27	Hs.24049	ESTs
4488	TTTTGTGCATT	2,00	0,27	Hs.238990	cyclin-dependent kinase inhibitor 1B (p27, Kip1)
4489	TGCAATAGGGA	2,00	0,27	Hs.235975	hypothetical protein DKFZp434D0412
4490	TGGTAGCAGTA	2,00	0,27	Hs.196437	hypothetical protein FLJ10788
4491	GGCTTGGGGAG	2,00	0,27	Hs.15953	hypothetical protein FLJ10120
4492	ACTCCAAAAAA	54,00	0,97	Hs.192810	Homo sapiens mRNA; cDNA DKFZp564H172 (from clone DKF
4493	TGGGGAGAGGA	16,00	0,71	Hs.75799	protease, serine, 8 (prostasin)
4494	TGCTTGACAAG	3,00	0,36	Hs.106127	RNA polymerase I 16 kDa subunit
4495	TAGGATGGGGG	8,00	0,56	Hs.76941	ATPase, Na <sup>+</sup> /K <sup>+</sup> transporting, beta 3 polypeptide
4496	TAGGTTGTCTA	114,00	1,14	Hs.279860	hypothetical protein FLJ20030
4497	TAAACTGAAAA	4,00	0,42	Hs.3491	ribosomal protein S14
4498	AAAACATTATG	2,00	0,27	Hs.80917	adaptor-related protein complex 3, sigma 1 subunit
4499	AATGTCCAGTA	2,00	0,27	Hs.26373	ESTs, Moderately similar to ALU1 HUMAN ALU SUBFAMILY
4500	GTGAAACTGCA	2,00	0,27	Hs.237055	EST
4501	GCACAGATTAC	2,00	0,27	Hs.158497	KIAA0724 gene product
4502	GCACCTGTCCG	2,00	0,27	Hs.1239	alanyl (membrane) aminopeptidase (aminopeptidase N,
4503	CTGGTGAGTGC	2,00	0,27	Hs.11902	MYLE protein
4504	ATGATGATGAT	9,00	0,59	Hs.79172	solute carrier family 25 (mitochondrial carrier; ade
4505	GGAGCGTGGGG	7,00	0,53	Hs.249982	cathepsin B
4506	CTCCCCCAAAA	5,00	0,46	Hs.283305	immunoglobulin heavy constant alpha 1
4507	AAAACCTGTAA	3,00	0,36	Hs.75914	coated vesicle membrane protein
4508	TGGCAGTCTGC	3,00	0,36	Hs.6179	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17 (72k
4509	TTGTGAGAATA	3,00	0,36	Hs.177425	KIAA0964 protein
4510	AAGGCGTTTCC	3,00	0,36	Hs.13255	KIAA0930 protein
4511	ATACTGTCACT	3,00	0,36	Hs.11441	chromosome 1 open reading frame 8
4512	CCTATTTACTG	23,00	0,79	Hs.113205	cytochrome c oxidase subunit IV

5	4513	GTACTGTAGCA	6,00	0,50	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of
	4514	TTCTTTCTCAC	1,00	0,14	Hs.9788	ESTs, Moderately similar to unnamed protein product
	4515	CTCAGAGAACA	1,00	0,14	Hs.9414	KIAA1488 protein
	4516	AAGCATCTCAG	1,00	0,14	Hs.84232	transcobalamin II; macrocytic anemia
10	4517	TAGATCTGTAT	1,00	0,14	Hs.83419	KIAA0252 protein
	4518	TACTTTATAAG	1,00	0,14	Hs.8230	a disintegrin-like and metalloprotease (repolysin t
	4519	CACAAATGCTG	1,00	0,14	Hs.80562	gelsolin (amyloidosis, Finnish type)
15	4520	CTGTGTCCAAG	1,00	0,14	Hs.79095	epidermal growth factor receptor pathway substrate 1
	4521	AAGAACTACAC	1,00	0,14	Hs.77546	KIAA0172 protein
	4522	GCAAGGAAAAA	1,00	0,14	Hs.77496	small nuclear ribonucleoprotein polypeptide G
20	4523	AAATGCAGTAG	1,00	0,14	Hs.75262	cathepsin O
	4524	GAAATTCAAAC	1,00	0,14	Hs.74649	cytochrome c oxidase subunit VIc
	4525	ATGCCTTTGAA	1,00	0,14	Hs.7298	biphenyl hydrolase-like (serine hydrolase; breast ep
25	4526	TTCCGTTCCCTT	1,00	0,14	Hs.52081	KIAA0867 protein
	4527	TCGGTGTCTGG	1,00	0,14	Hs.4953	golgi autoantigen, golgin subfamily a, 3
	4528	GTGGCTCAATT	1,00	0,14	Hs.4864	KIAA0892 protein
	4529	GGTTGGTGGTC	1,00	0,14	Hs.35276	KIAA0852 protein
30	4530	GGAGGTGCTCA	1,00	0,14	Hs.31895	ESTs, Weakly similar to B9 [H.sapiens]
	4531	GGCCTGGGGGT	1,00	0,14	Hs.267659	vav 3 oncogene
	4532	TTTGTTGTATG	1,00	0,14	Hs.26267	ESTs
	4533	GCATCTTCAAA	1,00	0,14	Hs.241510	interferon-induced protein 41, 30kD
35	4534	GAGAAGCCCCG	1,00	0,14	Hs.209099	ESTs, Weakly similar to ALU6_HUMAN ALU SUBFAMILY SP
	4535	ACAGGCAGAAA	1,00	0,14	Hs.200526	TNF receptor-associated factor 2
40	4536	GCGTTCAATAA	1,00	0,14	Hs.19720	Homo sapiens mRNA full length insert cDNA clone EURO
	4537	AAGCACTTCTG	1,00	0,14	Hs.189658	CGI-149 protein
	4538	CAGTCCCGGCT	1,00	0,14	Hs.189658	CGI-149 protein
45	4539	TATATACATTT	1,00	0,14	Hs.184211	peptidase (mitochondrial processing) beta
	4540	TGACTGTCACG	1,00	0,14	Hs.177776	Homo sapiens clone 23914 mRNA sequence
50	4541	GGCAGATTGCT	1,00	0,14	Hs.173259	uncharacterized bone marrow protein BM033
	4542	TTCTCGAGATG	1,00	0,14	Hs.161554	hypothetical protein FLJ20159
	4543	GGACCATTGAA	1,00	0,14	Hs.155244	pre-mRNA splicing factor similar to S. cerevisiae Pr
55	4544	CCTTTCTGTAA	1,00	0,14	Hs.143648	insulin receptor substrate 2
	4545	TGGAAATCAAG	1,00	0,14	Hs.13405	gephyrin
	4546	AAGCCAGTCTG	1,00	0,14	Hs.112378	LIM and senescent cell antigen-like domains 1
60	4547	ACTTTTCAAAA	1,00	0,14	Hs.108196	HSPC037 protein
	4548	TATGTATTTCT	1,00	0,14	Hs.102267	lysyl oxidase
	4549	GTGCTATTCTG	4,00	0,42	Hs.77873	Homo sapiens mRNA full length insert

					cDNA clone EURO	
4550	TCTGTCCTCAG	4,00	0,42	Hs.75216	protein tyrosine phosphatase, receptor type, F	
4551	GGGTGTGGTGG	4,00	0,42	Hs.25894	Homo sapiens mRNA; cDNA DKFZp564N123 (from clone DKF	5
4552	GCCCCCAATAA	66,00	1,03	Hs.227751	lectin, galactoside-binding, soluble, 1 (galectin 1)	
4553	AAATATGAGCT	3,00	0,36	Hs.181368	U5 snRNP-specific protein (220 kD), ortholog of S. c	10
4554	GAGTCAGGAGA	9,00	0,59	Hs.181271	CGI-120 protein	
4555	GGGGCCCCCTC	4,00	0,42	Hs.18528	Sjogren's syndrome nuclear autoantigen 1	15
4556	CTCACTTCTTA	4,00	0,42	Hs.165998	DKFZP564M2423 protein	
4557	CTCTGCCCTCC	4,00	0,42	Hs.115412	ESTs, Weakly similar to dJ68O2.2 [H.sapiens]	
4558	CTGTGTCTGTT	2,00	0,27	Hs.7833	selenium binding protein 1	20
4559	GACTATAGCGC	2,00	0,27	Hs.7036	N-Acetylglucosamine kinase	
4560	TTTTGTGTATT	2,00	0,27	Hs.42644	thioredoxin-like	
4561	AAGGAAGATTG	2,00	0,27	Hs.252692	hypothetical protein FLJ20343	
4562	TGCTCAGTGGT	2,00	0,27	Hs.194625	dynein, cytoplasmic, light intermediate polypeptide	25
4563	GCATTTAATA	28,00	0,84	Hs.275959	eukaryotic translation elongation factor 1 beta 2	
4564	CTGACCTGTGT	28,00	0,84	Hs.77961	major histocompatibility complex, class I, B	30
4565	AAACATTAGCC	3,00	0,36	Hs.82911	protein tyrosine phosphatase type IVA, member 2	
4566	CTTTGTTTAAT	1,00	0,14	Hs.95262	Homo sapiens mRNA; cDNA DKFZp434L235 (from clone DKF	35
4567	GAGAGGAGAGG	1,00	0,14	Hs.92002	guanine nucleotide binding protein (G protein), alpha	
4568	GAGAACTCCCC	1,00	0,14	Hs.82001	polycystic kidney disease 2 (autosomal dominant) -NO	40
4569	TAGTTGCAAT	1,00	0,14	Hs.77311	BTG family, member 3	
4570	GATGCTAACCA	1,00	0,14	Hs.76591	KIAA0887 protein	
4571	TACCTTTATTG	1,00	0,14	Hs.75761	SFRS protein kinase 1	45
4572	ATCACAGGTGA	1,00	0,14	Hs.7252	KIAA1224 protein	
4573	AACAAGTCTTT	1,00	0,14	Hs.69851	GAR1 protein	
4574	TGGGGGTTTCC	1,00	0,14	Hs.62954	ferritin, heavy polypeptide 1	
4575	GCCAAGACACA	1,00	0,14	Hs.5947	mel transforming oncogene (derived from cell line NK	50
4576	GAGACTGCAAT	1,00	0,14	Hs.5944	solute carrier family 11 (proton-coupled divalent me	
4577	TAAACAGGTGG	1,00	0,14	Hs.5473	ESTs, Moderately similar to ALU5_HUMAN ALU SUBFAMILY	55
4578	TCTGATCAGGA	1,00	0,14	Hs.50441	CGI-04 protein	
4579	AAGAGACATAG	1,00	0,14	Hs.46847	TRAF and TNF receptor-associated protein	60
4580	AAGAAGCGCAA	1,00	0,14	Hs.46784	potassium large conductance calcium-activated channe	
4581	GCACCCAACAC	1,00	0,14	Hs.4082	lectin, galactoside-binding, soluble, 8	65

					(galectin 8)
4582	AGGGACTTGTG	1,00	0,14	Hs.29331	carnitine palmitoyltransferase I, muscle
4583	TTTGCAAAAAA	1,00	0,14	Hs.286083	ESTs
4584	TGTGTGTGTAA	1,00	0,14	Hs.272328	KRAB-zinc finger protein synten
4585	TTTGAGTTCTT	1,00	0,14	Hs.24789	ESTs
4586	AACTCTAAGGA	1,00	0,14	Hs.238797	ESTs
4587	TGGTACTTCTC	1,00	0,14	Hs.22353	ESTs, Weakly similar to AF151847_1 CGI-89 protein [H]
4588	GGGTGAGGGGG	1,00	0,14	Hs.21840	Homo sapiens clone 24852 mRNA sequence
4589	GCTATTTCTTA	1,00	0,14	Hs.199009	Homo sapiens PCCX2 mRNA for protein containing CXXC
4590	GAGACGCATTT	1,00	0,14	Hs.184585	LIM domain only 2 (rhombotin-like 1)
4591	CTTGGTGCTGC	1,00	0,14	Hs.180842	ribosomal protein L13
4592	ACCCGGTACAG	1,00	0,14	Hs.173381	dihydropyrimidinase-like 2
4593	TATCCTCTGGC	1,00	0,14	Hs.154085	Homo sapiens cDNA FLJ20290 fis, clone HEP04540
4594	AAACACCAAAT	1,00	0,14	Hs.146388	microtubule-associated protein 7
4595	CCCAGCCACTT	1,00	0,14	Hs.126701	ribosomal protein S19
4596	GCAGTGCATCT	1,00	0,14	Hs.123373	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
4597	GAAGGTTGTGG	1,00	0,14	Hs.12017	KIAA0439 protein; homolog of yeast ubiquitin-protein
4598	AAAGGCAGGAA	1,00	0,14	Hs.118152	ESTs
4599	TATCAGTGCCT	1,00	0,14	Hs.117582	CGI-43 protein
4600	GCAAATGTACA	1,00	0,14	Hs.11238	KIAA0622 protein; Drosophila "multiple asters" (Mast
4601	CTTAGTCTAAA	1,00	0,14	Hs.108327	damage-specific DNA binding protein 1 (127kD)
4602	ATGAAATAGTA	1,00	0,14	Hs.107056	CED-6 protein
4603	GCTTGACATTG	1,00	0,14	Hs.103352	ESTs
4604	GTTCCCTGGCC	42,00	0,94	Hs.177415	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV)
4605	CTGCAACCTAA	3,00	0,36	Hs.50785	SEC22, vesicle trafficking protein (S. cerevisiae)-I
4606	TGTGGTGGTGT	5,00	0,46	Hs.83422	MLN51 protein
4607	GACAAAAGTC	2,00	0,27	Hs.9683	protein-kinase, interferon-inducible double stranded
4608	ATCTATGACCC	2,00	0,27	Hs.8179	hypothetical protein, clone 2746033
4609	TAACCGCAGAT	2,00	0,27	Hs.74376	olfactomedin related ER localized protein
4610	CCTGCCGTCGG	2,00	0,27	Hs.130541	KIAA1542 protein
4611	ACCTCCCACCC	2,00	0,27	Hs.118666	Human clone 23759 mRNA, partial cds
4612	GGGCCAATAAA	8,00	0,57	Hs.78605	DKFZP566I1024 protein
4613	AAAAAACCCAA	8,00	0,57	Hs.111680	endosulfine alpha
4614	TTCAATAAAAA	93,00	1,16	Hs.177592	ribosomal protein, large, P1
4615	TTCACTGCCGA	5,00	0,47	Hs.78089	ATPase, vacuolar, 14 kD
4616	GCTTTTCAGAC	4,00	0,42	Hs.78781	vascular endothelial growth factor B
4617	TAGTTGTAGGG	4,00	0,42	Hs.5324	hypothetical protein
4618	TTTGGTGTTTG	4,00	0,42	Hs.11050	F-box only protein 9
4619	TATCTTGCTTA	3,00	0,36	Hs.96334	ring finger protein 11



4620	TATCTGGTCTT	3,00	0,36	Hs.142258	signal transducer and activator of transcription 3 (	
4621	GGCTGGGCCTG	9,00	0,59	Hs.239782	H.sapiens clathrin light chain b gene	
4622	TGTCTGTGGTA	5,00	0,47	Hs.55296	HLA-B associated transcript-1	5
4623	AGGGCTTCCAA	104,00	1,21	Hs.29797	ribosomal protein L10	
4624	TATAGGCCGAA	2,00	0,28	Hs.92384	vitamin A responsive; cytoskeleton related	
4625	ACTGTTCTCTT	2,00	0,28	Hs.81360	Human clone 23722 mRNA sequence	10
4626	TCCTTTGTGCC	2,00	0,28	Hs.50252	Homo sapiens HSPC283 mRNA, partial cds	
4627	TTTATTGAATT	2,00	0,28	Hs.43910	CD164 antigen, sialomucin	
4628	TATATGGATGT	2,00	0,28	Hs.42758	ESTs	15
4629	TCTAGTCACTG	2,00	0,28	Hs.36565	ESTs	
4630	CAGCTCTTAGG	2,00	0,28	Hs.22208	Homo sapiens mRNA full length insert cDNA clone EURO	
4631	GGACCTTGGAG	3,00	0,36	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	20
4632	TATATTGATTG	3,00	0,36	Hs.77054	B-cell translocation gene 1, anti-proliferative	
4633	ATTACAAACCT	3,00	0,36	Hs.30376	hypothetical protein	
4634	CAGTGGGGTTA	3,00	0,36	Hs.17138	hypothetical protein FLJ20303	25
4635	CTCCTCACCTG	47,00	1,00	Hs.242908	lecithin-cholesterol acyltransferase	
4636	TACATTGCTTT	4,00	0,42	Hs.75104	RNA-binding protein S1, serine-rich domain	
4637	CTGGCTGCAAA	14,00	0,70	Hs.1342	cytochrome c oxidase subunit Vb	30
4638	GGTGGGGAGAT	7,00	0,54	Hs.157236	membrane protein of cholinergic synaptic vesicles	
4639	AAGCCTTGCTG	6,00	0,51	Hs.6289	growth factor receptor-bound protein 2	
4640	TTAGGGAGGAG	1,00	0,14	Hs.99995	intercellular adhesion molecule 3	35
4641	GAAAAGCTCCT	1,00	0,14	Hs.99843	DKFZP586N0721 protein	
4642	GAAGTCTCTGC	1,00	0,14	Hs.979	pyruvate dehydrogenase (lipoamide) beta	
4643	GATCTGAGGAG	1,00	0,14	Hs.96984	Homo sapiens cDNA FLJ20335 fis, clone HEP11429	40
4644	ATGAAAAGTGC	1,00	0,14	Hs.78743	zinc finger protein 131 (clone pHZ-10)	
4645	ATATGAAGCAT	1,00	0,14	Hs.7862	hypothetical protein FLJ20312	
4646	GGAGGGACCCC	1,00	0,14	Hs.78473	N-deacetylase/N-sulfotransferase (heparan glucosamin	45
4647	GGAGACTTCCT	1,00	0,14	Hs.77840	annexin A4	
4648	GCTCTGCCCTC	1,00	0,14	Hs.68257	general transcription factor IIF, polypeptide 1 (74k	50
4649	AGGTGTCTTTG	1,00	0,14	Hs.62264	KIAA0937 protein	
4650	AACAAATCCTT	1,00	0,14	Hs.5169	suppressor of G2 allele of SKP1, S. cerevisiae, homo	
4651	CAGGCGTGCAC	1,00	0,14	Hs.33818	RecQ protein-like 5	55
4652	TATAAATTTAA	1,00	0,14	Hs.30212	thyroid receptor interacting protein 15	
4653	ACACACAAAAA	1,00	0,14	Hs.279949	KIAA1007 protein	
4654	AAGCAAGAATG	1,00	0,14	Hs.24684	KIAA1376 protein	
4655	ACTTAAGGTTG	1,00	0,14	Hs.236494	RAB10, member RAS oncogene family	60
4656	GTGTCCTTGTC	1,00	0,14	Hs.226138	Homo sapiens mRNA; cDNA DKFZp566H2446 (from clon DK	

4657	CTCTCCTGCTC	1,00	0,14	Hs.21807	PR domain containing 4
4658	GCCAAGTGAAC	1,00	0,14	Hs.20225	tufelin-interacting protein
4659	AGGCCCCAGGG	1,00	0,14	Hs.187660	putative Rab5 GDP/GTP exchange factor homologue
4660	TAACAAGTTTC	1,00	0,14	Hs.179902	Homo sapiens CTL1 gene
4661	GTAGTCCAAAC	1,00	0,14	Hs.178617	ESTs, Weakly similar to AF151840_1 CGI-82 protein [H]
4662	GTGATGTCTGT	1,00	0,14	Hs.164026	ESTs
4663	GTCTACAATTG	1,00	0,14	Hs.161554	hypothetical protein FLJ20159
4664	ATAATTGACTA	1,00	0,14	Hs.15591	COP9 subunit 6 (MOV34 homolog, 34 kD)
4665	TTGGTGAAGGA	70,00	1,12	Hs.75968	thymosin, beta 4, X chromosome
4666	GCTTGTTAAGA	3,00	0,36	Hs.4113	S-adenosylhomocysteine hydrolase-like 1
4667	ATTGTGCTTGC	3,00	0,36	Hs.251531	proteasome (prosome, macropain) subunit, alpha type,
4668	AGGAAAAAAAA	3,00	0,36	Hs.180639	EST
4669	GCTGGGAGGGG	4,00	0,42	Hs.20733	ESTs
4670	AGTGTGCGCTT	2,00	0,28	Hs.83086	Homo sapiens GT212 mRNA
4671	AACTTGGCTGT	2,00	0,28	Hs.79107	mitogen-activated protein kinase 14
4672	GGGGACTGGTG	2,00	0,28	Hs.155342	protein kinase C, delta
4673	CCAGCTGCCAA	10,00	0,63	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T and BN75 tempe
4674	AATAGGTCCAA	57,00	1,08	Hs.113029	ribosomal protein S25
4675	TTGGCATTGTC	3,00	0,36	Hs.250911	Homo sapiens clone 23967 unknown mRNA, partial cds
4676	CCCCAGTTGCT	36,00	0,95	Hs.74451	calpain 4, small subunit (30K)
4677	GCATAATAGGT	90,00	1,26	Hs.184108	ribosomal protein L21 (gene or pseudogene)
4678	CTCTGATGCAG	2,00	0,28	Hs.80961	polymerase (DNA directed), gamma
4679	GTCATTATGCT	2,00	0,28	Hs.78305	RAB2, member RAS oncogene family
4680	TAAACTGTAA	2,00	0,28	Hs.3491	ribosomal protein S14
4681	CTAGCCAGCAG	2,00	0,28	Hs.24983	hypothetical protein from EUROIMAGE 2021883
4682	GCTAAACTCTG	2,00	0,28	Hs.207409	ESTs
4683	AGACGCTTCTG	2,00	0,28	Hs.203772	FSHD region gene 1
4684	GATCTGTTTCT	2,00	0,28	Hs.169743	Homo sapiens clone 25121 neuronal olfactomedin relat
4685	CTGGCCTGTGT	2,00	0,28	Hs.155191	villin 2 (ezrin)
4686	GCTGTTTAAAA	2,00	0,28	Hs.154320	ubiquitin-activating enzyme E1C (homologous to yeast
4687	CCCTGTAATAA	5,00	0,47	Hs.8518	selenoprotein N
4688	TCTGGGGACGA	5,00	0,47	Hs.74111	RNA-binding protein (autoantigenic)
4689	ATTCTTGCCG	5,00	0,47	Hs.25682	Homo sapiens HSPC262 mRNA, partial cds
4690	ATTAAATTCAG	3,00	0,36	Hs.218329	hypothetical protein
4691	CCTTTCAAGCA	3,00	0,36	Hs.198899	eukaryotic translation initiation factor 3, subunit
4692	TAATCCCAGCA	4,00	0,42	Hs.236710	EST
4693	TCTTCCCCAGT	4,00	0,42	Hs.14231	selenoprotein W, 1

4694	TGCCTGCACCA	41,00	1,00	Hs.135084	cystatin C (amyloid angiopathy and cerebral hemorrhage)
4695	CCGTGGTCGTG	10,00	0,63	Hs.99853	fibrillarin
4696	GGGAAACCCTG	5,00	0,47	Hs.161137	ESTs, Weakly similar to ALU2_HUMAN ALU SUBFAMILY SB
4697	GCTTCTGCATA	1,00	0,14	Hs.8886	hypothetical protein FLJ20424
4698	GTTGCATTTTC	1,00	0,14	Hs.81001	F-box only protein 25
4699	GTGATACGTTG	1,00	0,14	Hs.80306	Homo sapiens mRNA, clone:RES4-4
4700	CAGTTTGAAAT	1,00	0,14	Hs.77256	enhancer of zeste (Drosophila) homolog 2
4701	CAGTGATTCCA	1,00	0,14	Hs.75056	adaptor-related protein complex 3, delta 1 subunit
4702	CATATTTGTGA	1,00	0,14	Hs.6489	dynactin p62 subunit
4703	TACATTTGCAA	1,00	0,14	Hs.6349	Human Chromosome 16 BAC clone CIT987SK-A-362G6
4704	TAATTGCAGAT	1,00	0,14	Hs.4854	cyclin-dependent kinase inhibitor 2C (p18, inhibits
4705	CCATCCGCAGG	1,00	0,14	Hs.4437	ribosomal protein L28
4706	CAATGGAGCTT	1,00	0,14	Hs.30925	hypothetical protein FLJ10199
4707	TTGTACCACCT	1,00	0,14	Hs.29024	ESTs
4708	GCCTCCAGATT	1,00	0,14	Hs.278355	ESTs
4709	TAAAATAAAAG	1,00	0,14	Hs.271277	hypothetical protein from EUROIMAGE 363668
4710	GTATGGACTAT	1,00	0,14	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain 3
4711	AACCTGTTCTA	1,00	0,14	Hs.26761	DKFZP586L0724 protein
4712	TGTGGCCCACC	1,00	0,14	Hs.250870	mitogen-activated protein kinase kinase 5
4713	TTTGTGGTCAA	1,00	0,14	Hs.244099	EST, Weakly similar to EF2_HUMAN ELONGATION FACTOR 2
4714	ACATTTTTTAAC	1,00	0,14	Hs.177516	high density lipoprotein binding protein (vigilin)
4715	TGCCCCGCACT	1,00	0,14	Hs.169119	ESTs
4716	CCTGGGGGCCG	1,00	0,14	Hs.168157	nuclear transcription factor Y, gamma
4717	GATTTAAATCA	1,00	0,14	Hs.168005	transcriptional intermediary factor 1 gamma
4718	AGCCCTGGCTG	1,00	0,14	Hs.15896	pericentrin
4719	GGCGCACTCTG	1,00	0,14	Hs.151903	Homo sapiens clone 24706 mRNA sequence
4720	CAGGAGAACTG	1,00	0,14	Hs.150614	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAMILY SB2
4721	AAAACCTTTTGT	1,00	0,14	Hs.126219	hypothetical protein FLJ20081
4722	AACTCTCAATG	1,00	0,14	Hs.12150	retinal short-chain dehydrogenase/reductase retSDR2
4723	AGGAAACTGGG	1,00	0,14	Hs.11955	B9 protein
4724	TTTTGCAACAA	1,00	0,14	Hs.118739	ESTs, Weakly similar to JC2473 doc2 protein - human
4725	GGAAAATTGGT	1,00	0,14	Hs.115740	KIAA0210 gene product
4726	GAAGTGTGAGT	1,00	0,14	Hs.110044	ESTs
4727	TACACCAGCAA	1,00	0,14	Hs.105887	ESTs, Weakly similar to Homolog of rat Zymogen granu

4728	TGCAGCACGAG	18,00	0,78	Hs.110309	major histocompatibility complex, class I, F
4729	CTGGATGGGCA	6,00	0,52	Hs.44017	SIR2 (silent mating type information regulation 2, S
4730	CAGGGAGCGCC	3,00	0,36	Hs.8657	TPA inducible gene-1
4731	CGTGTGCCTGT	3,00	0,36	Hs.74649	cytochrome c oxidase subunit VIc
4732	TTCTCTCCACA	2,00	0,28	Hs.94446	polyamine-modulated factor 1
4733	CCCCATACTAC	2,00	0,28	Hs.57652	EGF-like-domain, multiple 2
4734	TTGTAATAAAA	2,00	0,28	Hs.283429	SMC (mouse) homolog, X chromosome
4735	TTTACAAATAA	2,00	0,28	Hs.23480	KIAA0493 protein
4736	TTAACCCTCTA	8,00	0,58	Hs.180877	H3 histone, family 3B (H3.3B)
4737	AAGGTAGCAGA	8,00	0,58	Hs.104125	adenylyl cyclase-associated protein
4738	GACCTCCTGCC	3,00	0,36	Hs.89449	mitogen-activated protein kinase kinase kinase 11
4739	TTACCATATCA	39,00	1,02	Hs.177461	ribosomal protein L39
4740	AAATACAGCAG	4,00	0,43	Hs.182429	protein disulfide isomerase-related protein
4741	CCCGTCCGGAA	145,00	1,66	Hs.180842	ribosomal protein L13
4742	TTGAGCCAGCC	11,00	0,66	Hs.91142	KH-type splicing regulatory protein (FUSE binding pr
4743	CCTGAGGTCAG	2,00	0,28	Hs.95196	ESTs, Weakly similar to T20B12.3 [C.elegans]
4744	TAACATTGGTG	2,00	0,28	Hs.79306	eukaryotic translation initiation factor 4E
4745	GTAGAAAAAAA	2,00	0,28	Hs.78890	numb (Drosophila) homolog
4746	GGGCTCTGAGC	2,00	0,28	Hs.6770	LCAT-like lysophospholipase
4747	CTTTTCATCAT	2,00	0,28	Hs.3726	x 003 protein
4748	TCACTGATCTT	2,00	0,28	Hs.3491	ribosomal protein S14
4749	GCTGGAATAAA	2,00	0,28	Hs.27728	hypothetical protein FLJ20211
4750	TTGGCCGGGCT	2,00	0,28	Hs.248488	EST
4751	AAAGTCTAGAA	15,00	0,75	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatosis 1)
4752	GAGCTTTTGAA	3,00	0,37	Hs.180638	Homo sapiens cDNA FLJ11066 fis, clone PLACE1004885
4753	TCCTAGCCTGT	4,00	0,43	Hs.74711	splicing factor similar to dnaJ
4754	CCTGAAATTTG	5,00	0,48	Hs.77492	heterogeneous nuclear ribonucleoprotein A0
4755	TTAATCCTAAA	5,00	0,48	Hs.150741	2',3'-cyclic nucleotide 3' phosphodiesterase
4756	ATAATTCTTTG	93,00	1,44	Hs.539	ribosomal protein S29
4757	ACATTTCAATTT	1,00	0,14	Hs.8966	integral membrane protein 1
4758	TCCAGGGCCGC	1,00	0,14	Hs.84128	ESTs, Weakly similar to S57447 HPBRII-7 protein - hu
4759	GAACCACAGGA	1,00	0,14	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylglucosyltransf
4760	AATATTTAGTG	1,00	0,14	Hs.75133	transcription factor 6-like 1 (mitochondrial transcr
4761	ACTTTTTGGCT	1,00	0,14	Hs.6968	KIAA1460 protein
4762	GAAGCAAAAAA	1,00	0,14	Hs.6278	DKFZP586B1621 protein
4763	GCCGCTGCCAG	1,00	0,14	Hs.6162	KIAA0771 protein
4764	CTCAGAACACT	1,00	0,14	Hs.5309	ESTs

4765	ATGGTCTCCTG	1,00	0,14	Hs.36565	ESTs
4766	TTTGTITTTAT	1,00	0,14	Hs.3622	procollagen-proline, 2-oxoglutarate 4-dioxygenase (p
4767	AGTACCTTATA	1,00	0,14	Hs.279898	PRO0529 protein
4768	CCTGAAAAAAA	1,00	0,14	Hs.279380	PRO1578 protein
4769	AATGCCCCACT	1,00	0,14	Hs.273230	hypothetical protein FLJ10830
4770	TCAGACTAGTT	1,00	0,14	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain 3
4771	TCTGGCAAAGA	1,00	0,14	Hs.267831	Rho GTPase activating protein 5
4772	AGGCGAGCTGC	1,00	0,14	Hs.241576	hypothetical protein PRO2577
4773	GTTTCATTTTGA	1,00	0,14	Hs.234149	hypothetical protein FLJ20647
4774	TTAAAGAGCCG	1,00	0,14	Hs.226133	growth arrest-specific 7
4775	GAATTTCCAG	1,00	0,14	Hs.2253	complement component 2
4776	AAAAATAAAGA	1,00	0,14	Hs.19414	ESTs, Weakly similar to INI7_HUMAN INTERFERON-ALPHA
4777	GCAACTTTTTG	1,00	0,14	Hs.183994	protein phosphatase 1, catalytic subunit, alpha isof
4778	AGCGGCTACAC	1,00	0,14	Hs.183487	interferon stimulated gene (20kD)
4779	TGCAACTACAA	1,00	0,14	Hs.182278	calmodulin 2 (phosphorylase kinase, delta)
4780	GGCCTGGAATT	1,00	0,14	Hs.171566	hypothetical protein
4781	TATTCCTGTGA	1,00	0,14	Hs.168075	karyopherin (importin) beta 2
4782	ATGCCCAATGT	1,00	0,14	Hs.155396	nuclear factor (erythroid-derived 2)-like 2
4783	GAAATAAAAAG	1,00	0,14	Hs.154156	myosin, light polypeptide 4, alkali; atrial, embryo
4784	GCCTTTCTAAT	1,00	0,14	Hs.149957	ribosomal protein S6 kinase, 90kD, polypeptide 1
4785	CATTTTACTGG	1,00	0,14	Hs.147189	HYA22 protein
4786	GCCAGATTGAG	1,00	0,14	Hs.146324	CGI-145 protein
4787	TTTTATTAAAG	1,00	0,14	Hs.108504	hypothetical protein FLJ20113
4788	AAGTGGAATAA	1,00	0,14	Hs.105850	KIAA0404 protein
4789	GATCTCACTGT	1,00	0,14	Hs.105235	KIAA0477 gene product
4790	GAGACTCCTGC	10,00	0,65	Hs.169902	solute carrier family 2 (facilitated glucose transpo
4791	TGCACTTCAAG	13,00	0,71	Hs.75445	SPARC-like 1 (mast9, hevin)
4792	AAAGAAAGTGG	5,00	0,48	Hs.151513	mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetyl
4793	TCCATCTGTTG	4,00	0,43	Hs.252189	syndecan 4 (amphiglycan, ryudocan)
4794	ATCCACCCGCC	3,00	0,37	Hs.251337	ESTs
4795	CTGCTTCCTGA	2,00	0,28	Hs.78921	A kinase (PRKA) anchor protein 1
4796	TGCTTATTGAA	2,00	0,28	Hs.5822	lectin, mannose-binding, 1
4797	ACTCACGATTG	2,00	0,28	Hs.4814	mannosidase, alpha, class 1B, member 1
4798	GGATGTGGAGG	2,00	0,28	Hs.31305	transducin-like enhancer of split 3, homolog of Dros
4799	AATTCCCGTCC	2,00	0,28	Hs.18349	HSPC145 protein
4800	AGCACATTTGA	8,00	0,59	Hs.80562	gelsolin (amyloidosis, Finnish type)
4801	CACTACACGGG	6,00	0,53	Hs.227729	FK506-binding protein 2 (13kD)
4802	GTTCAAAGACT	3,00	0,37	Hs.75260	mitogen inducible 2
4803	CTCAAGCACCA	3,00	0,37	Hs.279652	CGI-28 protein

4804	ACCACTTATCC	3,00	0,37	Hs.249982	cathepsin B
4805	GACATAAATCC	5,00	0,48	Hs.109281	Nef-associated factor 1
4806	GGTTCCTGGTG	2,00	0,28	Hs.3074	ESTs, Weakly similar to KIAA0386 [H.sapiens]
4807	ATTTCTGCTGG	2,00	0,28	Hs.279607	calpastatin
4808	GCTCTGTAAGC	2,00	0,28	Hs.268149	putative methyltransferase
4809	GTGAGACCCCC	2,00	0,28	Hs.235989	EST
4810	CTGTTAATAAA	2,00	0,28	Hs.19500	nuclear localization signal deleted in velocardiofac
4811	GTTGAGTAACA	2,00	0,28	Hs.184776	ribosomal protein L23a
4812	CAACTTTAGGG	2,00	0,28	Hs.170311	heterogeneous nuclear ribonucleoprotein D-like
4813	GCTACTATTAG	2,00	0,28	Hs.154443	minichromosome maintenance deficient (S. cerevisiae)
4814	ATGTGAAGAAT	2,00	0,28	Hs.13662	Homo sapiens clone 25036 mRNA sequence
4815	ACCTGCCCCCTC	2,00	0,28	Hs.125262	DKFZP586G1624 protein
4816	CCTGTCCTGCA	7,00	0,57	Hs.11417	Rab acceptor 1 (prenylated)
4817	CCTTTGTAAGT	5,00	0,49	Hs.78465	v-jun avian sarcoma virus 17 oncogene homolog
4818	AAGGACCTTTT	12,00	0,71	Hs.109051	glycoprotein, synaptic 2
4819	ATCGGGCCCCGG	10,00	0,66	Hs.274411	SCAN domain-containing 1
4820	AAAAATAAAGC	3,00	0,37	Hs.85100	WD repeat domain 1
4821	ACTGATCTGCA	3,00	0,37	Hs.264190	vacuolar protein sorting 35 (yeast homolog)
4822	TCTCTGCAAAA	3,00	0,37	Hs.25489	hypothetical protein FLJ20640
4823	AGCCTGGACTG	7,00	0,57	Hs.90107	cell membrane glycoprotein, 110000M(r) (surface anti
4824	CCCCGCCAAGT	8,00	0,60	Hs.169718	calponin 2
4825	TCAAAAAA	11,00	0,69	Hs.200188	deleted in lung and esophageal cancer 1
4826	TTATAACTGAA	7,00	0,57	Hs.79933	cyclin I
4827	TGCTGCCTCAG	2,00	0,28	Hs.30792	hook2 protein
4828	CTAGTCACTTC	2,00	0,28	Hs.18057	granulin
4829	AATGAGCAACT	2,00	0,28	Hs.17185	guanylate binding protein 2, interferon-inducible
4830	CAATTCCTTCA	2,00	0,28	Hs.170098	KIAA0372 gene product
4831	AGCTGGGATGG	2,00	0,28	Hs.15898	peroxisomal 2,4-dienoyl-CoA reductase
4832	CCACGTGGCTG	2,00	0,28	Hs.148932	semaphorin Rs, short form
4833	GCACCTTCTGG	2,00	0,28	Hs.132744	hypothetical protein
4834	CCCTGTTTTT	1,00	0,15	Hs.92030	ESTs
4835	TTTTTCTTCA	1,00	0,15	Hs.8262	lysosomal-associated membrane protein 2
4836	TTCTAGACCAT	1,00	0,15	Hs.78946	cullin 3
4837	GAGATGAAATG	1,00	0,15	Hs.75939	uridine monophosphate kinase
4838	GTCTGTGTATG	1,00	0,15	Hs.7481	ESTs, Weakly similar to similar to mitochondrial RNA
4839	CCAAGAGGAAA	1,00	0,15	Hs.74649	cytochrome c oxidase subunit VIc
4840	AATCAAGGTGT	1,00	0,15	Hs.73287	KIAA1235 protein
4841	CCCTGAGGCCA	1,00	0,15	Hs.6607	Homo sapiens mRNA; cDNA DKFZp566F164 (from clone DKF

4842	TCTGAAGACTT	1,00	0,15	Hs.5548	f-box and leucine-rich repeat protein 5	5
4843	TTGGATATGTG	1,00	0,15	Hs.554	Sjogren syndrome antigen A2 (60kD, ribonucleoprotein)	
4844	CATTGTCTTCA	1,00	0,15	Hs.5054	CGI-133 protein	
4845	TGTGAAGATTA	1,00	0,15	Hs.44829	ESTs	
4846	AAGTGAAGAGC	1,00	0,15	Hs.31945	hypothetical protein FLJ11071	
4847	TCGTCCTAGAA	1,00	0,15	Hs.286217	KIAA0685 gene product	10
4848	ACTGATAACAG	1,00	0,15	Hs.27182	phospholipase A2-activating protein	
4849	ATTTTGGATTG	1,00	0,15	Hs.26812	ESTs	
4850	CAGTGCCCAAC	1,00	0,15	Hs.26409	ESTs	
4851	CATTGGTAGAA	1,00	0,15	Hs.250911	Homo sapiens clone 23967 unknown mRNA, partial cds	15
4852	TGAAAATCAAA	1,00	0,15	Hs.239489	TIA1 cytotoxic granule-associated RNA-binding protei	
4853	AGGCTGCGGTG	1,00	0,15	Hs.209646	KIAA1118 protein	
4854	TAACTCCATTG	1,00	0,15	Hs.19822	SEC24 (S. cerevisiae) related gene family, member D	20
4855	CCGCCCTTCGG	1,00	0,15	Hs.180677	zinc finger protein 162	
4856	ACTTAACATTT	1,00	0,15	Hs.180532	heat shock 90kD protein 1, alpha	25
4857	AGGCTTCTAGC	1,00	0,15	Hs.17757	Homo sapiens mRNA; cDNA DKFZp434E1515 (from clone DK	
4858	GTGACTGCCAG	1,00	0,15	Hs.177536	metallocarboxypeptidase CPX-1	
4859	ATTAGTCAGAA	1,00	0,15	Hs.1735	inhibin, beta B (activin AB beta polypeptide)	30
4860	TTAACACTGTG	1,00	0,15	Hs.172069	DKFZP434C212 protein	
4861	AATTACCAAAG	1,00	0,15	Hs.170218	KIAA0251 protein	
4862	GTATCTTAATA	1,00	0,15	Hs.155489	NS1-associated protein 1	35
4863	TGTTCTCAAGT	1,00	0,15	Hs.154396	ESTs	
4864	CCTAAGGGAGA	1,00	0,15	Hs.153022	TATA box binding protein (TBP)-associated factor, RN	
4865	TCTCCACGAAG	1,00	0,15	Hs.149570	actin related protein 2/3 complex, subunit 4 (20 kD)	40
4866	GTTTGGATCTG	1,00	0,15	Hs.118836	myoglobin	
4867	TAAGATTAGAA	1,00	0,15	Hs.118631	timeless (Drosophila) homolog	
4868	TATTTGCTACA	1,00	0,15	Hs.102548	glucocorticoid receptor DNA binding factor 1	45
4869	GTGGATGGACT	3,00	0,37	Hs.6418	seven transmembrane domain orphan receptor	
4870	GGAATAAACC	3,00	0,37	Hs.3828	mevalonate (diphospho) decarboxylase	50
4871	ATCAGTGTGCA	3,00	0,37	Hs.194662	calponin 3, acidic	
4872	GCCATAAAATG	3,00	0,37	Hs.1908	proteoglycan 1, secretory granule	
4873	AAGTTGCTATT	23,00	0,92	Hs.78575	prosaposin (variant Gaucher disease and variant meta	
4874	CTCATAGCAGT	14,00	0,76	Hs.119252	tumor protein, translationally-controlled 1	55
4875	GGCTGAGAATG	6,00	0,54	Hs.106845	ESTs, Weakly similar to ALU6_HUMAN ALU SUBFAMILY SP	
4876	GGATGTGAAAG	9,00	0,64	Hs.177543	antigen identified by monoclonal antibodies 12E7, F2	60
4877	TTACACCTGTG	2,00	0,29	Hs.82794	centrin, EF-hand protein, 2	
4878	CCACCTGCTTT	2,00	0,29	Hs.7367	Homo sapiens glucocorticoid receptor	65

					AF-1 coactivato
5	4879	AGCACTGTACT	2,00	0,29	Hs.6375 uncharacterized hypothalamus protein HT010
	4880	CCCGGCTCCTC	2,00	0,29	Hs.31608 hypothetical protein FLJ20041
	4881	GTTTTCTGAA	2,00	0,29	Hs.31595 ESTs
	4882	TGCCTCCCATC	2,00	0,29	Hs.2437 eukaryotic translation initiation factor 2B, subunit
10	4883	GTGACGTGCAC	2,00	0,29	Hs.207390 ESTs, Moderately similar to ALU5_HUMAN ALU SUBFAMILY
	4884	GCTTGGCTCCC	2,00	0,29	Hs.175260 EST
	4885	GGGGGCAGGTC	2,00	0,29	Hs.107374 chromobox homolog 6
15	4886	CTTTTGTGCC	8,00	0,61	Hs.182238 GW128 protein
	4887	GAAGCAGGACC	67,00	1,46	Hs.180370 cofilin 1 (non-muscle)
	4888	TTGTGATGTAA	4,00	0,44	Hs.6975 PRO1073 protein
20	4889	AAGCGGGACCT	4,00	0,44	Hs.153436 N-acetyltransferase, homolog of S. cerevisiae ARD1
	4890	GTTTCTATCAA	4,00	0,44	Hs.12540 lysophospholipase I
	4891	GAGATCCGCAA	8,00	0,62	Hs.75348 proteasome (prosome, macropain) activator subunit 1
25	4892	ACAAAATAAAA	3,00	0,38	Hs.83469 nuclear factor (erythroid-derived 2)-like 1
	4893	CATTGCAGGAT	3,00	0,38	Hs.4288 hypothetical protein DKFZp434K046
	4894	GTCCCTCTCAA	2,00	0,29	Hs.92198 calcium-regulated heat-stable protein (24kD)
30	4895	TGAACAGTAAT	2,00	0,29	Hs.80120 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-ace
	4896	TCCAGAATCCT	2,00	0,29	Hs.7764 KIAA0469 gene product
	4897	AACAACCTGGCT	2,00	0,29	Hs.75243 bromodomain-containing 2
35	4898	CAGGTCAAGAA	2,00	0,29	Hs.179565 minichromosome maintenance deficient (S. cerevisiae)
	4899	CTGCCTCCGTG	2,00	0,29	Hs.12851 ESTs, Weakly similar to PSS1_HUMAN PHOSPHATIDYLSERIN
40	4900	ATTACACCACG	2,00	0,29	Hs.107014 membrane interacting protein of RGS16
	4901	TACCTGCAGAA	2,00	0,29	Hs.100000 S100 calcium-binding protein A8 (calgranulin A)
	4902	CCAAATGATGA	1,00	0,15	Hs.99519 ESTs
45	4903	TCACGCGCTCC	1,00	0,15	Hs.93231 ESTs
	4904	CTGGGATGCAG	1,00	0,15	Hs.89434 drebrin 1
	4905	CAACTATCCGT	1,00	0,15	Hs.87595 translocase of inner mitochondrial membrane 22 (yeas
50	4906	GCTTCATCAGA	1,00	0,15	Hs.76272 retinoblastoma-binding protein 2
	4907	ATACACTTTGT	1,00	0,15	Hs.75193 COP9 homolog
	4908	GCTTGGAGTTA	1,00	0,15	Hs.64322 hypothetical protein FLJ10913
	4909	GGGGCAGAGAG	1,00	0,15	Hs.6396 jumping translocation breakpoint
55	4910	GAAGCAAGAAA	1,00	0,15	Hs.6278 DKFZP586B1621 protein
	4911	TTGAAGTCAAA	1,00	0,15	Hs.3260 presenilin 1 (Alzheimer disease 3)
	4912	TGCAGGTACTG	1,00	0,15	Hs.278027 LIM domain kinase 2
	4913	GGGGAAATTGG	1,00	0,15	Hs.265960 hypothetical protein FLJ10563
60	4914	GAAATCCCAAT	1,00	0,15	Hs.24125 putative zinc finger protein
	4915	GGAAGAAGAAA	1,00	0,15	Hs.240062 hypothetical protein
	4916	GAGGAGGTGGA	1,00	0,15	Hs.22466 ubiquitin specific protease 19



4917	TAGAAATGTTTC	1,00	0,15	Hs.20985	sin3-associated polypeptide, 30kD
4918	ATGACTGCTGT	1,00	0,15	Hs.19525	ESTs
4919	GCATTCGCAGT	1,00	0,15	Hs.183842	ubiquitin B
4920	TTACACAGACT	1,00	0,15	Hs.182447	heterogeneous nuclear ribonucleoprotein C (C1/C2)
4921	CTGGGAGGGAG	1,00	0,15	Hs.154304	Homo sapiens chromosome 19, BAC 282485 (CIT-B-344H19)
4922	TTGTGTTCTTT	1,00	0,15	Hs.12305	DKFZP566B183 protein
4923	TTTTTCCTTAA	1,00	0,15	Hs.111911	ESTs
4924	AGCAGCCTTTT	1,00	0,15	Hs.10496	craniofacial development protein 1
4925	ATCCATCTGTG	4,00	0,45	Hs.63525	poly(rC)-binding protein 2
4926	CTTCTACTAAT	6,00	0,55	Hs.109857	Homo sapiens mRNA; cDNA DKFZp434H0820 (from clone DK
4927	CGCGTGCACAC	4,00	0,45	Hs.104640	HIV-1 inducer of short transcripts binding protein
4928	GTAGCAGGGCT	3,00	0,38	Hs.32797	ESTs
4929	TGCAGAACGGC	3,00	0,38	Hs.20776	CGI-91 protein
4930	TCTGCAATGAA	7,00	0,59	Hs.8170	hypothetical protein
4931	TGAGTGGACAG	4,00	0,45	Hs.3743	ESTs, Weakly similar to A28996 proline-rich protein
4932	CCAGGCTGCGT	4,00	0,45	Hs.149846	integrin, beta 5
4933	TTTCTGCTCCT	4,00	0,45	Hs.108124	ribosomal protein L41
4934	CTTTGCACTCT	2,00	0,29	Hs.78869	transcription elongation factor A (SII), 1
4935	GCTGTATAATT	2,00	0,29	Hs.74170	metallothionein 1E (functional)
4936	GGTTGAGTGTG	2,00	0,29	Hs.20529	ESTs, Weakly similar to ubiquitous TPR motif, Y isof
4937	TACAGTTCCT	2,00	0,29	Hs.20013	DKFZP564O2082 protein
4938	CCACTTTTTTAA	2,00	0,29	Hs.16492	DKFZP564G2022 protein
4939	GATCCGCTCTA	2,00	0,29	Hs.11615	map kinase phosphatase-like protein MK-STYX
4940	GTTTTCCGGTT	2,00	0,29	Hs.111449	CGI-94 protein
4941	AGTATGCCACT	2,00	0,29	Hs.110418	ESTs
4942	CAAGCAGGACA	7,00	0,59	Hs.179516	integral type I protein
4943	GCCGTGAGCAG	3,00	0,38	Hs.266514	hypothetical protein FLJ11342
4944	GAGTGAGACCC	10,00	0,70	Hs.125359	Thy-1 cell surface antigen
4945	ACCTCAGGAAA	15,00	0,84	Hs.177516	high density lipoprotein binding protein (vigilin)
4946	GGGCTGGGGTC	100,00	2,07	Hs.183698	ribosomal protein L29
4947	GACTCGCCAC	3,00	0,39	Hs.77171	minichromosome maintenance deficient (S. cerevisiae)
4948	GGACTTTCCTT	3,00	0,39	Hs.75789	N-myc downstream regulated
4949	TGAAAACACT	2,00	0,29	Hs.914	major histocompatibility complex, class II, DP alpha
4950	CTATGTGTTAC	2,00	0,29	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 9 (RNA
4951	TGGGTTTTTAA	2,00	0,29	Hs.63525	poly(rC)-binding protein 2
4952	CATTTAGATTT	2,00	0,29	Hs.3566	ART-4 protein
4953	CCTGGAATCCC	2,00	0,29	Hs.270605	ESTs, Weakly similar to alternatively spliced produc
4954	TGAATGATTTT	2,00	0,29	Hs.152707	glioblastoma amplified sequence

4955	GCCAGAAGGGG	1,00	0,15	Hs.90825	ESTs
4956	AAGAAATGCAA	1,00	0,15	Hs.8984	Homo sapiens chromosome 14 BAC 98L12
4957	CTCTTATTTCA	1,00	0,15	Hs.89072	ESTs
4958	TGTGTGTTAGC	1,00	0,15	Hs.76297	G protein-coupled receptor kinase 6
4959	ACCGCACAAAT	1,00	0,15	Hs.75232	SEC14 ( <i>S. cerevisiae</i> )-like 1
4960	TGGCCCTTTCA	1,00	0,15	Hs.70838	hypothetical protein PRO0971
4961	GGCTTTGTACG	1,00	0,15	Hs.49282	hypothetical protein FLJ11088
4962	TTCGTATTACA	1,00	0,15	Hs.46743	McKusick-Kaufman syndrome
4963	TTCTGTGTATA	1,00	0,15	Hs.3530	TLS-associated serine-arginine protein
4964	TGTGACACTGA	1,00	0,15	Hs.3273	Ts translation elongation factor, mitochondrial
4965	GGCTGAATTTT	1,00	0,15	Hs.31921	KIAA0648 protein
4966	AAACCTGAGAA	1,00	0,15	Hs.29724	ESTs, Weakly similar to CDEP [H.sapiens]
4967	TCTTCAGTAGC	1,00	0,15	Hs.2934	ribonucleotide reductase M1 polypeptide
4968	GAGCTCAAGAT	1,00	0,15	Hs.285780	Homo sapiens mRNA; cDNA DKFZp434A012 (from clone DKF
4969	TATGGGGTCCAC	1,00	0,15	Hs.278408	hypothetical protein
4970	ATGATGCCTCT	1,00	0,15	Hs.27657	KIAA0802 protein
4971	GTTAAACCCTG	1,00	0,15	Hs.256030	ESTs, Weakly similar to KIAA0004 [H.sapiens]
4972	TAATAAGCACT	1,00	0,15	Hs.25497	MAX binding protein
4973	GGAGGGGAGGC	1,00	0,15	Hs.19513	CGI-63 protein
4974	TTATCCTTCAC	1,00	0,15	Hs.188882	Homo sapiens clone 23872 mRNA sequence
4975	AATATTAAGAC	1,00	0,15	Hs.168103	prp28, U5 snRNP 100 kd protein
4976	AAGTGCATTTG	1,00	0,15	Hs.167420	ESTs
4977	TAATGAAATTG	1,00	0,15	Hs.15020	homolog of mouse quaking QKI (KH domain RNA binding
4978	CACCTCATCCC	1,00	0,15	Hs.125078	ornithine decarboxylase antizyme 1
4979	AACAAATTCTT	1,00	0,15	Hs.118722	fucosyltransferase 8 (alpha (1,6) fucosyltransferase
4980	GGGCTTGGTAT	1,00	0,15	Hs.107882	hypothetical protein FLJ10659
4981	GGCTGGGGGCC	50,00	1,47	Hs.75721	profilin 1
4982	TATGTGATTTG	3,00	0,39	Hs.5216	HSPC028 protein
4983	ACAACACTACA	3,00	0,39	Hs.27744	RAB3A, member RAS oncogene family
4984	ATGGCCATAGA	3,00	0,39	Hs.155206	serine/threonine kinase 25 (Ste20, yeast homolog)
4985	AAAGCAGCACA	3,00	0,39	Hs.108802	N-ethylmaleimide-sensitive factor
4986	ACTTGAGCCG	8,00	0,65	Hs.177656	calmodulin 1 (phosphorylase kinase, delta)
4987	TGCGCGCCCTG	4,00	0,46	Hs.15093	hypothetical protein
4988	AAGATAATGCC	4,00	0,46	Hs.102696	MCT-1 protein
4989	AGCACGACCCG	2,00	0,30	Hs.89434	drebrin 1
4990	TAGTAGATGCT	2,00	0,30	Hs.74649	cytochrome c oxidase subunit VIc
4991	CCTCACTTTCT	2,00	0,30	Hs.155560	calnexin
4992	TTAGTTAAGCA	3,00	0,39	Hs.33642	archain 1
4993	ACATCCTCACC	3,00	0,39	Hs.279554	proteasome (prosome, macropain) 26S subunit, non-ATP

4994	TCAGCTGGCCC	3,00	0,39	Hs.256583	interleukin enhancer binding factor 3, 90kD
4995	GCCTTCCAATA	30,00	1,20	Hs.76053	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA)
4996	CTCCCCCAAGC	5,00	0,52	Hs.283305	immunoglobulin heavy constant alpha 1
4997	CCCTCCTGGGG	8,00	0,66	Hs.95867	Homo sapiens EST00098 gene, last exon
4998	GAATCACTGCC	5,00	0,52	Hs.14454	chromosome 2 open reading frame 1
4999	TTCTCTCAACT	3,00	0,39	Hs.27445	unknown
5000	TAACCAAACAC	3,00	0,39	Hs.274147	Homo sapiens partial mRNA for NICE-4 protein, 3' end
5001	TCATTTTCCAA	4,00	0,46	Hs.187958	solute carrier family 6 (neurotransmitter transporte
5002	GAAATTTGAAA	2,00	0,30	Hs.79457	hypothetical protein FLJ20519
5003	TCAAGAAACAT	2,00	0,30	Hs.78580	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1
5004	CAAATAAAATG	2,00	0,30	Hs.71465	squalene epoxidase
5005	GTTCTCAGGAA	2,00	0,30	Hs.6968	KIAA1460 protein
5006	GTGTAAATGGA	2,00	0,30	Hs.286131	CGI-101 protein
5007	CCACACCGGTA	2,00	0,30	Hs.284279	heme oxygenase (decycling) 2
5008	AGGTCTGCCAG	2,00	0,30	Hs.201967	aldo-keto reductase family 1, member C2 (dihydrodiol
5009	TAGATGTGATG	1,00	0,15	Hs.99841	ESTs, Weakly similar to dJ1108D11.1 [H.sapiens]
5010	TAATAAAACCC	1,00	0,15	Hs.94810	Human DNA sequence from clone RP5-1170K4 on chromoso
5011	ACCCACCTGCA	1,00	0,15	Hs.9100	ESTs
5012	GAGCCTCATCC	1,00	0,15	Hs.83715	Sjogren syndrome antigen B (autoantigen La)
5013	TGGGAAGAGGG	1,00	0,15	Hs.80261	enhancer of filamentation 1 (cas-like docking; Crk-a
5014	CGGCAGGAAAA	1,00	0,15	Hs.78019	Homo sapiens clone 24432 mRNA sequence
5015	ATGTATAATAA	1,00	0,15	Hs.67052	vacuolar protein sorting 26 (yeast homolog)
5016	GGTCCAGCATC	1,00	0,15	Hs.4791	KIAA0376 protein
5017	TTTAATCTCAG	1,00	0,15	Hs.4104	hypothetical protein
5018	AGATTACTGAT	1,00	0,15	Hs.3991	ESTs
5019	TGTTGGGTTCT	1,00	0,15	Hs.3628	mitogen-activated protein kinase kinase kinase
5020	CAAGAGAGTAG	1,00	0,15	Hs.30332	glutamine-fructose-6-phosphate transaminase 2
5021	TGACACAGCCA	1,00	0,15	Hs.29390	ESTs
5022	CTGAATTCAGT	1,00	0,15	Hs.28739	ESTs
5023	AATATTGTCCG	1,00	0,15	Hs.283322	hypothetical protein
5024	ACTTCACAAAG	1,00	0,15	Hs.27556	ESTs
5025	GTTTTGTGGGA	1,00	0,15	Hs.267263	hypothetical protein
5026	TTTCATCCACT	1,00	0,15	Hs.25515	KIAA0362 protein
5027	GTAAACAATA	1,00	0,15	Hs.24758	ESTs
5028	TTTCATTAATC	1,00	0,15	Hs.247043	type 1 tumor necrosis factor receptor

					shedding amino
5	5029	GGGAAACTCCA	1,00	0,15	Hs.235390 Homo sapiens mRNA; cDNA DKFZp761B101 (from clone DKF
	5030	TGCCTGTGAAA	1,00	0,15	Hs.228289 EST
	5031	ATGCATTGTTT	1,00	0,15	Hs.198308 tryptophan rich basic protein
	5032	CTGTGATTGTG	1,00	0,15	Hs.195175 CASP8 and FADD-like apoptosis regula- tor
10	5033	CCAAAATTCTA	1,00	0,15	Hs.193700 Homo sapiens mRNA; cDNA DKFZp586I0324 (from clone DK
	5034	GACCTGCACTC	1,00	0,15	Hs.172278 syntrophin, beta 2 (dystrophin-associated protein A1
15	5035	CCTCTGGCAGC	1,00	0,15	Hs.166235 ESTs, Moderately similar to ALU5_HUMAN ALU SUBFAMILY
	5036	GCAGAAGCACA	1,00	0,15	Hs.16134 serine/threonine kinase 10
	5037	GTGATGTGCAC	1,00	0,15	Hs.141683 ESTs
20	5038	AAAACCTGAAA	1,00	0,15	Hs.118890 glycogen synthase kinase 3 alpha
	5039	TATAATAAATA	1,00	0,15	Hs.10758 NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18kD
	5040	GACGACACGAG	55,00	1,65	Hs.153177 ribosomal protein S28
25	5041	TGGCCCCCGCC	5,00	0,53	Hs.93649 upstream transcription factor 2, c-fos interacting
	5042	TAATCCTCAAG	4,00	0,47	Hs.78409 collagen, type XVIII, alpha 1
30	5043	GTTCTGGTTTA	11,00	0,77	Hs.241336 Homo sapiens mRNA; cDNA DKFZp564G0422 (from clone DK
	5044	TAAGTAGCAAA	6,00	0,58	Hs.239625 integral membrane protein 2B
	5045	GCTTACCTTTC	8,00	0,67	Hs.7753 calumenin
	5046	CCACTCCTCCA	4,00	0,47	Hs.82890 defender against cell death 1
35	5047	CAGCGCTTTGA	4,00	0,47	Hs.7274 DKFZP434P1750 protein
	5048	GTA CTCCAGTT	2,00	0,30	Hs.279857 PTD013 protein
	5049	GCAGGAGGTGA	2,00	0,30	Hs.11441 chromosome 1 open reading frame 8
40	5050	GGAGCTGCTGC	2,00	0,30	Hs.110950 Homo sapiens clone 25007 mRNA se- quence
	5051	GCCCCGCCCTC	5,00	0,53	Hs.280666 Homo sapiens chromosome 19, cosmid R32184
	5052	GAGGGAGTTTC	107,00	2,61	Hs.76064 ribosomal protein L27a
45	5053	TTCTCCACGC	3,00	0,40	Hs.183373 src homology 3 domain-containing pro- tein HIP-55
	5054	GCCTGGGCTGG	7,00	0,63	Hs.112184 DKFZP586J0619 protein
	5055	GACAGTGTGGG	4,00	0,47	Hs.279863 nuclear mitotic apparatus protein 1
50	5056	AATCCAGGAGG	5,00	0,53	Hs.89674 dolichyl-diphosphooligosaccharide- protein glycosyltr
	5057	CCCCCTGGATC	31,00	1,30	Hs.275243 S100 calcium-binding protein A6 (calcy- clin)
55	5058	TACAGTATGTT	7,00	0,64	Hs.170171 glutamate-ammonia ligase (glutamine synthase)
	5059	CCCATCATCCC	8,00	0,68	Hs.109051 glycoprotein, synaptic 2
	5060	GAGGAGGGTGA	4,00	0,48	Hs.75318 tubulin, alpha 1 (testis specific)
60	5061	GTCACAGTCCT	3,00	0,40	Hs.155321 serum response factor (c-fos serum response element-
	5062	GATGCCCTCCT	3,00	0,40	Hs.143648 insulin receptor substrate 2

5063	GCCAGACCCCT	3,00	0,40	Hs.108945	KIAA0515 protein
5064	TGCCTGTGGCC	2,00	0,30	Hs.7678	cellular retinoic acid-binding protein 1
5065	GGAAGAGCACT	2,00	0,30	Hs.75268	sialyltransferase 4C (beta-galactosidase alpha-2,3-s
5066	CCCTCTGTGAT	2,00	0,30	Hs.74649	cytochrome c oxidase subunit VIc
5067	ATTGGCTGGGC	2,00	0,30	Hs.57764	protein phosphatase 1A (formerly 2C), magnesium-depe
5068	GCATTGAGTGT	2,00	0,30	Hs.161554	hypothetical protein FLJ20159
5069	TTTCCACTTAA	2,00	0,30	Hs.101813	solute carrier family 9 (sodium/hydrogen exchanger),
5070	CGGCACATCCA	1,00	0,16	Hs.92357	galactokinase 1
5071	ATACCAGATAC	1,00	0,16	Hs.9071	progesterone membrane binding protein
5072	AAGCACCTTGA	1,00	0,16	Hs.89862	TNFRSF1A-associated via death domain
5073	GGGGTCCCAAA	1,00	0,16	Hs.6815	ESTs
5074	TGTGAAAATAA	1,00	0,16	Hs.62349	ras association (RaiGDS/AF-6) domain containing prot
5075	TCAAGAAATAA	1,00	0,16	Hs.61418	microfibrillar-associated protein 1
5076	CTGGTACCTGT	1,00	0,16	Hs.5813	ESTs, Moderately similar to 2109260A B cell growth f
5077	ACTCATCTGAC	1,00	0,16	Hs.5320	hypothetical protein
5078	AGGTATGGAGA	1,00	0,16	Hs.43654	hypothetical protein FLJ20561
5079	GGCACACCTTA	1,00	0,16	Hs.41127	Homo sapiens cDNA FLJ10745 fis, clone NT2RP3001676
5080	ATTGTAGACAA	1,00	0,16	Hs.39871	KIAA0727 protein
5081	GTCATATTTCC	1,00	0,16	Hs.32990	DKFZP566F084 protein
5082	TTGGAGGAGAG	1,00	0,16	Hs.32978	proprotein convertase subtilisin/kexin type 7
5083	AGAGCAGGTAC	1,00	0,16	Hs.262095	ESTs, Weakly similar to P137_HUMAN GPI-ANCHORED PROT
5084	TGGGTCTGGAT	1,00	0,16	Hs.25328	ESTs
5085	TGGAGAGAATA	1,00	0,16	Hs.249247	heterogeneous nuclear protein similar to rat helix d
5086	CCCAGGAGCAG	1,00	0,16	Hs.22051	Homo sapiens mRNA; cDNA DKFZp434O119 (from clone DKF
5087	ACACTAAGACG	1,00	0,16	Hs.170253	ESTs, Weakly similar to rabaptin-4 [H.sapiens]
5088	GTCAGAACACC	1,00	0,16	Hs.169832	zinc finger protein 42 (myeloid-specific retinoic ac
5089	GTATAAACGAA	1,00	0,16	Hs.166982	phosphatidylinositol glycan, class F
5090	CCCCCTCCTTA	1,00	0,16	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (from clone DKF
5091	GAAATGTATGC	1,00	0,16	Hs.142939	ESTs
5092	TCCTCTCACCA	1,00	0,16	Hs.12151	hypothetical protein FLJ11286
5093	GTGCTACTTCT	1,00	0,16	Hs.119129	collagen, type IV, alpha 1
5094	AATTCCAATC	1,00	0,16	Hs.117582	CGI-43 protein
5095	AGCTCCAGAT	1,00	0,16	Hs.111334	ferritin, light polypeptide
5096	TGTGAGGGCAT	1,00	0,16	Hs.103808	hypothetical protein FLJ20602
5097	TTCCCTGTGTA	1,00	0,16	Hs.102548	glucocorticoid receptor DNA binding factor 1
5098	TGCCTCTGCGG	18,00	1,01	Hs.75564	CD151 antigen

5099	GTAAAAAAAAA	21,00	1,09	Hs.77495	KIAA0242 protein
5100	GAACGCCTAAT	8,00	0,69	Hs.173381	dihydropyrimidinase-like 2
5101	TCAGACGCAGC	40,00	1,54	Hs.250655	prothymosin, alpha (gene sequence 28)
5102	AGCTGTCTCAA	3,00	0,40	Hs.99766	Homo sapiens mRNA; cDNA DKFZp564J0323 (from clone DK
5103	ACGACAAAGCT	3,00	0,40	Hs.83920	peptidylglycine alpha-amidating monooxygenase
5104	CCCTTCTGCCA	3,00	0,40	Hs.6214	KIAA0731 protein
5105	ATAGCTGGGGC	3,00	0,40	Hs.3446	mitogen-activated protein kinase kinase 1
5106	GTTTCAGGAGT	3,00	0,40	Hs.156114	protein tyrosine phosphatase, non- receptor type subs
5107	CCTGTGTGCAT	3,00	0,40	Hs.11611	KIAA1424 protein
5108	CCCCCAATGCT	3,00	0,40	Hs.115232	splicing factor 3a, subunit 2, 66kD
5109	GGACCACTGAA	86,00	2,46	Hs.119598	ribosomal protein L3
5110	TTTAAAAAAAA	2,00	0,31	Hs.74088	early growth response 3
5111	GGGCAGGGGAA	2,00	0,31	Hs.57672	hypothetical protein FLJ20248
5112	TTGAGAGATGA	2,00	0,31	Hs.3758	COP9 complex subunit 7a
5113	AAGCAAAAGGT	2,00	0,31	Hs.28505	ubiquitin-conjugating enzyme E2H (ho- mologous to yeas
5114	TGAAAAGCTTA	2,00	0,31	Hs.2384	tumor protein D52
5115	GCTCTGTTCAT	2,00	0,31	Hs.18192	Ser/Arg-related nuclear matrix protein (plenty of pr
5116	TTGAAGTGGTT	2,00	0,31	Hs.179972	hypothetical protein FLJ10154
5117	CGGAGCCGGCT	2,00	0,31	Hs.117582	CGI-43 protein
5118	GTCTGACCCCA	6,00	0,60	Hs.173902	protein phosphatase 2 (formerly 2A), regulatory subu
5119	CGACCCACGCG	30,00	1,35	Hs.169401	apolipoprotein E
5120	TACATAATTAC	7,00	0,65	Hs.120980	(Manual assignment) ORF-less transcript in MEN1 regi
5121	GCTGAAGATGA	3,00	0,41	Hs.78202	SWI/SNF related, matrix associated, actin dependent
5122	TGCTGTGCATA	8,00	0,70	Hs.147916	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3
5123	CAGCCCAACCG	7,00	0,65	Hs.28081	eukaryotic translation initiation factor 3, subunit
5124	CCCTGGGTTCT	54,00	1,92	Hs.111334	ferritin, light polypeptide
5125	CTGTGGCCGGA	3,00	0,41	Hs.284296	Homo sapiens SURF-4 mRNA, complete cds
5126	CCTGTAAAGCC	2,00	0,31	Hs.9691	Homo sapiens cDNA FLJ11255 fis, clone PLACE1008902
5127	GCTTTTCCTGT	2,00	0,31	Hs.75277	Homo sapiens mRNA; cDNA DKFZp586M141 (from clone DKF
5128	ACCCTGGGCAC	2,00	0,31	Hs.220324	Human DNA sequence from clone 283E3 on chromosome 1p
5129	GCAGAGCCTTG	2,00	0,31	Hs.20768	HSPC189 protein
5130	AATATCTGACT	2,00	0,31	Hs.118021	active BCR-related gene
5131	GACATCCTGTC	1,00	0,16	Hs.87627	(Manual assignment) MEMOREC SAS10
5132	ATTTAGACCAG	1,00	0,16	Hs.84790	KIAA0225 protein
5133	TGCTGTGACCA	1,00	0,16	Hs.78465	v-jun avian sarcoma virus 17 oncogene

					homolog
5134	ATCGTGGAGGA	1,00	0,16	Hs.727	inhibin, beta A (activin A, activin AB alpha polypep
5135	TATTCAATTAC	1,00	0,16	Hs.7045	GL004 protein
5136	TCTTTGTCTAA	1,00	0,16	Hs.6838	ESTs
5137	GCCAAAGTGTT	1,00	0,16	Hs.5831	tissue inhibitor of metalloproteinase 1 (erythroid p
5138	GATCCAAATGT	1,00	0,16	Hs.42650	ZW10 interactor
5139	GAGGCTTAATA	1,00	0,16	Hs.30819	hypothetical protein
5140	AGGGGAGAGGA	1,00	0,16	Hs.285999	trinucleotide repeat containing 15
5141	AGAGAAAAAAA	1,00	0,16	Hs.285038	Human XIST, coding sequence "a" mRNA (locus DXS399E)
5142	GATGTTGTCCA	1,00	0,16	Hs.279607	calpastatin
5143	CCCAATACTCT	1,00	0,16	Hs.26110	hypothetical protein
5144	GAAATTGGTCT	1,00	0,16	Hs.249247	heterogeneous nuclear protein similar to rat helix d
5145	AACGAGTATTC	1,00	0,16	Hs.241578	U6 snRNA-associated Sm-like protein LSm8
5146	TGCCAAAAAAA	1,00	0,16	Hs.19261	dystonia 1, torsion (autosomal dominant; torsin A)
5147	GGTGCACCCGG	1,00	0,16	Hs.183454	Homo sapiens mRNA; cDNA DKFZp434N1221 (from clone DK
5148	TCTAGCATTTT	1,00	0,16	Hs.179260	ESTs, Moderately similar to T12543 hypothetical prot
5149	AGCTTTGTAGA	1,00	0,16	Hs.16364	hypothetical protein FLJ10955
5150	CCCAAGGTCTT	1,00	0,16	Hs.153818	ESTs
5151	AACCAATACAG	1,00	0,16	Hs.146161	ESTs, Weakly similar to KIAA0859 protein [H.sapiens]
5152	CTTTTTAAATC	1,00	0,16	Hs.119222	suppression of tumorigenicity 13 (colon carcinoma) (
5153	GCTCCTGAGCC	1,00	0,16	Hs.111988	PR/SET domain containing protein 07
5154	GAGAAACATTT	1,00	0,16	Hs.101619	ESTs
5155	CAAAATGCAAA	1,00	0,16	Hs.10029	cathepsin C
5156	TGGAATGCTGG	12,00	0,87	Hs.7744	NADH dehydrogenase (ubiquinone) flavoprotein 1 (51kD
5157	ACCTTGTGCCC	5,00	0,55	Hs.878	sorbitol dehydrogenase
5158	TGGAGTGGAGG	17,00	1,05	Hs.3764	guanylate kinase 1
5159	CTCCACAAATT	4,00	0,49	Hs.278426	PDGF associated protein
5160	AGAAATCACTG	2,00	0,31	Hs.282266	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chai
5161	TGCAGGTGTGT	2,00	0,31	Hs.20993	high-glucose-regulated protein 8
5162	CCTGCAGTCCC	2,00	0,31	Hs.141746	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX
5163	CCCAAACTTTG	2,00	0,31	Hs.109438	Homo sapiens clone 24775 mRNA sequence
5164	GGGTGCAAAAA	3,00	0,42	Hs.249495	heterogeneous nuclear ribonucleoprotein A1
5165	CTATCAGTTTT	3,00	0,42	Hs.194625	dynein, cytoplasmic, light intermediate polypeptide
5166	ATTCTCCAGTA	73,00	2,49	Hs.234518	ribosomal protein L23

5167	GCAAAGAAAA	4,00	0,50	Hs.3844	LIM domain only 4
5168	ATGAGCTGACC	7,00	0,68	Hs.695	cystatin B (stefin B)
5169	TAATTTGCATT	3,00	0,42	Hs.79368	epithelial membrane protein 1
5170	AAACACTCTTG	3,00	0,42	Hs.151134	oxidase (cytochrome c) assembly 1-like
5171	CCAACAAGAAT	4,00	0,50	Hs.82749	transmembrane 4 superfamily member 2
5172	TTAAAGGCCGG	4,00	0,50	Hs.79086	ribosomal protein, mitochondrial, L3
5173	GCCGAGACCAA	2,00	0,32	Hs.61258	argininosuccinate lyase
5174	GTTTAAGTTAA	2,00	0,32	Hs.30029	ESTs
5175	CCTTGCTTTTA	2,00	0,32	Hs.278736	cell division cycle 42 (GTP-binding protein, 25kD)
5176	TGAGGACACAG	2,00	0,32	Hs.14541	cullin 1
5177	TTGGGAATCCC	1,00	0,16	Hs.9547	hypothetical protein FLJ10916
5178	CATTTTTCCCC	1,00	0,16	Hs.90336	ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton
5179	ACTCAAATCTT	1,00	0,16	Hs.7953	HSPC041 protein
5180	TAATTTTAACT	1,00	0,16	Hs.78867	protein tyrosine phosphatase, receptor-type, Z polyp
5181	CAGGTGTCTTT	1,00	0,16	Hs.77100	general transcription factor IIE, polypeptide 2 (bet
5182	ACTGGTGAGAG	1,00	0,16	Hs.76728	ESTs
5183	AAAATAAAGCT	1,00	0,16	Hs.74649	cytochrome c oxidase subunit VIc
5184	ACTCACTGCAG	1,00	0,16	Hs.60377	KIAA1298 protein
5185	TTAAAATTGCC	1,00	0,16	Hs.444	serine/threonine kinase 19
5186	AACCAGGTGGA	1,00	0,16	Hs.44095	hypothetical protein FLJ20018
5187	TAGGTCAGGAC	1,00	0,16	Hs.43666	protein tyrosine phosphatase type IVA, member 3
5188	GTGGCGGCACC	1,00	0,16	Hs.43112	Homo sapiens mRNA; cDNA DKFZp434B1620 (from clone DK
5189	CCCACAACCCG	1,00	0,16	Hs.38205	from HeLa cyclin-dependent kinase 2 interacting prot
5190	GAATTGAGCTT	1,00	0,16	Hs.36787	chromodomain helicase DNA binding protein 2
5191	TGTTCTTTGCA	1,00	0,16	Hs.3376	hypothetical protein FLJ10743
5192	GCTTCCTCTGC	1,00	0,16	Hs.27262	Homo sapiens clone 25110 mRNA sequence
5193	GGATACAACAC	1,00	0,16	Hs.272458	protein phosphatase 3 (formerly 2B), catalytic subun
5194	GTAGTCACCGC	1,00	0,16	Hs.26630	ATP-binding cassette, sub-family A (ABC1), member 3
5195	GCACAAGAGTG	1,00	0,16	Hs.25892	ESTs
5196	GCCTCCAGCCT	1,00	0,16	Hs.23100	ESTs
5197	TAAACATTGTC	1,00	0,16	Hs.23060	DKFZP564F0522 protein
5198	CAAATTACAAT	1,00	0,16	Hs.22393	density-regulated protein
5199	CTTACAGCCAC	1,00	0,16	Hs.195969	ESTs
5200	ACTGCACCACT	1,00	0,16	Hs.185910	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
5201	TTACAATGCTG	1,00	0,16	Hs.184013	ESTs, Highly similar to unnamed protein product [H.s
5202	TCCTACGGAAA	1,00	0,16	Hs.108708	calcium/calmodulin-dependent protein kinase 2



5203	GCTGTTCAATG	3,00	0,42	Hs.77306	survival of motor neuron 1, telomeric
5204	ATATAATCTGA	3,00	0,42	Hs.621	lectin, galactoside-binding, soluble, 3 (galectin 3)
5205	CTAATAAACTT	3,00	0,42	Hs.279583	CGI-81 protein
5206	CAGGATCCAGA	6,00	0,63	Hs.119222	suppression of tumorigenicity 13 (colon carcinoma) (
5207	CGGATAACCAG	7,00	0,69	Hs.5181	proliferation-associated 2G4, 38kD
5208	GTGTATCTTTT	5,00	0,57	Hs.73965	splicing factor, arginine/serine-rich 2
5209	CTCCACCTGGT	2,00	0,32	Hs.75835	phosphomannomutase 1
5210	TCAACTGGTTC	2,00	0,32	Hs.75812	phosphoenolpyruvate carboxykinase 2 (mitochondrial)
5211	AAATTTTAAAA	2,00	0,32	Hs.74649	cytochrome c oxidase subunit VIc
5212	ACCCACAGTGC	2,00	0,32	Hs.67896	7-60 protein
5213	AGGCCTGGGCC	2,00	0,32	Hs.6163	ESTs, Weakly similar to myotonic dystrophy kinase [H
5214	TCAGTGCGCAG	2,00	0,32	Hs.5534	ESTs
5215	CTGAGGTGATG	2,00	0,32	Hs.26367	Homo sapiens mRNA; cDNA DKFZp564M1178 (from clone DK
5216	CCACTCCACTC	2,00	0,32	Hs.190452	KIAA0365 gene product
5217	GCCTGCTCCCT	2,00	0,32	Hs.16725	hypothetical protein FLJ10111
5218	GACTGTGCCAC	11,00	0,88	Hs.5120	dynein, cytoplasmic, light polypeptide
5219	TGATCTCCAAA	8,00	0,74	Hs.83190	fatty acid synthase
5220	AAGAAAGTTCT	5,00	0,58	Hs.10729	hypothetical protein
5221	TAACAGAAAGG	3,00	0,43	Hs.97496	YY1 transcription factor
5222	ATGGCTAAGCT	3,00	0,43	Hs.82280	regulator of G-protein signalling 10
5223	GATGGGGACAA	3,00	0,43	Hs.118724	DR1-associated protein 1 (negative cofactor 2 alpha)
5224	AATTCAATTAA	4,00	0,51	Hs.211568	eukaryotic translation initiation factor 4 gamma, 1
5225	AGCAAAGTGA	4,00	0,51	Hs.182579	leucine aminopeptidase
5226	CCTCGGAAAAT	30,00	1,56	Hs.2017	ribosomal protein L38
5227	ATGGCCCATAC	2,00	0,32	Hs.282975	carboxylesterase 2 (intestine, liver)
5228	CACCACGGGCC	2,00	0,32	Hs.273219	breast cancer anti-estrogen resistance 1
5229	CGGATAAGGCC	2,00	0,32	Hs.256526	nuclear prelamin A recognition factor
5230	CCTTGGGCCTA	2,00	0,32	Hs.14963	chromatin-specific transcription elongation factor,
5231	TATAACTTGTA	2,00	0,32	Hs.132955	BCL2/adenovirus E1B 19kD-interacting protein 3-like
5232	GCACCTTATTG	2,00	0,32	Hs.125078	ornithine decarboxylase antizyme 1
5233	CACATCTCTGA	2,00	0,32	Hs.10248	Homo sapiens cDNA FLJ20167 fis, clone COL09512
5234	CCTTGTCCAGC	2,00	0,32	Hs.101067	GCN5 (general control of amino-acid synthesis, yeast
5235	AGCTGGTTTCC	6,00	0,65	Hs.286027	etoposide-induced mRNA
5236	TTCCCTCGTGA	3,00	0,43	Hs.80758	aspartyl-tRNA synthetase
5237	CGCACCATTGC	5,00	0,58	Hs.94672	GCN5 (general control of amino-acid synthesis, yeast
5238	ATATTCTGCCT	1,00	0,17	Hs.96900	hypothetical protein
5239	CTCCCAAGCTC	1,00	0,17	Hs.9452	KIAA0770 protein
5240	CAAGCTTGGTC	1,00	0,17	Hs.86858	ribosomal protein S6 kinase, 70kD,

					polypeptide 1
5	5241	GTCATCACTGG	1,00	0,17	Hs.8535 hypothetical protein bA395L14.2
	5242	CCCTGTTTCAGC	1,00	0,17	Hs.78824 tyrosine kinase with immunoglobulin and epidermal gr
	5243	GACTGGAAAAA	1,00	0,17	Hs.743 Fc fragment of IgE, high affinity I, recep- tor for; g
10	5244	GACCCTTCTCC	1,00	0,17	Hs.6580 Homo sapiens clone 23718 mRNA se- quence
	5245	GGCAGGAGTAG	1,00	0,17	Hs.62661 guanylate binding protein 1, interferon- inducible, 6
15	5246	TGCTAGGAAGG	1,00	0,17	Hs.55235 sphingomyelin phosphodiesterase 2, neutral membrane
	5247	TGTTGTATTTG	1,00	0,17	Hs.48902 ESTs
	5248	GTGGCACCCGC	1,00	0,17	Hs.47305 ESTs, Weakly similar to LONN_HUMAN MITOCHONDRIAL LON
20	5249	AAACTCACGCC	1,00	0,17	Hs.3337 transmembrane 4 superfamily member 1
	5250	TGTATGGCTGG	1,00	0,17	Hs.284269 Homo sapiens calpain 3 (CAPN3) mRNA, complete cds, a
	5251	GCTTAAATTAA	1,00	0,17	Hs.282283 baculoviral IAP repeat-containing 2
25	5252	AGAAGATTTAT	1,00	0,17	Hs.250746 ESTs
	5253	ACCTGGCCTGA	1,00	0,17	Hs.20225 tuftelin-interacting protein
	5254	CTGTACATACT	1,00	0,17	Hs.197298 NS1-binding protein
30	5255	ATGCTGGGGAG	1,00	0,17	Hs.19701 Homo sapiens mRNA for P53TG1-D, complete cds
	5256	GCAATAATGGT	1,00	0,17	Hs.19614 gemin4
	5257	GCTGGCCGGAA	1,00	0,17	Hs.184367 GTPase activating protein-like
	5258	CGCTGGTTCCC	1,00	0,17	Hs.179943 ribosomal protein L11
35	5259	CAGGGGCTGGG	1,00	0,17	Hs.155983 KIAA0677 gene product
	5260	CGTTTAATCAT	1,00	0,17	Hs.155218 E1B-55kDa-associated protein 5
	5261	CTCCCAGGTCA	1,00	0,17	Hs.152720 M-phase phosphoprotein 6
	5262	AGCCCTCAACA	1,00	0,17	Hs.139240 DKFZP564F1422 protein
40	5263	GACTGAATGTA	1,00	0,17	Hs.109259 ESTs, Weakly similar to alternatively spliced produc
	5264	GTAATGCATAT	1,00	0,17	Hs.109150 SH3-domain binding protein 5 (BTK- associated)
45	5265	GTGAGGGCACA	1,00	0,17	Hs.107382 KIAA1517 protein
	5266	CCCTGGCAATG	5,00	0,59	Hs.273369 uncharacterized hematopoietic stem/progenitor cells
	5267	ACGCAGGGAGA	53,00	2,29	Hs.180532 heat shock 90kD protein 1, alpha
50	5268	CCCGGGAGCGA	4,00	0,52	Hs.75807 carboxy terminal LIM domain protein 1
	5269	GAGGCCATCCC	4,00	0,52	Hs.70830 U6 snRNA-associated Sm-like protein LSm7
	5270	GGCTGGTCTCC	6,00	0,65	Hs.86185 Alu-binding protein with zinc finger do- main
55	5271	GAGGGCCTTGT	2,00	0,33	Hs.90303 tuberous sclerosis 2
	5272	GTGACAGAATT	2,00	0,33	Hs.77837 UDP-glucose pyrophosphorylase 2
	5273	CTTTTCACTTC	2,00	0,33	Hs.279919 ring-box 1
60	5274	TGTGTTGTGTC	2,00	0,33	Hs.279806 Homo sapiens mRNA; cDNA DKFZp434E109 (from clone DKF
	5275	TGGGGTGGAGT	2,00	0,33	Hs.26403 glutathione transferase zeta 1 (maleyla-

					cetoacetate i
5276	GATTCAACCAA	2,00	0,33	Hs.168213	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J S
5277	CCGTCATCCTG	2,00	0,33	Hs.153591	Not56 (D. melanogaster)-like protein
5278	AGCTGAGCTAA	2,00	0,33	Hs.118243	deoxyribonuclease II, lysosomal
5279	CAATAAATGTT	48,00	2,18	Hs.179779	ribosomal protein L37
5280	GCAGGGCCTCA	13,00	1,01	Hs.92323	FXD domain-containing ion transport regulator 3
5281	CAGTTACTTAG	9,00	0,83	Hs.279920	tyrosine 3-monooxygenase/tryptophan 5- monooxygenase
5282	TTCCTGGTAGT	6,00	0,66	Hs.181043	KIAA0788 protein
5283	GTTTTCAATCA	5,00	0,60	Hs.173736	ancient ubiquitous protein 1
5284	CCCTCCTCTCC	2,00	0,33	Hs.83173	cyclin D3
5285	TCCCTGGCAGA	2,00	0,33	Hs.70327	cysteine-rich protein 2
5286	GACACGAACAA	2,00	0,33	Hs.25829	ras-related protein
5287	CTGGGATGTCG	2,00	0,33	Hs.20159	CGI-92 protein
5288	GTGTTCTGACT	2,00	0,33	Hs.15832	DKFZP586P2220 protein
5289	GCTATGCTCCC	2,00	0,33	Hs.13094	hypothetical protein PRO2207
5290	GCCCCTCAGCA	2,00	0,33	Hs.11184	hypothetical protein FLJ20419
5291	CCCCCTGCCCT	7,00	0,73	Hs.177596	hypothetical protein FLJ10350
5292	AGAAAGATGTC	11,00	0,93	Hs.78225	annexin A1
5293	TTTACAGCTGG	3,00	0,44	Hs.89981	diacylglycerol kinase, zeta (104kD)
5294	GTTGTAAATA	3,00	0,44	Hs.7869	lysophosphatidic acid acyltransferase- delta
5295	CTGCCTCCTTA	4,00	0,53	Hs.7918	uncharacterized hypothalamus protein HSMNP1
5296	TCACCTTCAAG	1,00	0,17	Hs.74002	nuclear receptor coactivator 1
5297	TTTTATAAGGA	1,00	0,17	Hs.73986	CDC-like kinase 2
5298	CCTTGTCCTCT	1,00	0,17	Hs.69743	GM2 ganglioside activator protein
5299	AGTGTTTGTAG	1,00	0,17	Hs.5420	hypothetical protein FLJ20695
5300	AGAACAAAGGC	1,00	0,17	Hs.50785	SEC22, vesicle trafficking protein (S. cerevisiae)-l
5301	GGCAAAAAAAA	1,00	0,17	Hs.2953	ribosomal protein S15a
5302	GCCTCCACAGC	1,00	0,17	Hs.285813	ESTs
5303	GCACAAGTTCT	1,00	0,17	Hs.284174	hypothetical protein FLJ20216
5304	GTTGGGTAGAA	1,00	0,17	Hs.282990	Human DNA sequence from clone RP1- 28H20 on chromosom
5305	AGGTCAGGAAA	1,00	0,17	Hs.249429	EST
5306	GTCATTTTCTA	1,00	0,17	Hs.232058	transcription factor 8 (represses inter- leukin 2 expr
5307	TCTTCCCTCAG	1,00	0,17	Hs.215683	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY
5308	GGTTGATCACC	1,00	0,17	Hs.19699	Conserved gene telomeric to alpha globin cluster
5309	TTTCAAGTGGT	1,00	0,17	Hs.17820	Rho-associated, coiled-coil containing protein kinas
5310	CCGGGTTATTT	1,00	0,17	Hs.169138	RPA-binding trans-activator
5311	CCGCCCCCAGC	1,00	0,17	Hs.167927	islet cell autoantigen 1 (69kD)
5312	GTGTTGACTGC	1,00	0,17	Hs.153639	hypothetical SBB103 protein
5313	TGAAACGGAAG	1,00	0,17	Hs.12940	zinc-fingers and homeoboxes 1

5314	GTGCTCAGCCT	1,00	0,17	Hs.12909	ESTs, Weakly similar to unnamed protein product [H.s]
5315	ACCTGGTGTCT	1,00	0,17	Hs.111988	PR/SET domain containing protein 07
5316	GCAGAGAAAAA	1,00	0,17	Hs.109606	coronin, actin-binding protein, 1A
5317	TAAGTGACTGT	1,00	0,17	Hs.103755	receptor-interacting serine-threonine kinase 2
5318	CACAGAGTCCT	4,00	0,53	Hs.75140	low density lipoprotein-related protein-associated p
5319	TAAACTGTTTC	9,00	0,85	Hs.3491	ribosomal protein S14
5320	TTCACAGATTT	3,00	0,44	Hs.8107	Homo sapiens mRNA; cDNA DKFZp586B0918 (from clone DK
5321	AGCTGATCAGC	3,00	0,44	Hs.78223	N-acylaminoacyl-peptide hydrolase
5322	TTCATTGTAGA	4,00	0,53	Hs.6527	G protein-coupled receptor 56
5323	TGCCATCTGTA	4,00	0,53	Hs.23960	cyclin B1
5324	GCCTCCTGTCA	2,00	0,33	Hs.7765	chromosome 16 open reading frame 5
5325	CACTGTGACCT	2,00	0,33	Hs.284271	cytochrome b5 reductase 1 (B5R.1)
5326	GGGCTGCTCTT	2,00	0,33	Hs.155829	KIAA0676 protein
5327	CCCAGGACACC	2,00	0,33	Hs.110443	Homo sapiens mRNA; cDNA DKFZp761O051 (from clone DKF
5328	ATGTTGCCCT	2,00	0,33	Hs.10882	HMG-box containing protein 1
5329	TGCTAAAAAAA	6,00	0,68	Hs.146550	myosin, heavy polypeptide 9, non-muscle
5330	GGGGAGGGGGC	3,00	0,45	Hs.89781	upstream binding transcription factor, RNA polymeras
5331	GCCAGACACCC	3,00	0,45	Hs.3804	DKFZP564C1940 protein
5332	TACTCTTGGCA	14,00	1,11	Hs.2730	heterogeneous nuclear ribonucleoprotein L
5333	TAGGCCCAAGT	4,00	0,54	Hs.78880	ilvB (bacterial acetolactate synthase)-like
5334	CCAACCGTGCT	8,00	0,81	Hs.75207	glyoxalase I
5335	GGTGACCACCA	4,00	0,54	Hs.83623	nuclear receptor subfamily 1, group I, member 3
5336	GCATTTGACAG	2,00	0,34	Hs.74649	cytochrome c oxidase subunit VIc
5337	GGTGCGGCTGG	2,00	0,34	Hs.188882	Homo sapiens clone 23872 mRNA sequence
5338	TTGTGATTAAT	2,00	0,34	Hs.18442	E-1 enzyme
5339	GGAGAGACAGG	2,00	0,34	Hs.170980	ESTs, Weakly similar to CBF1 interacting corepressor
5340	TCAGTTTGTC	10,00	0,92	Hs.15318	HS1 binding protein
5341	GTGCCTAGGGA	3,00	0,45	Hs.12854	ATRAP protein
5342	AGTATCTGGGA	3,00	0,45	Hs.11538	actin related protein 2/3 complex, subunit 1A (41 kD)
5343	TCAATCAAGAT	9,00	0,87	Hs.75544	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase
5344	TGGCTGGGAAA	6,00	0,69	Hs.172684	vesicle-associated membrane protein 8 (endobrevin)
5345	TAAGAAGCCCC	1,00	0,17	Hs.94318	ESTs
5346	CAGGCACTGAA	1,00	0,17	Hs.91065	hypothetical protein DKFZp761B2423
5347	GGGTTTTTCTG	1,00	0,17	Hs.83583	actin related protein 2/3 complex, subunit 2 (34 kD)
5348	GAGAAGACACG	1,00	0,17	Hs.8037	ESTs

5349	TGCAGAAGTAG	1,00	0,17	Hs.77770	adaptor-related protein complex 3, mu 2 subunit
5350	TTGTCCGGGCT	1,00	0,17	Hs.75064	tubulin-specific chaperone c
5351	GATTTTAATGT	1,00	0,17	Hs.7370	phosphatidylinositol transfer protein, beta
5352	CCTCTTGTAAT	1,00	0,17	Hs.66170	HSKM-B protein
5353	CCCTGGCTGTA	1,00	0,17	Hs.58127	ESTs
5354	TGATGTGGAAT	1,00	0,17	Hs.5687	protein phosphatase 1B (formerly 2C), magnesium-depe
5355	AAATGACTATA	1,00	0,17	Hs.43071	ESTs, Weakly similar to AF151900_1 CGI-142 protein [
5356	GAGGTTAGATT	1,00	0,17	Hs.283712	hypothetical protein
5357	ATGCTGTCTGC	1,00	0,17	Hs.26471	Homo sapiens clone HQ0692
5358	AGTTGAGTCCT	1,00	0,17	Hs.262476	S-adenosylmethionine decarboxylase 1
5359	CCCCACTAAAC	1,00	0,17	Hs.21036	Homo sapiens mRNA; cDNA DKFZp434A1010 (from clone DK
5360	TGCTTGTGGTT	1,00	0,17	Hs.176600	WD-repeat protein
5361	TACGGGGGCCA	1,00	0,17	Hs.173043	metastasis-associated 1-like 1
5362	CCGTGAAAAAA	1,00	0,17	Hs.159448	surfeit 2
5363	TAACAAACCTG	1,00	0,17	Hs.15422	ESTs
5364	TTTCTGTGAAC	1,00	0,17	Hs.14415	CGI-108 protein
5365	CAATATCTTG	1,00	0,17	Hs.114404	ESTs
5366	GATGTGAAAAG	1,00	0,17	Hs.106148	Homo sapiens mRNA; cDNA DKFZp434G0972 (from clone DK
5367	GCCACGTGGAG	1,00	0,17	Hs.103665	villin-like
5368	CACAAACGGTA	105,00	4,52	Hs.195453	ribosomal protein S27 (metalloprotein 1)
5369	CGGAGGTGGGA	3,00	0,45	Hs.2491	DiGeorge syndrome critical region gene 2
5370	ATGGTGGTGGC	3,00	0,45	Hs.238030	secretory carrier membrane protein 2
5371	GCATATTAAAA	3,00	0,45	Hs.178658	RAD23 (S. cerevisiae) homolog B
5372	GGTGAGACCTG	17,00	1,29	Hs.80423	prostatic binding protein
5373	ACGCCCTGCTC	2,00	0,34	Hs.898	dystrophin myotonic-protein kinase
5374	AGGACTTCTGA	2,00	0,34	Hs.43847	ESTs, Weakly similar to SFR7_HUMAN SPLICING FACTOR.
5375	ATCCGTGCCCT	6,00	0,70	Hs.141011	calmodulin 3 (phosphorylase kinase, delta)
5376	AAAAGAACTT	15,00	1,21	Hs.172182	poly(A)-binding protein, cytoplasmic 1
5377	GGTGGATGTGC	5,00	0,64	Hs.178728	methyl-CpG binding domain protein 3
5378	GTAGGGGCCTC	1,00	0,18	Hs.82208	acyl-Coenzyme A dehydrogenase, very long chain
5379	TAATTTGAAAA	1,00	0,18	Hs.6523	similar to rat smooth muscle protein SM-20
5380	AGGCCACCTCA	1,00	0,18	Hs.6084	frequenin (Drosophila) homolog
5381	ACTCTTGTTGG	1,00	0,18	Hs.5378	spondin 1, (f-spondin) extracellular matrix protein
5382	TGGAAGCTTTC	1,00	0,18	Hs.5308	ESTs
5383	ATACATAATAA	1,00	0,18	Hs.4994	transducer of ERBB2, 2
5384	GGGCCGCTCAG	1,00	0,18	Hs.37656	KIAA0602 protein
5385	TACCAAGCCAG	1,00	0,18	Hs.31388	ESTs
5386	AATGCGGGAAA	1,00	0,18	Hs.259836	ESTs, Moderately similar to

					ALUC_HUMAN !!!! ALU CLAS
5387	AGGCTTTATGG	1,00	0,18	Hs.24385	Human hbc647 mRNA sequence
5388	TGATGAGTGCT	1,00	0,18	Hs.21657	ESTs
5389	TAAAACCCTAT	1,00	0,18	Hs.211582	myosin, light polypeptide kinase
5390	GCCACAGCCAG	1,00	0,18	Hs.198037	KIAA0599 protein
5391	GGGCTCCAGGA	1,00	0,18	Hs.184227	F-box only protein 21
5392	AGCGGAGTCTG	1,00	0,18	Hs.181013	phosphoglycerate mutase 1 (brain)
5393	CTTATGGTCCC	1,00	0,18	Hs.179608	retinol dehydrogenase homolog
5394	GAAGTCATTTT	1,00	0,18	Hs.164478	ESTs, Weakly similar to AF161483_1 HSPC134 [H.sapien]
5395	TGTTTGGTTTC	1,00	0,18	Hs.161554	hypothetical protein FLJ20159
5396	AGAGCTCACTA	1,00	0,18	Hs.13845	ESTs
5397	CCTGTAAATCC	1,00	0,18	Hs.109654	hypothetical protein FLJ11271
5398	AGCTGTTCTGC	3,00	0,46	Hs.249495	heterogeneous nuclear ribonucleoprotein A1
5399	GAGGCCAGTGA	3,00	0,46	Hs.2280	ribophorin I
5400	TGTAATCAATA	11,00	1,02	Hs.249495	heterogeneous nuclear ribonucleoprotein A1
5401	GATATCAGTCT	2,00	0,35	Hs.66394	ring finger protein 4
5402	CTTCTGCTGGG	2,00	0,35	Hs.17144	short-chain dehydrogenase/reductase 1
5403	AACTGCTTCAA	8,00	0,85	Hs.11538	actin related protein 2/3 complex, subunit 1A (41 kD)
5404	ACGGTGATGTC	5,00	0,64	Hs.10453	ESTs
5405	GCCTCCTCCCA	14,00	1,19	Hs.170120	muscle specific gene
5406	GCCCCTGCCTC	3,00	0,47	Hs.283667	hypothetical protein DKFZp547H084
5407	TGCGGAGGCCC	3,00	0,47	Hs.25723	Sjogren's syndrome/scleroderma autoan- tigen 1
5408	CTTATGGTTGA	4,00	0,57	Hs.14084	ring finger protein 7
5409	TAATACTTTTG	2,00	0,35	Hs.90527	HSPC128 protein
5410	TAAGCATTAAG	2,00	0,35	Hs.8180	syndecan binding protein (syntenin)
5411	ACAGTGTTAAA	2,00	0,35	Hs.74649	cytochrome c oxidase subunit VIc
5412	TTTGTGGGCAG	2,00	0,35	Hs.39619	ESTs, Weakly similar to RCN1_HUMAN RETICULOCALBIN 1
5413	TGGTCCCTCTC	2,00	0,35	Hs.36587	protein phosphatase 1, regulatory sub- unit 7
5414	GTTTCTAATAA	2,00	0,35	Hs.239298	microtubule-associated protein 4
5415	CAATTGTAAAT	2,00	0,35	Hs.18792	thioredoxin-like, 32kD
5416	GCACTTTGAGG	2,00	0,35	Hs.103382	phospholipid scramblase 3
5417	ATCAAGGGTGT	32,00	2,06	Hs.157850	ribosomal protein L9
5418	AGGGGCGCAGA	4,00	0,57	Hs.97616	SH3-domain GRB2-like 1
5419	GGCTGATGTGG	10,00	0,99	Hs.75280	glycyl-tRNA synthetase
5420	GCAGCCATCCG	81,00	4,17	Hs.4437	ribosomal protein L28
5421	CTTCTGTGAT	7,00	0,80	Hs.2533	aldehyde dehydrogenase 9 (gamma- aminobutyraldehyde d
5422	AAGGAAGCTGC	1,00	0,18	Hs.9914	folliculin
5423	GTGTTCTCCG	1,00	0,18	Hs.91299	unknown gene
5424	ACATAATAAAG	1,00	0,18	Hs.90077	TG-interacting factor (TALE family ho- meobox)
5425	ACGTCTCTATT	1,00	0,18	Hs.8551	PRP4/STK/WD splicing factor
5426	TTGATGCCCTA	1,00	0,18	Hs.7871	hypothetical protein FLJ10081

5427	GACACCAACTA	1,00	0,18	Hs.77500	ubiquitin specific protease 4 (proto-oncogene)
5428	TGCCCAGCAAA	1,00	0,18	Hs.76297	G protein-coupled receptor kinase 6
5429	ATACATACTGT	1,00	0,18	Hs.74313	ESTs
5430	GAGGCCAATGC	1,00	0,18	Hs.6151	KIAA0235 protein
5431	TCTGCAGGGGA	1,00	0,18	Hs.59509	ESTs
5432	ACTACTAAATA	1,00	0,18	Hs.5437	Tax1 (human T-cell leukemia virus type I) binding pr
5433	GCTGGTTCCTG	1,00	0,18	Hs.34516	Homo sapiens mRNA; cDNA DKFZp434E0211 (from clone DK
5434	TGCCATATAAG	1,00	0,18	Hs.32271	hypothetical protein FLJ10846
5435	ACCCAATTTGT	1,00	0,18	Hs.30348	ESTs
5436	ACCAAATATTT	1,00	0,18	Hs.250641	tropomyosin 4
5437	GGACAGAACCC	1,00	0,18	Hs.171835	hypothetical protein FLJ10889
5438	GTGATTATGAT	1,00	0,18	Hs.170318	hypothetical protein FLJ10147
5439	TCACAGTGCCT	3,00	0,47	Hs.81008	filamin B, beta (actin-binding protein-278)
5440	GCTCCACTGGA	3,00	0,47	Hs.75709	mannose-6-phosphate receptor (cation dependent)
5441	GTGCCCTGTTG	5,00	0,66	Hs.278411	NCK-associated protein 1
5442	CCCGGGGCCTC	2,00	0,35	Hs.90691	nucleophosmin/nucleoplasmin 3
5443	CACCTGTCCTT	2,00	0,35	Hs.54457	CD81 antigen (target of antiproliferative antibody 1
5444	CTGGAGGCACA	2,00	0,35	Hs.283976	Homo sapiens clone TCBA00888 mRNA sequence
5445	GAGAGGGCAGA	2,00	0,35	Hs.26412	ESTs, Weakly similar to KIAA0544 protein [H.sapiens]
5446	AATCCGACTCT	2,00	0,35	Hs.211577	kinectin 1 (kinesin receptor)
5447	CTTTTCAGCAA	4,00	0,58	Hs.79474	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase
5448	GGGCGGGGGCG	2,00	0,36	Hs.99890	polymerase (DNA directed), delta 1, catalytic subuni
5449	GAGCGCAGCGA	2,00	0,36	Hs.83727	cleavage and polyadenylation specific factor 1, 160k
5450	TCCTGCCCTCA	2,00	0,36	Hs.80598	transcription elongation factor A (SII), 2
5451	TGTGGGAACCA	2,00	0,36	Hs.7750	Novel human gene mapping to chromosome 1
5452	CCAGATTTTGG	2,00	0,36	Hs.4788	nicastrin
5453	ATATTGTCAA	2,00	0,36	Hs.3903	Homo sapiens mRNA; cDNA DKFZp762L106 (from clone DKF
5454	CACTGCATATG	2,00	0,36	Hs.196177	phosphorylase kinase, gamma 2 (testis)
5455	GAGCATAATA	2,00	0,36	Hs.170065	Wiskott-Aldrich syndrome-like
5456	CGCCGCCGGCT	66,00	3,76	Hs.182825	ribosomal protein L35
5457	GGGGTGCTGTG	5,00	0,67	Hs.166161	dynamitin 1
5458	AAGCCAGGACA	8,00	0,90	Hs.10326	coatamer protein complex, subunit epsilon
5459	TTTCTAGTTTG	11,00	1,09	Hs.111894	membrane nucleoside transporter
5460	GGCAACGTGGT	6,00	0,76	Hs.80162	Huntingtin interacting protein K
5461	AAGACAGTGGC	102,00	5,46	Hs.184109	ribosomal protein L37a
5462	GAGGGGAGGAA	1,00	0,19	Hs.83634	host cell factor C1 (VP16-accessory protein)

5	5463	TAAATGTTGAT	1,00	0,19	Hs.83572	Human clone 23721 mRNA sequence
	5464	CCTGCCACCCC	1,00	0,19	Hs.6133	ESTs, Highly similar to JC5772 tissue-specific calpa
	5465	AACTCTCCCC	1,00	0,19	Hs.57222	nurim (nuclear envelope membrane protein)
	5466	GGAGTAAGGGG	1,00	0,19	Hs.5163	ESTs
10	5467	ATCGCGACACT	1,00	0,19	Hs.4864	KIAA0892 protein
	5468	GCGAAAAAAA	1,00	0,19	Hs.4746	Homo sapiens mRNA; cDNA DKFZp761M16121 (from clone D
	5469	TGTGCTGAGAG	1,00	0,19	Hs.284136	PRO2047 protein
	5470	CTTTTAGGCCT	1,00	0,19	Hs.23202	ESTs
15	5471	CCTGTACTCCC	1,00	0,19	Hs.229434	EST
	5472	CACTCACACAA	1,00	0,19	Hs.2280	ribophorin I
	5473	TGTATTCAGCA	1,00	0,19	Hs.21765	hypothetical protein of unknown function
20	5474	TGGGAAACCTG	1,00	0,19	Hs.211568	eukaryotic translation initiation factor 4 gamma, 1
	5475	ATGCTGCCAAA	1,00	0,19	Hs.210749	proline synthetase co-transcribed (bacterial homolog
	5476	CCAGCAGCTTC	1,00	0,19	Hs.200317	KIAA1404 protein
25	5477	AGACAGTAATA	1,00	0,19	Hs.127610	acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain
	5478	TATTTCAAGTA	1,00	0,19	Hs.12373	adenylate cyclase 6
	5479	TGGCTAGATTT	1,00	0,19	Hs.11463	UMP-CMP kinase
30	5480	CACTCTGGAAT	1,00	0,19	Hs.110707	H326
	5481	CTGCCCTAGTA	1,00	0,19	Hs.106730	chromosome 22 open reading frame 3
	5482	AAGCTGAGTGG	7,00	0,83	Hs.79024	heterogeneous nuclear ribonucleoprotein M
35	5483	TTGCTGGAGAA	4,00	0,59	Hs.197114	RNA binding protein; AT-rich element binding factor
	5484	GCAGCTAATTT	3,00	0,49	Hs.8207	GK001 protein
	5485	AGAGCAAGTAC	3,00	0,49	Hs.78050	small acidic protein
40	5486	CTTGATTAAAC	2,00	0,36	Hs.284265	Homo sapiens pRGR1 mRNA, partial cds
	5487	GCCCCGAAGCT	2,00	0,36	Hs.278675	bromodomain-containing 4
	5488	TGAAAGTAACA	2,00	0,36	Hs.256583	interleukin enhancer binding factor 3, 90kD
45	5489	ACATCATCGAT	57,00	3,51	Hs.182979	ribosomal protein L12
	5490	TTTACAAAGAG	5,00	0,68	Hs.75360	carboxypeptidase E
	5491	AAGCCCAGGCT	3,00	0,49	Hs.19610	DKFZP564N1362 protein
50	5492	ATCCACATCGC	8,00	0,92	Hs.119503	HSPC025
	5493	ACTGGCTGCTG	5,00	0,69	Hs.74649	cytochrome c oxidase subunit VIc
	5494	TGTGTGTTTGT	5,00	0,69	Hs.226117	H1 histone family, member 0
	5495	TTCCCCTTCCT	2,00	0,37	Hs.75730	signal recognition particle receptor ('docking prote
55	5496	GGGGAAGGGCA	2,00	0,37	Hs.65377	ESTs
	5497	CCCTGAATCCC	2,00	0,37	Hs.184592	Human clone A9A2BRB5 (CAC)n/(GTG)n repeat-containing
60	5498	AATGAACAATA	2,00	0,37	Hs.11342	ninjurin 1
	5499	GTTTGGCAGTG	6,00	0,78	Hs.283690	hypothetical protein
	5500	GAGGCCTCAGC	3,00	0,50	Hs.11184	hypothetical protein FLJ20419



5501	TTCTGGCTGCG	7,00	0,86	Hs.119251	ubiquinol-cytochrome c reductase core protein I	
5502	TGGTACACGTA	11,00	1,15	Hs.279574	CGI-39 protein	
5503	GAGGGCCGGTG	6,00	0,78	Hs.36727	hypothetical protein FLJ10903	5
5504	GAAAAAATAAA	1,00	0,19	Hs.94925	dihydroorotate dehydrogenase	
5505	GTTGTAAATAA	1,00	0,19	Hs.92033	Homo sapiens cDNA FLJ10181 fis, clone HEMBA1004227,	
5506	AGGTGCCTCGG	1,00	0,19	Hs.84285	ubiquitin-conjugating enzyme E2I (homologous to yeas	10
5507	CTTTCCTTTTC	1,00	0,19	Hs.80658	uncoupling protein 2 (mitochondrial, proton carrier)	
5508	ATTTTTGCCCT	1,00	0,19	Hs.79372	retinoid X receptor, beta	15
5509	TTCCACCAACC	1,00	0,19	Hs.75618	RAB11A, member RAS oncogene family	
5510	TAGGAGATTTT	1,00	0,19	Hs.74597	stromal interaction molecule 1	
5511	TGGAAGAATGG	1,00	0,19	Hs.6774	ESTs	
5512	TTCATTATAGG	1,00	0,19	Hs.6315	acetylserotonin O-methyltransferase-like	20
5513	GGCCTGTGTGA	1,00	0,19	Hs.4973	hypothetical protein	
5514	AACTAACATTT	1,00	0,19	Hs.3297	ribosomal protein S27a	
5515	CTGTATTAAAA	1,00	0,19	Hs.28264	Homo sapiens mRNA; cDNA DKFZp564L0822 (from clone DK	25
5516	TTGCTATGAAA	1,00	0,19	Hs.26549	ESTs	
5517	TTACTCTTTCT	1,00	0,19	Hs.2533	aldehyde dehydrogenase 9 (gamma-aminobutyraldehyde d	
5518	ACTTATGTTTA	1,00	0,19	Hs.234896	geminin	30
5519	CTGTTATAGGA	1,00	0,19	Hs.206521	YME1 (S.cerevisiae)-like 1	
5520	ATGGCTCACAC	1,00	0,19	Hs.154879	DiGeorge syndrome critical region gene DGS1	
5521	TTTTCCCACCA	1,00	0,19	Hs.153937	activated p21cdc42Hs kinase	35
5522	TTTCTGAAAAA	1,00	0,19	Hs.109646	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6	
5523	GACCTCACTGT	1,00	0,19	Hs.109047	ESTs, Weakly similar to 2119210A mucin [H.sapiens]	40
5524	GTTTTTTTTTAA	1,00	0,19	Hs.10114	ESTs, Weakly similar to unnamed protein product [H.s	
5525	CTGTCCTTGTG	5,00	0,70	Hs.6101	Human DNA sequence from clone 511E16 on chromosome 6	45
5526	CCACCCCGAAT	15,00	1,41	Hs.74637	testis enhanced gene transcript	
5527	TATGACTTAAT	7,00	0,87	Hs.173737	Homo sapiens mRNA, clone:PO2ST9	
5528	GCCCCAGCGAG	3,00	0,50	Hs.238296	ADP-ribosylation factor binding protein GGA1	50
5529	CTGACCGGTGC	2,00	0,37	Hs.8068	hematopoietic PBX-interacting protein	
5530	TGTGTGCCACT	2,00	0,37	Hs.72925	chromosome 11 open reading frame 13	
5531	AATTGCCACTG	2,00	0,37	Hs.61389	ESTs, Weakly similar to unnamed protein product [H.s	55
5532	ACAAAAAATAA	2,00	0,37	Hs.274387	Homo sapiens mRNA; cDNA DKFZp434A1520 (from clone DK	
5533	TGAATGTCAAG	2,00	0,37	Hs.230767	EST	
5534	TACGAAGTTCT	2,00	0,37	Hs.19105	translocase of inner mitochondrial membrane 17 (yeas	60
5535	CTGAGTCTCCC	9,00	1,03	Hs.77269	guanine nucleotide binding protein (G	

					protein), alph
5	5536	GAGGCGATCAG	4,00	0,61	Hs.30783 hypothetical protein FLJ20850
	5537	GCCCCCACTC	3,00	0,50	Hs.75074 mitogen-activated protein kinase-activated protein k
	5538	CACTCGTGTGA	3,00	0,50	Hs.146409 wingless-type MMTV integration site family, member 4
10	5539	GGAGAAGATGA	3,00	0,50	Hs.132415 prefoldin 2
	5540	TTTGGTCTTTT	3,00	0,50	Hs.109773 hypothetical protein FLJ20625
	5541	GGGGGACGGCT	7,00	0,89	Hs.21346 hypothetical protein LOC58481
	5542	TAGTCCCTCTT	2,00	0,38	Hs.84264 acidic protein rich in leucines
15	5543	TATGCGTTTGG	2,00	0,38	Hs.76611 ESTs
	5544	ATTTTGTGTCA	2,00	0,38	Hs.75056 adaptor-related protein complex 3, delta 1 subunit
	5545	GACTCTGGTGC	12,00	1,26	Hs.2953 ribosomal protein S15a
20	5546	GCAGGTCAGCC	3,00	0,51	Hs.78950 branched chain keto acid dehydrogenase E1, alpha pol
	5547	CAGACTTTTTT	3,00	0,51	Hs.74649 cytochrome c oxidase subunit VIc
	5548	TTCAGTTGCTT	3,00	0,51	Hs.26700 Homo sapiens cDNA FLJ10309 fis, clone NT2RM2000287
25	5549	TAGAAACCAGA	3,00	0,51	Hs.194662 calponin 3, acidic
	5550	ACTCGCTCTGT	3,00	0,51	Hs.11669 laminin, alpha 5
	5551	CTGGGTTAATA	99,00	6,16	Hs.126701 ribosomal protein S19
30	5552	CCGTCCAAGGG	57,00	3,91	Hs.80617 ribosomal protein S16
	5553	GAGTGAAAGAC	2,00	0,38	Hs.5811 hypothetical protein FLJ20467
	5554	GAGCTCCACAG	2,00	0,38	Hs.3407 protein kinase (cAMP-dependent, catalytic) inhibitor
35	5555	AAAGTGGA AAA	2,00	0,38	Hs.203613 ESTs, Weakly similar to ALUB_HUMAN !!!! ALU CLASS B
	5556	AATGGGGGTTA	1,00	0,19	Hs.94308 Homo sapiens cDNA FLJ10447 fis, clone NT2RP1000851
40	5557	CTTTGCTTTTT	1,00	0,19	Hs.84264 acidic protein rich in leucines
	5558	GTACGAATGGC	1,00	0,19	Hs.82065 interleukin 6 signal transducer (gp130, oncostatin M
	5559	TGAAGGTGGAT	1,00	0,19	Hs.7840 calcineurin binding protein 1
45	5560	GAATGAGCAAC	1,00	0,19	Hs.6686 ESTs
	5561	GCTGCAAAGGA	1,00	0,19	Hs.61628 calcium binding atopy-related autoantigen 1
	5562	CTAGATTCCCT	1,00	0,19	Hs.46783 ESTs
50	5563	TCTGTAGGCTG	1,00	0,19	Hs.38694 ESTs
	5564	CAGGGCTCGCG	1,00	0,19	Hs.29288 Homo sapiens mRNA; cDNA DKFZp434P174 (from clone DKF
	5565	CCTGGGTCCTG	1,00	0,19	Hs.285845 Homo sapiens cDNA FLJ20358 fis, clone HEP16618
55	5566	GAGAGGAAACT	1,00	0,19	Hs.275425 hypothetical protein
	5567	TGGTTCTATAT	1,00	0,19	Hs.26213 Human DNA sequence from clone RP3-447F3 on chromosom
60	5568	TGCCTATAGCC	1,00	0,19	Hs.258445 EST
	5569	CACCCTGTACA	1,00	0,19	Hs.25450 solute carrier family 29 (nucleoside transporters),
	5570	AAGGAGAATGG	1,00	0,19	Hs.22119 Homo sapiens cDNA FLJ20318 fis, clone

					HEP08704
5571	CACGACTGTTC	1,00	0,19	Hs.184779	Homo sapiens mRNA; cDNA DKFZp586B1922 (from clon DK
5572	ATTTTCTTTA	1,00	0,19	Hs.182741	TIA1 cytotoxic granule-associated RNA-binding protei
5573	AATGGTTAGCC	1,00	0,19	Hs.103657	hypothetical protein PRO2219
5574	GTGGCATCACC	6,00	0,82	Hs.14317	hypothetical protein Nop10p
5575	AGCACCTCCAG	87,00	5,62	Hs.75309	eukaryotic translation elongation factor 2
5576	CCAAAATTAGG	3,00	0,51	Hs.239737	C-terminal binding protein 1
5577	TTTGTGACTGT	6,00	0,82	Hs.239737	C-terminal binding protein 1
5578	GTGCACTGAGC	23,00	2,01	Hs.181244	major histocompatibility complex, class I, A
5579	CTCAAAAAAAAA	4,00	0,63	Hs.165998	DKFZP564M2423 protein
5580	TTGGGGAAACA	2,00	0,38	Hs.81029	biliverdin reductase A
5581	AGGCTGTGTTC	2,00	0,38	Hs.79	aminoacylase 1
5582	GGGGCTGTGGC	2,00	0,38	Hs.331	general transcription factor IIIC, polypeptide 1 (al
5583	TGTGTGTGTGT	2,00	0,38	Hs.285681	WS basic-helix-loop-helix leucine zipper protein
5584	CTTCTGTCTCC	2,00	0,38	Hs.108824	ESTs, Weakly similar to cDNA EST yk415c12.5 comes fr
5585	AACGTGCAGGG	6,00	0,83	Hs.160786	argininosuccinate synthetase
5586	GATAGTTGTGG	5,00	0,74	Hs.77558	thyroid hormone receptor interactor 7
5587	CAAGGATCTAC	5,00	0,74	Hs.31989	DKFZP586G1722 protein
5588	ATCAAGTTCGA	5,00	0,74	Hs.108082	ESTs, Weakly similar to Ydr472wp [S.cerevisiae]
5589	CAGGGGAGTGG	3,00	0,53	Hs.79396	N-methylpurine-DNA glycosylase
5590	CTCCAATAAAA	3,00	0,53	Hs.278559	talín
5591	CCTTATATTIG	3,00	0,53	Hs.118174	tetratricopeptide repeat domain 3
5592	TTACGATGAAT	2,00	0,39	Hs.6335	phosphatidylinositol-4-phosphate 5-kinase, type II,
5593	CCACACACCGT	2,00	0,39	Hs.4877	CGI-51 protein
5594	GACTAGTGCCT	2,00	0,39	Hs.181551	ESTs
5595	GCAGCTCAGAT	1,00	0,20	Hs.81648	Homo sapiens cDNA FLJ11021 fis, clone PLACE1003704,
5596	ACTCCAGCTGA	1,00	0,20	Hs.7763	vesicle docking protein p115
5597	GTGTCGCATCT	1,00	0,20	Hs.7734	Homo sapiens cDNA FLJ20684 fis, clone KAIA3469
5598	TGGAAAAAAAAA	1,00	0,20	Hs.61255	fructose-1,6-bisphosphatase 2
5599	GTAATTAAAC	1,00	0,20	Hs.57664	Homo sapiens mRNA full length insert cDNA clone EURO
5600	CAGTATCCCAG	1,00	0,20	Hs.4994	transducer of ERBB2, 2
5601	AATCGCTAATA	1,00	0,20	Hs.47986	Homo sapiens mRNA; cDNA DKFZp586H051 (from clone DKF
5602	CCAGTTTGTAT	1,00	0,20	Hs.42331	ephrin-A4
5603	AATAAAATTAG	1,00	0,20	Hs.271980	mitogen-activated protein kinase 6
5604	AGGAGCCTTAG	1,00	0,20	Hs.25059	A kinase (PRKA) anchor protein 8
5605	AATATGGTACA	1,00	0,20	Hs.236774	high-mobility group (nonhistone chromosomal) protein
5606	AATTTACTTCC	1,00	0,20	Hs.1742	IQ motif containing GTPase activating

					protein 1
5607	CCGGTTGGCAA	1,00	0,20	Hs.13740	ESTs
5608	TTTGGAAGAAA	1,00	0,20	Hs.12482	glyceronephosphate O-acyltransferase
5609	GCTCATTAAAG	1,00	0,20	Hs.112237	ESTs
5610	TCCACGCACCA	4,00	0,64	Hs.82023	hypothetical protein similar to mouse Fbw5
5611	ACTTACCTGCT	19,00	1,84	Hs.174031	cytochrome c oxidase subunit VIb
5612	TCTGCTTACAG	7,00	0,94	Hs.74267	ribosomal protein L15
5613	ATGACTCAAGG	5,00	0,76	Hs.239752	nuclear receptor subfamily 2, group F, member 6
5614	GATGAACACTG	2,00	0,39	Hs.32826	CGI-130 protein
5615	TCGCCCAGGCG	2,00	0,39	Hs.26870	ESTs
5616	ACAAGAATTGT	3,00	0,54	Hs.80919	synaptophysin-like protein
5617	TACCCACCCCT	9,00	1,13	Hs.7647	MYC-associated zinc finger protein (purine-binding t
5618	AGCCTGCAGAA	6,00	0,87	Hs.10927	hypothetical protein R33729_1
5619	GGATTCCAGTT	3,00	0,54	Hs.5321	ARP3 (actin-related protein 3, yeast) homolog
5620	GGAGTCTAACT	3,00	0,54	Hs.240170	ESTs, Moderately similar to alternatively spliced pr
5621	GGAGTGTGCGT	2,00	0,40	Hs.4944	ESTs, Weakly similar to AIF1_HUMAN ALLOGRAFT INFLAMM
5622	GAAATCCGCAC	2,00	0,40	Hs.279854	mannosidase, alpha, class 2B, member 1
5623	TCTGTAACACC	2,00	0,40	Hs.260622	butyrate-induced transcript 1
5624	TTCTGGCACTG	2,00	0,40	Hs.20237	DKFZP566C134 protein
5625	GGCTCAAAACT	1,00	0,20	Hs.90625	Human DNA sequence from clone 475B7 on chromosome Xq
5626	GTGGCCCCGGC	1,00	0,20	Hs.77575	ESTs
5627	TCTCTGCCTCT	1,00	0,20	Hs.77365	hypothetical protein FLJ11000
5628	TTCTGTAGCCC	1,00	0,20	Hs.5541	ATPase, Ca++ transporting, ubiquitous
5629	AATGGAGACTT	1,00	0,20	Hs.2943	signal recognition particle 19kD
5630	GAGGGCCTTCA	1,00	0,20	Hs.284233	NICE-5 protein
5631	GTGAGGCCCCG	1,00	0,20	Hs.272193	Homo sapiens cDNA FLJ20149 fis, clone COL08213
5632	TACCCACAGAG	1,00	0,20	Hs.26209	ESTs
5633	TTACCGTCCCC	1,00	0,20	Hs.25601	chromodomain helicase DNA binding protein 3
5634	GGAAGATGATG	1,00	0,20	Hs.19762	ESTs, Weakly similar to unknown [D.melanogaster]
5635	GAGGGAAATGG	1,00	0,20	Hs.12862	radical fringe (Drosophila) homolog
5636	AAGCTGTGTCT	1,00	0,20	Hs.108332	ubiquitin-conjugating enzyme E2D 2 (homologous to ye
5637	CACAGGGCCAT	1,00	0,20	Hs.107812	ESTs, Weakly similar to PSF_HUMAN PTB-ASSOCIATED SPL
5638	GTAGATGCAAG	1,00	0,20	Hs.101047	transcription factor 3 (E2A immunoglobulin enhancer
5639	TCAGCGGAGAA	1,00	0,20	Hs.100469	myeloid/lymphoid or mixed-lineage leukemia (trithora
5640	GTGACTGCCAC	5,00	0,78	Hs.84183	diphtheria toxin resistance protein re-

					quired for diph
5641	GGCCTGCTGCT	10,00	1,24	Hs.9634	ESTs, Highly similar to C10 [H.sapiens]
5642	AAGGAAGCAAT	4,00	0,67	Hs.194703	adaptor-related protein complex 4, mu 1 subunit
5643	AAATGCCACAC	8,00	1,07	Hs.65450	reticulon 4
5644	TGTGTTGAGAG	150,00	10,78	Hs.275221	hypothetical protein FLJ20061
5645	CTGCTGAGTGA	6,00	0,89	Hs.79259	hypothetical protein
5646	CCTGCTCCCTG	4,00	0,67	Hs.184601	solute carrier family 7 (cationic amino acid transpo
5647	GTAGAAAAGAA	2,00	0,40	Hs.75056	adaptor-related protein complex 3, delta 1 subunit
5648	AGCCTGTTGCA	2,00	0,40	Hs.182885	ESTs, Weakly similar to M03F8.2 [C.elegans]
5649	TGGAGGTGGGG	2,00	0,40	Hs.182625	VAMP (vesicle-associated membrane protein)-associate
5650	TGGCCCTCCAG	2,00	0,40	Hs.181015	signal transducer and activator of transcription 6,
5651	CCGTTCTGGAT	2,00	0,40	Hs.173638	Homo sapiens partial TCF-4 gene for T-cell transcrip
5652	GTGTTGGGGGT	3,00	0,55	Hs.55016	ESTs
5653	TGATGTTTGAC	5,00	0,79	Hs.75416	DAZ associated protein 2
5654	TCACAAGCAAA	23,00	2,31	Hs.146763	nascent-polypeptide-associated complex alpha polypep
5655	TCAGAGAATAA	2,00	0,41	Hs.99486	ESTs
5656	CATCCCGTGAC	2,00	0,41	Hs.81118	leukotriene A4 hydrolase
5657	TTAAGACTTCA	2,00	0,41	Hs.80562	gelsolin (amyloidosis, Finnish type)
5658	ACTTGCGAATA	2,00	0,41	Hs.77735	fibrogenic lymphokine
5659	TCTGGGGAAAT	1,00	0,21	Hs.87417	cathepsin L2
5660	GTGTACCGGAT	1,00	0,21	Hs.8517	pleckstrin homology, Sec7 and coiled/coiled domains 2
5661	ACGCTCATCGT	1,00	0,21	Hs.81217	frizzled (Drosophila) homolog 2
5662	TTCTTTTTTAC	1,00	0,21	Hs.75682	autoantigen
5663	ATGCAGAGATT	1,00	0,21	Hs.7137	clones 23667 and 23775 zinc finger protein
5664	TCACAACTTC	1,00	0,21	Hs.61828	amyloid beta precursor protein-binding protein 1, 59
5665	AGACTATATTT	1,00	0,21	Hs.56542	X-prolyl aminopeptidase (aminopeptidase P) 1, solubl
5666	CCTGAAAAGCT	1,00	0,21	Hs.3964	Homo sapiens clone 24877 mRNA sequence
5667	TTTCTGTTTTA	1,00	0,21	Hs.31189	ESTs, Weakly similar to ALU2_HUMAN ALU SUBFAMILY SB
5668	TTTCTTTTTGA	1,00	0,21	Hs.286236	eukaryotic translation initiation factor 5
5669	TTGTTGGTCAA	1,00	0,21	Hs.285950	ESTs
5670	GGAGCCAGCTG	1,00	0,21	Hs.279894	PRO1659 protein
5671	CAGAAGTGTC	1,00	0,21	Hs.278441	KIAA0015 gene product
5672	ATGGGGAGAGA	1,00	0,21	Hs.24989	ESTs
5673	GCGTGACTTCT	1,00	0,21	Hs.22897	ESTs, Weakly similar to AF161483_1 HSPC134 [H.sapien
5674	CAAAAGCTTAT	1,00	0,21	Hs.21941	ADQ21 protein

5	5675	GCTTCGTGCTG	1,00	0,21	Hs.208912	Novel human gene mapping to chromosome 22
	5676	AAAGTGGCTAC	1,00	0,21	Hs.183868	glucuronidase, beta
	5677	GCTAGTGAAAT	1,00	0,21	Hs.181406	endothelin converting enzyme 1
	5678	CTAAACTTTTT	1,00	0,21	Hs.180919	inhibitor of DNA binding 2, dominant negative helix-
10	5679	CCTGTAACCCT	1,00	0,21	Hs.151777	Human translation initiation factor eIF-2alpha mRNA,
	5680	CCTCCAGCCCC	1,00	0,21	Hs.146428	collagen, type V, alpha 1
	5681	CTGTCTGTTCT	1,00	0,21	Hs.101174	microtubule-associated protein tau
15	5682	TGGGCAAAGCC	58,00	4,85	Hs.2186	eukaryotic translation elongation factor 1 gamma
	5683	TGCGGCTGGTT	3,00	0,56	Hs.74617	dynactin 1 (p150, Glued (Drosophila) homolog)
20	5684	AAGTGGGTGCC	6,00	0,92	Hs.119475	cold inducible RNA-binding protein
	5685	TGCCCAGGATT	2,00	0,41	Hs.91448	MKP-1 like protein tyrosine phosphatase
	5686	TCTGTATCCCC	2,00	0,41	Hs.724	thyroid hormone receptor, alpha (avian erythroblasti
25	5687	GCTTAACCTGG	7,00	1,03	Hs.77508	glutamate dehydrogenase 1
	5688	GTATTCCCCTT	7,00	1,03	Hs.117176	poly(A)-binding protein, nuclear 1
	5689	CTTGAGCAATA	6,00	0,93	Hs.848	FK506-binding protein 4 (59kD)
	5690	GTGATCATTA	1,00	0,21	Hs.8949	ESTs, Weakly similar to AF126780_1 retinal short-cha
30	5691	AAAATCTGCCA	1,00	0,21	Hs.878	sorbitol dehydrogenase
	5692	GATGGAGCCCT	1,00	0,21	Hs.74649	cytochrome c oxidase subunit VIc
	5693	CTCAGGAAGCT	1,00	0,21	Hs.7019	signal-induced proliferation-associated gene 1
35	5694	GCTTTGTATCC	1,00	0,21	Hs.286078	E2k
	5695	ACCAGGTCCAC	1,00	0,21	Hs.285445	solute carrier family 5 (sodium-dependent vitamin tr
40	5696	CTGGCCGACTT	1,00	0,21	Hs.274149	proline and glutamic acid rich nuclear protein
	5697	GGGAACGGAGG	1,00	0,21	Hs.267831	Rho GTPase activating protein 5
	5698	AATGGATTATT	1,00	0,21	Hs.247452	FabG (beta-ketoacyl-[acyl-carrier-protein] reductase
45	5699	AAGATAAACTC	1,00	0,21	Hs.19015	ESTs, Weakly similar to NR54_HUMAN 54 KDA NUCLEAR RN
	5700	TGGCTGGCCAC	1,00	0,21	Hs.174142	colony stimulating factor 1 receptor, formerly McDon
50	5701	CTTGTGATCCC	1,00	0,21	Hs.173042	KIAA1143 protein
	5702	GTAAAAA	1,00	0,21	Hs.135183	centaurin-alpha
	5703	TGGGGCCGCAG	1,00	0,21	Hs.126759	ESTs
	5704	TCTTTTGGGG	1,00	0,21	Hs.120854	ESTs
55	5705	CTTTTGTTTC	1,00	0,21	Hs.108319	thyroid hormone receptor-associated protein, 150 kDa
	5706	CATAGTTTATAG	1,00	0,21	Hs.106823	H.sapiens gene from PAC 42616, similar to syntaxin 7
60	5707	GCTGATTGGCA	1,00	0,21	Hs.104476	ESTs
	5708	TGGTTGCGACA	1,00	0,21	Hs.101408	branched chain aminotransferase 2, mitochondrial

5709	TTACTAAATGG	6,00	0,94	Hs.155560	calnexin
5710	TACTAATAAAA	5,00	0,83	Hs.11565	ESTs, Weakly similar to F15D4.3 [C.elegans]
5711	CCTTCTGGTGG	3,00	0,58	Hs.82643	protein tyrosine kinase 9
5712	ATGACACTCAC	4,00	0,71	Hs.82306	destrin (actin depolymerizing factor)
5713	GCTCCCAGACT	7,00	1,06	Hs.5097	synaptogyrin 2
5714	GGAAGGGAGGC	6,00	0,95	Hs.279581	hypothetical protein FLJ20568
5715	TAACCCAGCAG	3,00	0,58	Hs.7043	succinate-CoA ligase, GDP-forming, alpha subunit
5716	TAAAAAAAAA	17,00	2,01	Hs.98658	budding uninhibited by benzimidazoles 1 (yeast homol
5717	TTTTGTAAATA	2,00	0,43	Hs.75607	myristoylated alanine-rich protein kinase C substrat
5718	GGCATTGTTCA	2,00	0,43	Hs.3128	polymerase (RNA) II (DNA directed) polypeptide H
5719	TTGGGTTTTGA	2,00	0,43	Hs.261239	ESTs, Moderately similar to ALU8 HUMAN ALU SUBFAMILY
5720	CCTGGATAAAT	2,00	0,43	Hs.181634	Human Chromosome 16 BAC clone CIT987SK-A-61E3
5721	GGCAATATGGT	2,00	0,43	Hs.160823	ESTs
5722	GAAAAGAGATT	1,00	0,22	Hs.92145	ESTs
5723	TCTGTTAATAA	1,00	0,22	Hs.89434	drebrin 1
5724	TACATTCACCT	1,00	0,22	Hs.82043	D123 gene product
5725	GTTCTCCCTTC	1,00	0,22	Hs.49657	Homo sapiens mRNA; cDNA DKFZp547N084 (from clone DKF
5726	CTGTGCTCTAA	1,00	0,22	Hs.42500	ADP-ribosylation factor-like 5
5727	TGGGCTGGGGT	1,00	0,22	Hs.3416	adipose differentiation-related protein
5728	GAAGAACAAGT	1,00	0,22	Hs.28491	spermidine/spermine N1-acetyltransferase
5729	GGAAGATGTTC	1,00	0,22	Hs.284158	Homo sapiens mRNA; cDNA DKFZp762B195 (from clone DKF
5730	TTAATAAAATA	1,00	0,22	Hs.2707	G1 to S phase transition 1
5731	ACCTTGGGCAA	1,00	0,22	Hs.19554	chromosome 1 open reading frame 2
5732	TGTACCTAACT	1,00	0,22	Hs.18272	ESTs
5733	TGGCTTATTAA	1,00	0,22	Hs.18021	hypothetical protein FLJ20446
5734	TTGTGATACTA	1,00	0,22	Hs.175417	ESTs
5735	GGCTTTCCCTG	1,00	0,22	Hs.171802	ESTs, Weakly similar to hypothetical protein [H.sapi
5736	TGTTTAATACA	1,00	0,22	Hs.143601	Homo sapiens cDNA FLJ20678 fis, clone KAIA4163
5737	CACCACCACAC	1,00	0,22	Hs.123319	EST, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE
5738	GGGAGCATTAA	1,00	0,22	Hs.117582	CGI-43 protein
5739	GGGAGGAGGGT	1,00	0,22	Hs.112159	ESTs
5740	TGGACCCCCCG	3,00	0,59	Hs.173501	ESTs, Moderately similar to AF151825_1 CGI-67 protei
5741	GTA CTGTATGC	4,00	0,73	Hs.180446	karyopherin (importin) beta 1
5742	GTGTGTTTGTA	19,00	2,26	Hs.118787	transforming growth factor, beta-induced, 68kD
5743	CGCAGTGCCT	13,00	1,70	Hs.76159	ATPase, H+ transporting, lysosomal

					(vacuolar proton
5	5744	AGTGCCGTGTG	2,00	0,43	Hs.76391 myxovirus (influenza) resistance 1, homolog of murin
	5745	GCCTGAGGGGC	2,00	0,43	Hs.14927 ESTs, Moderately similar to TNRC_HUMAN LYMPHOTOXIN-B
	5746	TCTCAATTCTT	5,00	0,86	Hs.146409 wingless-type MMTV integration site family, member 4
10	5747	TTCATTATAAT	9,00	1,32	Hs.250655 prothymosin, alpha (gene sequence 28)
	5748	GATGAGTCTCG	10,00	1,43	Hs.233952 proteasome (prosome, macropain) subunit, alpha type,
15	5749	ATGGAAAGGAA	2,00	0,44	Hs.243901 Homo sapiens cDNA FLJ20738 fis, clone HEP08257
	5750	TGCTGCTTGAA	2,00	0,44	Hs.12152 APMCF1 protein
	5751	TGTTAGCCTGT	1,00	0,22	Hs.92384 vitamin A responsive; cytoskeleton related
20	5752	TTTTCTGAGTG	1,00	0,22	Hs.82238 POP4 (processing of precursor, S. cerevisiae) homol
	5753	ACCAAAGTGTG	1,00	0,22	Hs.77608 splicing factor, arginine/serine-rich 9
25	5754	TGAATACTACT	1,00	0,22	Hs.76507 LPS-induced TNF-alpha factor
	5755	TCAAGTCCAGA	1,00	0,22	Hs.75867 solute carrier family 20 (phosphate transporter), me
	5756	TGTACTTCCTA	1,00	0,22	Hs.75485 ornithine aminotransferase (gyrate atrophy)
30	5757	GAGGCAGAAGA	1,00	0,22	Hs.6179 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17 (72k
	5758	TGCCTATAGTC	1,00	0,22	Hs.55158 ESTs, Weakly similar to weak similarity to TPR domai
35	5759	GAAAGATTGGA	1,00	0,22	Hs.5076 sorting nexin 12
	5760	GTCTTCTTAAT	1,00	0,22	Hs.279884 DNAJ domain-containing
	5761	GAAGGCACCAT	1,00	0,22	Hs.26706 CGI-121 protein
	5762	AATGGCACTTA	1,00	0,22	Hs.26023 KIAA1041 protein
40	5763	GATGAGCGGCT	1,00	0,22	Hs.227637 chromosome 22 open reading frame 2
	5764	TGACTGCTGCT	1,00	0,22	Hs.214372 ESTs
	5765	GCCCAGGGACC	1,00	0,22	Hs.205421 EST
	5766	TAAATGTCCTG	1,00	0,22	Hs.193331 ESTs
45	5767	GAGAATCTGAT	1,00	0,22	Hs.184352 ESTs, Weakly similar to cDNA EST EMBL:D36107 comes f
	5768	TGTTTTGGAAC	1,00	0,22	Hs.176657 RAN binding protein 3
	5769	TGTAAGTTTTG	1,00	0,22	Hs.161554 hypothetical protein FLJ20159
50	5770	TTGTAGCTCAA	1,00	0,22	Hs.159384 KIAA0138 gene product
	5771	TGGTCAAGGTG	1,00	0,22	Hs.13996 ESTs
	5772	TATGTGCCACT	1,00	0,22	Hs.122579 hypothetical protein FLJ10461
	5773	TATGCCCTATC	1,00	0,22	Hs.115740 KIAA0210 gene product
55	5774	ACTGCTGTCTA	1,00	0,22	Hs.10724 Homo sapiens HDCMD11P mRNA, partial cds
	5775	AATCTGGTTGC	1,00	0,22	Hs.103804 heterogeneous nuclear ribonucleoprotein U (scaffold
60	5776	AGGAAAGCTGC	54,00	5,44	Hs.76437 ribosomal protein L36
	5777	ACAGTGCTTGC	5,00	0,88	Hs.80350 protein phosphatase 2 (formerly 2A), catalytic subun



5778	GCCCCCCCCGTG	3,00	0,61	Hs.85573	Homo sapiens mRNA; cDNA DKFZp566N034 (from clone DKF
5779	GAGCGGCCTCT	3,00	0,61	Hs.77868	ORF
5780	ACATCGTAGGG	3,00	0,61	Hs.108408	CGI-78 protein
5781	CAAGGGTAAGA	7,00	1,13	Hs.76224	EGF-containing fibulin-like extracellular matrix pro
5782	TTGTAATCGTG	21,00	2,55	Hs.125078	ornithine decarboxylase antizyme 1
5783	GCAAAAAAAAAA	19,00	2,37	Hs.76293	thymosin, beta 10
5784	GGGTGTGTATT	2,00	0,45	Hs.83347	angio-associated, migratory cell protein
5785	ATACTGCTGCT	2,00	0,45	Hs.82919	cullin 2
5786	ACCATAATGTG	2,00	0,45	Hs.821	zinc finger protein homologous to Zfp92 in mouse
5787	GACTTGGAGGC	2,00	0,45	Hs.77783	membrane-associated tyrosine- and threonine-specific
5788	GACAGACATCA	2,00	0,45	Hs.7517	Homo sapiens mRNA; cDNA DKFZp434O1230 (from clone DK
5789	CAGGTTGACAG	2,00	0,45	Hs.69235	transportin-SR
5790	GTGCATCCCGA	4,00	0,76	Hs.165843	casein kinase 2, beta polypeptide
5791	TTTTTAATGTT	7,00	1,14	Hs.181307	H3 histone, family 3A
5792	TCTATAGAGTT	2,00	0,45	Hs.7351	cyclic AMP phosphoprotein, 19 kD
5793	TTTATTGAAAA	2,00	0,45	Hs.43910	CD164 antigen, sialomucin
5794	CGATCAGTTTG	2,00	0,45	Hs.34906	ESTs
5795	CTGGGAGGAGG	2,00	0,45	Hs.26518	transmembrane 4 superfamily member 7
5796	CTGGTTTCTCC	2,00	0,45	Hs.258503	p53 inducible protein
5797	CCTAGGACCTG	2,00	0,45	Hs.149570	actin related protein 2/3 complex, subunit 4 (20 kD)
5798	AAGGCCACCGG	2,00	0,45	Hs.1384	O-6-methylguanine-DNA methyltransferase
5799	TAAAGTGTCTG	2,00	0,45	Hs.132875	Homo sapiens HSPC309 mRNA, partial cds
5800	TTTAGGGGGAA	2,00	0,45	Hs.108319	thyroid hormone receptor-associated protein, 150 kDa
5801	TACAATTGTGA	2,00	0,45	Hs.107260	hypothetical protein DKFZp586H0623
5802	GACTGCGTGCC	3,00	0,62	Hs.3760	KIAA0948 protein
5803	CGTGGGGTGCC	4,00	0,77	Hs.92679	ESTs, Weakly similar to microtubule-based motor [H.s
5804	AGCTTGGACAG	1,00	0,23	Hs.92700	DKFZP564O243 protein
5805	TATGTTGAGAA	1,00	0,23	Hs.6241	phosphoinositide-3-kinase, regulatory subunit, polyp
5806	CTACAATAAAT	1,00	0,23	Hs.57100	ESTs
5807	TATCCTGGTAA	1,00	0,23	Hs.284291	sorting nexin 6
5808	CAAATAAACTT	1,00	0,23	Hs.25978	ESTs
5809	CTGCCCTGGGA	1,00	0,23	Hs.252259	ribosomal protein S3
5810	CCAGAAAGAAT	1,00	0,23	Hs.245188	tissue inhibitor of metalloproteinase 3 (Sorsby fund
5811	ATCTCTTTCCC	1,00	0,23	Hs.241521	ESTs, Highly similar to serine protease [H.sapiens]
5812	TCTGTTATTGG	1,00	0,23	Hs.182698	hypothetical protein FLJ10024
5813	GAGCACATCAG	1,00	0,23	Hs.173497	Sec23 (S. cerevisiae) homolog B
5814	CCATCCAGTGA	1,00	0,23	Hs.155140	casein kinas 2, alpha 1 polypeptide

5815	GCCGGCCCGGC	1,00	0,23	Hs.133230	ribosomal protein S15
5816	CAAACCATCCG	1,00	0,23	Hs.125170	ESTs
5817	TTCTCTACACA	5,00	0,91	Hs.114360	transforming growth factor beta-stimulated protein T
5818	GAGGGTGGCGC	3,00	0,63	Hs.81687	non-metastatic cells 3, protein expressed in
5819	TTGTCCAGAGG	3,00	0,63	Hs.14839	polymerase (RNA) II (DNA directed) polypeptide G
5820	CTTGTAATCCT	7,00	1,16	Hs.265827	interferon, alpha-inducible protein (clone IFI-6-16)
5821	GGCTGATTTT	2,00	0,46	Hs.81361	heterogeneous nuclear ribonucleoprotein A/B
5822	TGCTCTGTGTA	2,00	0,46	Hs.70186	suppressor of Ty (S.cerevisiae) 5 homolog
5823	TATGTAATATG	2,00	0,46	Hs.41569	phosphatidic acid phosphatase type 2A
5824	CCACAACCTGG	2,00	0,46	Hs.101742	Human DNA sequence from clone 321D2 on chromosome 16
5825	GAAAAATGGTT	49,00	5,38	Hs.283106	hemoglobin, gamma A
5826	ACGGAACAATA	8,00	1,29	Hs.8272	prostaglandin D2 synthase (21kD, brain)
5827	TAAAAGACAAA	3,00	0,63	Hs.77196	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)
5828	CTCAACATCTC	44,00	4,98	Hs.73742	ribosomal protein, large, P0
5829	CAATCACAAAA	2,00	0,46	Hs.76288	calpain 2, (m/II) large subunit
5830	AATGCAAGATA	2,00	0,46	Hs.182643	transcription elongation factor B (SIII), polypeptid
5831	CCCCTCCCCAG	2,00	0,46	Hs.150540	Homo sapiens chromosome 22q13 BAC clone CIT987SK-384
5832	AGCTCTCCCTG	48,00	5,42	Hs.82202	ribosomal protein L17
5833	GATGTCTCTAG	3,00	0,64	Hs.74368	transmembrane protein (63kD), endoplasmic reticulum/
5834	AATAAAGTTGT	4,00	0,79	Hs.117176	poly(A)-binding protein, nuclear 1
5835	TGGCCAAAAAA	1,00	0,24	Hs.95044	ESTs
5836	AATAGCTGATT	1,00	0,24	Hs.90011	adenylosuccinate synthase
5837	CCCGGCCTTAA	1,00	0,24	Hs.81907	ESTs, Moderately similar to ALU4 HUMAN ALU SUBFAMILY
5838	GAGGAAGGCTC	1,00	0,24	Hs.78771	phosphoglycerate kinase 1
5839	CTATTTAGGGA	1,00	0,24	Hs.7736	hypothetical protein
5840	CTAGCAGAGCA	1,00	0,24	Hs.4747	dyskeratosis congenita 1, dyskerin
5841	GCCTGTGGGTT	1,00	0,24	Hs.43549	uncharacterized hematopoietic stem/progenitor cells
5842	TTTTGGATGTA	1,00	0,24	Hs.286047	Homo sapiens ubiquitin-conjugating enzyme variant Ku
5843	ACCGGGGTGAA	1,00	0,24	Hs.182874	guanine nucleotide binding protein (G protein) alpha
5844	GCCCCGGAGCC	1,00	0,24	Hs.17528	amyloid beta (A4) precursor protein-binding, family
5845	AAGACAGAGCA	1,00	0,24	Hs.169854	ESTs, Weakly similar to hypothetical protein [H.sapi
5846	GGGCAGAATAT	1,00	0,24	Hs.168670	peroxisomal farnesylated protein
5847	TGATCGCGGCT	1,00	0,24	Hs.135906	ESTs
5848	GACAATGCCAG	5,00	0,93	Hs.155433	ATP synthase, H+ transporting, mito-

					chondrial F1 comp
5849	AGACAAGCTGG	4,00	0,80	Hs.166975	splicing factor, arginine/serine-rich 5
5850	GCTGGTGCCTG	4,00	0,80	Hs.125359	Thy-1 cell surface antigen
5851	GCTAAAAAAA	3,00	0,64	Hs.256697	histidine triad nucleotide-binding protein
5852	TACTAAAAAAG	3,00	0,64	Hs.173611	NADH dehydrogenase (ubiquinone) Fe-S protein 2 (49kD)
5853	CTGGGTCTCCA	4,00	0,80	Hs.180842	ribosomal protein L13
5854	GTATTTAACAT	2,00	0,47	Hs.9006	VAMP (vesicle-associated membrane protein)-associate
5855	GAAAAAATGTT	2,00	0,47	Hs.194329	ESTs, Weakly similar to AF125535_1 pp21 homolog [H.s]
5856	GGGGGGTGGAG	2,00	0,47	Hs.189583	putative protein similar to nessy (Drosophila)
5857	TCAAGAAATTA	2,00	0,47	Hs.152978	proteasome (prosome, macropain) activator subunit 3
5858	GAATCCGATTT	2,00	0,47	Hs.151536	RAB13, member RAS oncogene family
5859	GCCGCTTCTAG	3,00	0,65	Hs.75813	polycystic kidney disease 1 (autosomal dominant)
5860	AGCGTGTGATG	2,00	0,47	Hs.74649	cytochrome c oxidase subunit VIc
5861	GAGGGACTTGG	2,00	0,47	Hs.32246	ESTs, Weakly similar to AF123303_1 calcium-binding t
5862	CAAGCAAATA	2,00	0,47	Hs.116449	ESTs
5863	AGGAGCAAAGG	5,00	0,96	Hs.76289	biliverdin reductase B (flavin reductase (NADPH))
5864	GCCCTGACCTT	1,00	0,24	Hs.97871	ESTs, Moderately similar to hypothetical protein [H.
5865	AGTAAACTTC	1,00	0,24	Hs.9552	binders of Arl Two
5866	TCTAAAGAATG	1,00	0,24	Hs.92918	hypothetical protein
5867	TATCTTCTAAG	1,00	0,24	Hs.82314	hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyha
5868	GTTCTATTTAA	1,00	0,24	Hs.8033	hypothetical protein FLJ11164
5869	CCAGGCACTGT	1,00	0,24	Hs.74649	cytochrome c oxidase subunit VIc
5870	GCTGCCTGCCT	1,00	0,24	Hs.71962	ESTs
5871	CTAAAACTGGT	1,00	0,24	Hs.69993	ESTs
5872	AACCTGGCCTC	1,00	0,24	Hs.6780	protein tyrosine kinase 9-like (A6-related protein)
5873	TACACCAAGAA	1,00	0,24	Hs.6449	hypothetical protein FLJ20542
5874	GAGCTGCAGGG	1,00	0,24	Hs.6294	hypothetical protein DKFZp434L1435 similar to valyl
5875	TGTATATGGTG	1,00	0,24	Hs.279849	KIAA0438 gene product
5876	CTTGAGTCACA	1,00	0,24	Hs.261023	Human DNA sequence from clone RP3-500L14 on chromoso
5877	CTTTGTTTTGC	1,00	0,24	Hs.2271	endothelin 1
5878	GATTTAAAAAA	1,00	0,24	Hs.187991	DKFZP564A122 protein
5879	TGATGATGTTG	1,00	0,24	Hs.11050	F-box only protein 9
5880	CTGGCTCCATC	1,00	0,24	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-binding)
5881	CTCACACATTA	5,00	0,97	Hs.150101	lysosomal-associated membrane protein 1
5882	GGGCCAGGGGA	5,00	0,97	Hs.111099	ESTs, Weakly similar to alpha-1 type I

					collagen [H.s	
	5883	GGCCCGGCTTT	2,00	0,48	Hs.283639	ESTs
5	5884	TGAGGCAGGGA	2,00	0,48	Hs.154546	syntaxin 5A
	5885	GGCAAGAAGAA	27,00	3,59	Hs.111611	ribosomal protein L27
	5886	CATCTAAACTG	7,00	1,25	Hs.180900	Williams-Beuren syndrome chromosome region 1
10	5887	TGTTTCATCATC	6,00	1,12	Hs.65450	reticulon 4
	5888	CAGCAGAAGCA	14,00	2,14	Hs.283975	small EDRK-rich factor 2
	5889	TTGAATTCCCC	6,00	1,13	Hs.171921	sema domain, immunoglobulin domain (Ig), short basic
15	5890	ACAGTCTTGCC	2,00	0,48	Hs.77665	KIAA0102 gene product
	5891	AGCACTTTTGC	2,00	0,48	Hs.103419	fasciculation and elongation protein zeta 2 (zygin I)
	5892	GAGCAGCGCCC	7,00	1,27	Hs.112408	S100 calcium-binding protein A7 (psoriasin 1)
20	5893	AGTTTGGGCTG	1,00	0,25	Hs.9911	ESTs
	5894	GTGTTGAGAGA	1,00	0,25	Hs.77502	methionine adenosyltransferase II, alpha
	5895	CCCCTGCTGCT	1,00	0,25	Hs.6272	Homo sapiens mRNA; cDNA DKFZp761P0114 (from clone DK
25	5896	GCCTGTTTGTA	1,00	0,25	Hs.5613	Homo sapiens mRNA; cDNA DKFZp564E2222 (from clone DK
	5897	TACGCTTGGTC	1,00	0,25	Hs.284271	cytochrome b5 reductase 1 (B5R.1)
	5898	TGGGGATTACC	1,00	0,25	Hs.274393	Homo sapiens unknown mRNA
30	5899	TGGTTTATTAA	1,00	0,25	Hs.23023	ESTs
	5900	TCCAGGGCTCT	1,00	0,25	Hs.22824	MYB binding protein (P160) 1a
	5901	CCAGTAGAAGT	1,00	0,25	Hs.226799	HSPC039 protein
	5902	TGGTTTTGTAT	1,00	0,25	Hs.184339	KIAA0175 gene product
35	5903	TAAATTTTAAA	1,00	0,25	Hs.180370	cofilin 1 (non-muscle)
	5904	GTGTGGGAGAT	1,00	0,25	Hs.16331	ESTs
	5905	GAAGTGCCCAT	1,00	0,25	Hs.10491	KIAA1237 protein
40	5906	CTAGCCTCACG	48,00	6,03	Hs.14376	actin, gamma 1
	5907	TGCCTGCTCCT	3,00	0,68	Hs.93678	ESTs
	5908	GCCGCCTGCCT	2,00	0,49	Hs.850	IMP (inosine monophosphate) dehydrogenase 1
45	5909	AGCCGGGCTTT	2,00	0,49	Hs.57079	ESTs
	5910	GAGGGGATGTA	2,00	0,49	Hs.223025	RAB31, member RAS oncogene family
	5911	ACTTTGAATGA	2,00	0,49	Hs.19077	CGI-113 protein
	5912	CTGCCCGCCTG	2,00	0,49	Hs.15961	dynactin 3 (p22)
50	5913	CTGTTGGTGAT	38,00	5,03	Hs.3463	ribosomal protein S23
	5914	TGTGCTCAGGG	1,00	0,25	Hs.92261	pyruvate dehydrogenase kinase, isoenzyme 2
	5915	TTCTTTGGGAA	1,00	0,25	Hs.9095	Homo sapiens mRNA; cDNA DKFZp434N1710 (from clone DK
55	5916	GGCATCAGGGG	1,00	0,25	Hs.8361	hypothetical protein, estradiol-induced
	5917	TCTGCAAGAAG	1,00	0,25	Hs.81281	hypothetical protein
	5918	CGTGGCCACGG	1,00	0,25	Hs.77221	choline kinase
60	5919	GTGTGCTTAGA	1,00	0,25	Hs.72071	hypothetical protein FLJ20038
	5920	GTGGGGAGGAC	1,00	0,25	Hs.7165	zinc finger protein 259
	5921	TCTGTCAATCT	1,00	0,25	Hs.65234	hypothetical protein FLJ20596
	5922	AATAAACGTGT	1,00	0,25	Hs.57304	Ras-related GTP-binding protein

5923	AGCGCCTTCCT	1,00	0,25	Hs.49005	hypothetical protein
5924	CTCAGCCTGAA	1,00	0,25	Hs.3496	ESTs
5925	GCAGTGCCACT	1,00	0,25	Hs.34068	ESTs
5926	CTAGAAGTACA	1,00	0,25	Hs.32500	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3)
5927	ATTTTGTCGTG	1,00	0,25	Hs.29147	hypothetical protein FLJ11015
5928	GATTTTCAGCTC	1,00	0,25	Hs.280978	hypothetical protein FLJ10496
5929	TCACAGCAAGG	1,00	0,25	Hs.279944	replication initiation region protein (60kD)
5930	GCTGGGCGGCT	1,00	0,25	Hs.272788	Homo sapiens cDNA FLJ20205 fis, clone COLF1506
5931	AGGATATCCAG	1,00	0,25	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidop- sis homolog)
5932	TATTTCACTAAA	1,00	0,25	Hs.21858	trinucleotide repeat containing 3
5933	GGCCTCCAGCC	1,00	0,25	Hs.184669	zinc finger protein 144 (Mel-18)
5934	ATTTGTATCTA	1,00	0,25	Hs.181363	ESTs
5935	AGTAAGCTCCC	1,00	0,25	Hs.172788	ALEX3 protein
5936	CCCTCGCATTG	1,00	0,25	Hs.153850	Human DNA sequence from clone 321D2 on chromosome 16
5937	GAGAGAAGAGT	1,00	0,25	Hs.13476	UDP-Gal:betaGlcNAc beta 1,4- galacto- syltransferase,
5938	GATTACTTGCC	1,00	0,25	Hs.100915	peroxisomal biogenesis factor 16
5939	TTCTTATTTTA	3,00	0,69	Hs.75916	splicing factor 3b, subunit 2, 145kD
5940	GGGTCAAAGG	8,00	1,45	Hs.181307	H3 histone, family 3A
5941	GAGTTGGCAGT	4,00	0,86	Hs.258730	heme-regulated initiation factor 2-alpha kinase
5942	GCCTTTCCCTC	4,00	0,86	Hs.12064	ubiquitin specific protease 22
5943	GCATATGAGCA	2,00	0,50	Hs.7149	ESTs, Weakly similar to hypothetical protein [H.sapi
5944	AACAGAATATG	2,00	0,50	Hs.69469	dendritic cell protein
5945	TGTGCTAAATG	27,00	3,82	Hs.250895	ribosomal protein L34
5946	GAAATGTAAGA	9,00	1,59	Hs.63525	poly(rC)-binding protein 2
5947	TGAAGAGAATT	3,00	0,69	Hs.82306	destrin (actin depolymerizing factor)
5948	CTGCTTAAGGG	2,00	0,50	Hs.76662	ESTs, Weakly similar to KIAA0946 pro- tein [H.sapiens]
5949	GCTCAGGTCTG	2,00	0,50	Hs.181406	endothelin converting enzyme 1
5950	TTCTTGCTTAA	2,00	0,50	Hs.169895	ubiquitin-conjugating enzyme E2L 6
5951	TTTCTTAAAGG	4,00	0,88	Hs.197114	RNA binding protein; AT-rich element binding factor
5952	TAGAATGCAAA	1,00	0,26	Hs.7946	KIAA1288 protein
5953	CTTCCCACTCT	1,00	0,26	Hs.6845	ESTs, Weakly similar to JC4903 UDP- galactose transpo
5954	AAATCCTAGAA	1,00	0,26	Hs.6592	ESTs, Weakly similar to salivary proline- rich protei
5955	ACAGCTAATTA	1,00	0,26	Hs.4310	eukaryotic translation initiation factor 1A
5956	TTTCATCTGTA	1,00	0,26	Hs.285013	putative human HLA class II associated protein I
5957	CGTGTGAGAG	1,00	0,26	Hs.284136	PRO2047 protein
5958	TCTACTGTTAG	1,00	0,26	Hs.240615	Human DNA sequence from clone RP3- 460J8 on chromosom
5959	TAAATAAAGCA	1,00	0,26	Hs.214783	ESTs

5960	AACTGGGTCTG	1,00	0,26	Hs.182215	ADP-ribosylation factor-like 3
5961	AATACATCAAA	1,00	0,26	Hs.178761	26S proteasome-associated pad1 homolog
5962	CCTGAGTTGAT	1,00	0,26	Hs.13201	clone FLB4739
5963	AAATCTCTGGT	1,00	0,26	Hs.109315	KIAA1415 protein
5964	TGCTACGATCT	1,00	0,26	Hs.103135	ESTs
5965	GCGACAGCTCC	9,00	1,64	Hs.184582	ribosomal protein L24
5966	ATACAATAAAA	3,00	0,71	Hs.151734	nuclear transport factor 2 (placental protein 15)
5967	GAGGCCGACCC	2,00	0,51	Hs.74631	basigin
5968	GCAAGACCCCA	2,00	0,51	Hs.200595	KIAA0562 gene product
5969	GGCCGCTGCTC	2,00	0,51	Hs.151531	protein phosphatase 3 (formerly 2B), catalytic subun
5970	GGTGAGACACT	12,00	2,05	Hs.164280	solute carrier family 25 (mitochondrial carrier; ade
5971	TCTGTTTATCA	7,00	1,36	Hs.180394	signal recognition particle 14kD (homologous Alu RNA
5972	TGCTGGGTGGG	4,00	0,89	Hs.198273	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8
5973	TCACCTGTAGG	2,00	0,51	Hs.78921	A kinase (PRKA) anchor protein 1
5974	CTTGACACACA	2,00	0,51	Hs.286236	eukaryotic translation initiation factor 5
5975	TGAAGGAGCCG	12,00	2,09	Hs.89399	ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 comp
5976	CTTTGATGTTT	3,00	0,72	Hs.85100	WD repeat domain 1
5977	TCGTCTTTATC	13,00	2,23	Hs.75538	ribosomal protein S7
5978	ATGGCAAGGGA	7,00	1,39	Hs.118724	DR1-associated protein 1 (negative cofactor 2 alpha)
5979	AGTAAAAAAA	1,00	0,26	Hs.9552	binder of Arl Two
5980	CAGTGGAATGC	1,00	0,26	Hs.811	ubiquitin-conjugating enzyme E2B (RAD6 homolog)
5981	GTGTCCTGTAG	1,00	0,26	Hs.6166	hypothetical protein FLJ11196
5982	CAAAGGCTCT	1,00	0,26	Hs.5392	potassium channel modulatory factor
5983	TATAGTGGCTA	1,00	0,26	Hs.5326	Homo sapiens SSX4 protein gene, partial cds; OATL1 p
5984	GTTCTCTTTGT	1,00	0,26	Hs.285458	Homo sapiens mRNA; cDNA DKFZp434G012 (from clone DKF
5985	CACAAGCTTCA	1,00	0,26	Hs.284176	hypothetical protein PRO2221
5986	ACGTGAGTGCT	1,00	0,26	Hs.279932	CGI-105 protein
5987	TCTTCTGCTTT	1,00	0,26	Hs.278429	hepatocellular carcinoma-associated antigen 59
5988	CCTTCCCTGAG	1,00	0,26	Hs.26584	diaphanous (Drosophila, homolog) 1
5989	CCTGGAGGGGC	1,00	0,26	Hs.265327	Human DNA sequence from clone RP4-756G23 on chromoso
5990	TGGATGCTGTT	1,00	0,26	Hs.26516	hypothetical protein FLJ10604
5991	CAGCCCTCCCG	1,00	0,26	Hs.250857	calcium/calmodulin-dependent protein kinase (CaM kin
5992	TATGGTACCAA	1,00	0,26	Hs.242710	ESTs
5993	AGAGACTCTTG	1,00	0,26	Hs.227391	DKFZP547E1010 protein
5994	CAGCCATAAAA	1,00	0,26	Hs.21332	hypothetical protein FLJ20724
5995	AAGCTGTATAA	1,00	0,26	Hs.153423	hexabrachion (tenascin C, cytotactin)

5996	TGGCCTAATAT	1,00	0,26	Hs.1501	syndecan 2 (heparan sulfate proteoglycan 1, cell sur
5997	TTGCTGTAGAC	1,00	0,26	Hs.14125	p53 regulated PA26 nuclear protein
5998	TTACTGCCTAG	1,00	0,26	Hs.12921	ESTs
5999	TAGCTGCCTTT	1,00	0,26	Hs.117582	CGI-43 protein
6000	CTGGGTTGTGA	1,00	0,26	Hs.10669	KIAA1249 protein
6001	TGGTTTGCCTA	3,00	0,73	Hs.6459	ESTs, Moderately similar to unnamed protein product
6002	CTCATCAGCTT	5,00	1,08	Hs.104125	adenylyl cyclase-associated protein
6003	CACCCCCAGGC	2,00	0,52	Hs.7301	G protein pathway suppressor 2
6004	CAAAAAAAAAA	14,00	2,41	Hs.112272	histone deacetylase 8
6005	CCGCCGAAGTT	5,00	1,08	Hs.182979	ribosomal protein L12
6006	TGTACCTGTAA	33,00	4,95	Hs.278242	tubulin, alpha, ubiquitous
6007	AAAAAAAAAAG	3,00	0,73	Hs.180842	ribosomal protein L13
6008	TGGATCAACCA	4,00	0,92	Hs.286030	caveolin 1 caveolae protein, 22kD
6009	GAAGTGTGTCC	2,00	0,53	Hs.5298	CGI-45 protein
6010	CCCAATTTTCA	2,00	0,53	Hs.46405	polymerase (RNA) II (DNA directed) polypeptide F
6011	CAGATTTGCAT	2,00	0,53	Hs.155986	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 24
6012	GGTCCCCTACC	2,00	0,53	Hs.151761	KIAA0100 gene product
6013	AATCCTGTGGA	39,00	5,84	Hs.178551	ribosomal protein L8
6014	AGGGGATTCCC	3,00	0,74	Hs.75412	Arginine-rich protein
6015	CTTTCTTTGAG	5,00	1,10	Hs.4909	dickkopf (Xenopus laevis) homolog 3
6016	AGAGACAAGTC	2,00	0,53	Hs.98614	ribosome binding protein 1 (dog 180kD homolog)
6017	TGTTTTCGCCT	2,00	0,53	Hs.83916	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex,
6018	GGCCCACACCC	2,00	0,53	Hs.77978	Homo sapiens HRIHFB2007 mRNA, partial cds
6019	GTGAAACATTA	1,00	0,27	Hs.30352	ribosomal protein S6 kinase, 52kD, polypeptide 1
6020	GATTTGAAATG	1,00	0,27	Hs.273307	signal recognition particle 68kD
6021	CACAGTCAAAA	1,00	0,27	Hs.250712	calcium channel, voltage-dependent, beta 3 subunit
6022	TAACCCAACAA	1,00	0,27	Hs.1869	phosphoglucosyltransferase 1
6023	TGGGAAAACCTC	1,00	0,27	Hs.153028	cytochrome b-561
6024	AAATCGATGAG	1,00	0,27	Hs.13580	ESTs, Weakly similar to AF180920_1 cyclin L ania-6a
6025	GGAAGATGAAC	1,00	0,27	Hs.12255	hypothetical protein FLJ10656
6026	AGGTTTTGCCT	1,00	0,27	Hs.102469	putative nuclear protein
6027	GCCCTCGGCCG	4,00	0,93	Hs.17883	protein phosphatase 1G (formerly 2C), magnesium-depe
6028	CGGAGACCCTA	3,00	0,74	Hs.74497	nuclease sensitive element binding protein 1
6029	AATGAAAAAAA	3,00	0,74	Hs.11393	RAD51 (S. cerevisiae) homolog C
6030	CTGCTATACGA	17,00	2,94	Hs.180946	ribosomal protein L5
6031	CCACTCCTCAA	7,00	1,45	Hs.82890	defender against cell death 1
6032	CCCAACCCCTG	3,00	0,75	Hs.169488	dentatorubral-pallidoluysian atrophy (atrophin-1)

5	6033	CCTGAGCCCGG	5,00	1,12	Hs.68571	VPS28 protein
	6034	GCGCTGGAGTG	7,00	1,47	Hs.110695	ESTs, Weakly similar to B0495.6 [C.elegans]
	6035	TGGCAGCTTTT	3,00	0,76	Hs.6153	CGI-48 protein
	6036	CAGCTTCACCT	2,00	0,55	Hs.179606	nuclear RNA helicase, DECD variant of DEAD box famil
10	6037	AGTGGCTGTGT	1,00	0,28	Hs.5486	clone FLB5214
	6038	ACTCCTTCCTC	1,00	0,28	Hs.256290	S100 calcium-binding protein A11 (cal-gizzarin)
	6039	GCAAATCTGAA	1,00	0,28	Hs.242894	ADP-ribosylation factor-like 1
15	6040	TAAAGGTTTTT	1,00	0,28	Hs.241520	transcriptional coactivator
	6041	CCTTTTGGGTT	1,00	0,28	Hs.2288	visinin-like 1
	6042	AAAGGAATAAT	1,00	0,28	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586I2022 (from clone DK
20	6043	ATTTTAACAAA	1,00	0,28	Hs.155218	E1B-55kDa-associated protein 5
	6044	AACCAGGTGTG	1,00	0,28	Hs.153880	polymerase (RNA) mitochondrial (DNA directed)
	6045	TTTGTGTCAAA	1,00	0,28	Hs.15093	hypothetical protein
25	6046	GGTCCCGTTCC	1,00	0,28	Hs.11081	ESTs, Weakly similar to S57447 HPBRIL-7 protein - hu
	6047	ACAAAAGACAA	1,00	0,28	Hs.103391	Human insulin-like growth factor binding protein 5 (
30	6048	CCTTGGTTTTG	3,00	0,76	Hs.75875	ubiquitin-conjugating enzyme E2 variant 1
	6049	TTCTCCCAAAT	3,00	0,76	Hs.75617	collagen, type IV, alpha 2
	6050	TGGTAGTTACC	3,00	0,76	Hs.66881	Homo sapiens mRNA; cDNA DKFZp434A1518 (from clone DK
35	6051	TTTGTTAAAC	3,00	0,76	Hs.111244	hypothetical protein
	6052	CTTCGAAACTC	4,00	0,96	Hs.51299	NADH dehydrogenase (ubiquinone) flavoprotein 2 (24kD
40	6053	GCAGTCGCTTG	5,00	1,15	Hs.100002	HSPC162 protein
	6054	GCTGAAGGAAA	2,00	0,55	Hs.75569	v-rel avian reticuloendotheliosis viral oncogene hom
	6055	GCCTCCTGAGT	2,00	0,55	Hs.108689	sterol regulatory element binding transcription fact
45	6056	TGAGGCCAGGC	4,00	0,97	Hs.79162	structure specific recognition protein 1
	6057	GTCTGGGGCTT	16,00	2,93	Hs.75725	transgelin 2
	6058	TTGGGGTTTCC	83,00	12,69	Hs.62954	ferritin, heavy polypeptide 1
	6059	TCAGCCTTCTG	6,00	1,34	Hs.179986	flotillin 1
50	6060	ATCGCTTTCTA	14,00	2,65	Hs.177486	amyloid beta (A4) precursor protein (protease nexin-
	6061	CTTTTGTTTGG	2,00	0,56	Hs.5094	ring finger protein 10
55	6062	CAAATGCAAAG	2,00	0,56	Hs.11817	nudix (nucleoside diphosphate linked moiety X)-type
	6063	AGCACTGCAGC	2,00	0,56	Hs.111039	N-myristoyltransferase 1
	6064	TAGGAAACACC	1,00	0,28	Hs.8765	RNA helicase-related protein
	6065	GACGTTCACTG	1,00	0,28	Hs.75888	phosphogluconate dehydrogenase
60	6066	TATGCTGTTAT	1,00	0,28	Hs.5663	ESTs
	6067	TTAGTCAGGCT	1,00	0,28	Hs.50984	sarcoma amplified sequence
	6068	GCCCATTTTAT	1,00	0,28	Hs.226318	carbon catabolite repressor protein

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					(CCR4)-associati
6069	GAACGCTGAAG	1,00	0,28	Hs.155983	KIAA0677 gene product
6070	TATCCTAGGGT	1,00	0,28	Hs.142613	Homo sapiens cDNA FLJ10281 fis, clone HEMBB1001289
6071	TCAACAGCAGG	1,00	0,28	Hs.11556	ESTs
6072	TCCATCAAGAA	6,00	1,36	Hs.79387	proteasome (prosome, macropain) 26S subunit, ATPase,
6073	TAGCCGCTGAG	4,00	0,99	Hs.75932	N-ethylmaleimide-sensitive factor attachment protein
6074	GGCCCTCTGAG	5,00	1,18	Hs.161362	protein (peptidyl-prolyl cis/trans isomerase) NIMA-i
6075	GGTCCAGTGTT	14,00	2,70	Hs.181013	phosphoglycerate mutase 1 (brain)
6076	GGTGGAGCAGA	2,00	0,56	Hs.6846	Homo sapiens mRNA; cDNA DKFZp761J1410 (from clone DK
6077	GCGGCGGCGAG	2,00	0,56	Hs.5662	guanine nucleotide binding protein (G protein), beta
6078	TGTGGGAAATC	2,00	0,56	Hs.251754	secretory leukocyte protease inhibitor (antileukopro
6079	AGTTCCACCAG	2,00	0,56	Hs.182626	chromosome 22 open reading frame 5
6080	GATGTTAATTG	2,00	0,56	Hs.171501	ubiquitin specific protease 11
6081	AACTCTTGAAG	7,00	1,55	Hs.58189	eukaryotic translation initiation factor 3, subunit
6082	GAAGATGTGGG	11,00	2,22	Hs.250911	Homo sapiens clone 23967 unknown mRNA, partial cds
6083	AACAGAAGCAA	6,00	1,38	Hs.74649	cytochrome c oxidase subunit VIc
6084	GTGACAGACAT	3,00	0,79	Hs.75117	interleukin enhancer binding factor 2, 45kD
6085	GCTCAGCTGGA	10,00	2,07	Hs.223241	eukaryotic translation elongation factor 1 delta (gu
6086	TGCTTTGGGAT	7,00	1,56	Hs.84344	CGI-135 protein
6087	GGCTCCTCGAG	4,00	1,00	Hs.179600	TAP binding protein (tapasin)
6088	GCTCCGAGCGT	5,00	1,20	Hs.80617	ribosomal protein S16
6089	CCTAGCTGGAT	48,00	8,01	Hs.182937	peptidylprolyl isomerase A (cyclophilin A)
6090	GTGGACCCCAA	4,00	1,01	Hs.74562	siah binding protein 1; FBP interacting repressor; p
6091	GCTTTACTTTG	3,00	0,80	Hs.8966	integral membrane protein 1
6092	ACCTTCCTAGT	3,00	0,80	Hs.6454	chromosome 19 open reading frame 3
6093	AGGAAAAGATG	2,00	0,57	Hs.82520	Human 1.1 kb mRNA upregulated in retinoic acid treat
6094	GTAGGAGCTGG	2,00	0,57	Hs.81728	unc119 (C.elegans) homolog
6095	ATTGACCGCTG	2,00	0,57	Hs.177766	ADP-ribosyltransferase (NAD <sup>+</sup> ; poly (ADP-ribose) poly
6096	GAGGACTTGCG	1,00	0,29	Hs.8768	hypothetical protein FLJ10849
6097	GCATTTTGTA	1,00	0,29	Hs.85616	TOLLIP protein
6098	GGCTGGGTTTT	1,00	0,29	Hs.74870	H2.0 (Drosophila)-like homeo box 1
6099	CGTGAACAATT	1,00	0,29	Hs.7045	GL004 protein
6100	TTCCCAAAGGC	1,00	0,29	Hs.64904	ADP-ribosylation factor related protein 1
6101	TTCACCAGGGC	1,00	0,29	Hs.63243	Homo sapiens cDNA FLJ10041 fis, clone HEMBA1001022
6102	GTACTCTACTT	1,00	0,29	Hs.52184	hypothetical protein FLJ20618

5	6103	CTGGTGGTGCC	1,00	0,29	Hs.49427	Gem-interacting protein
	6104	TTCCCTGGGAA	1,00	0,29	Hs.35096	KIAA1538 protein
	6105	CTGGGGGAGGG	1,00	0,29	Hs.274122	erythrocyte membrane protein band 4.9 (dematin)
	6106	GCTGTACAAAG	1,00	0,29	Hs.250911	Homo sapiens clone 23967 unknown mRNA, partial cds
10	6107	TGACCTATTTTC	1,00	0,29	Hs.214646	KIAA0447 gene product
	6108	ATCAGTGTGAA	1,00	0,29	Hs.194662	calponin 3, acidic
	6109	AGGAAAGCCAG	1,00	0,29	Hs.19012	Rab9 effector p40
	6110	CCGAAGTCGAG	1,00	0,29	Hs.169872	ESTs
15	6111	GAGAAAGAGGC	1,00	0,29	Hs.16420	Npw38-binding protein NpwBP
	6112	GCACCTATTGA	1,00	0,29	Hs.16178	apoptosis antagonizing transcription factor
	6113	TCTTCGTCCTG	1,00	0,29	Hs.14891	myelin protein zero-like 1
20	6114	CCACCGCACTT	1,00	0,29	Hs.115325	RAB7, member RAS oncogene family-like 1
	6115	GAAGTGGAGAA	1,00	0,29	Hs.109150	SH3-domain binding protein 5 (BTK-associated)
25	6116	TTGGGCACTAG	1,00	0,29	Hs.102402	Mad4 homolog
	6117	GTTGACTTACA	1,00	0,29	Hs.10065	hypothetical protein 23851
	6118	AACTTGCCCAT	8,00	1,75	Hs.111611	ribosomal protein L27
	6119	GTGTTGCACAA	20,00	3,73	Hs.165590	ribosomal protein S13
30	6120	TGGAGAGCAAC	4,00	1,01	Hs.4113	S-adenosylhomocysteine hydrolase-like 1
	6121	CTCACTTTTTT	4,00	1,02	Hs.76722	CCAAT/enhancer binding protein (C/EBP), delta
35	6122	TGACTGGCAGT	4,00	1,02	Hs.119663	CD59 antigen p18-20 (antigen identified by monoclonal)
	6123	GAGGCGCTGGG	2,00	0,58	Hs.76366	BCL2-antagonist of cell death
	6124	GTGGGGTGACA	2,00	0,58	Hs.250905	hypothetical protein
40	6125	TTTTACTCACA	2,00	0,58	Hs.183706	adducin 1 (alpha)
	6126	CAATAAACTGA	11,00	2,29	Hs.150580	putative translation initiation factor
	6127	ACTGAAGGCGC	3,00	0,81	Hs.92208	a disintegrin and metalloproteinase domain 15 (metar)
45	6128	CTTCTCACCGT	3,00	0,81	Hs.84285	ubiquitin-conjugating enzyme E2I (homologous to yeas)
	6129	TGGAAGTGTGA	3,00	0,81	Hs.279751	sialic acid binding Ig-like lectin 8
	6130	AAGAATCTGAA	3,00	0,81	Hs.183435	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1
50	6131	GGAAGGACAGA	4,00	1,03	Hs.106876	Vacuolar proton-ATPase, subunit D; V-ATPase, subunit
	6132	GTAAGATTTGA	6,00	1,42	Hs.279939	mitochondrial carrier homolog 1
55	6133	TTAAACCTCAA	7,00	1,61	Hs.170311	heterogeneous nuclear ribonucleoprotein D-like
	6134	CACCACGGTGT	3,00	0,82	Hs.241471	RNB6
	6135	GTAGCAAAAAA	2,00	0,58	Hs.183842	ubiquitin B
	6136	GTCCCAAAATG	1,00	0,30	Hs.99908	nuclear receptor coactivator 4
60	6137	TCGGTTACAAG	1,00	0,30	Hs.98614	ribosome binding protein 1 (dog 180kD homolog)
	6138	GTCAGACTGTA	1,00	0,30	Hs.93199	lanosterol synthase (2,3-oxidosqualene-

					lanosterol cy
6139	TAATCTTTACT	1,00	0,30	Hs.90744	proteasome (prosome, macropain) 26S subunit, non-ATP
6140	TTAGTCTTCAG	1,00	0,30	Hs.82712	fragile X mental retardation, autosomal homolog 1
6141	TCATAGTTCAG	1,00	0,30	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (so
6142	TTTGGAGCATT	1,00	0,30	Hs.7773	ESTs, Weakly similar to A4P_HUMAN INTESTINAL MEMBRAN
6143	GGAGAGAAAAC	1,00	0,30	Hs.70945	ESTs
6144	GGCCAGTGTTG	1,00	0,30	Hs.40094	Human DNA sequence from clone 167A19 on chromosome 1
6145	CTACTCTTCTA	1,00	0,30	Hs.180532	heat shock 90kD protein 1, alpha
6146	TTTTAACAAAA	1,00	0,30	Hs.169370	FYN oncogene related to SRC, FGR, YES
6147	TATGTATGTTG	1,00	0,30	Hs.144477	hypothetical protein PRO2975
6148	AGGGGAAAATA	1,00	0,30	Hs.119537	GAP-associated tyrosine phosphoprotein p62 (Sam68)
6149	ATGGCAGAGAC	1,00	0,30	Hs.104335	Human DNA sequence from clone RP3-402G11 on chromoso
6150	GCCTGCTGGGC	16,00	3,22	Hs.2706	glutathione peroxidase 4 (phospholipid hydroperoxida
6151	GTTTCTTCCCT	4,00	1,05	Hs.117582	CGI-43 protein
6152	CCGGACCTGTG	2,00	0,59	Hs.117582	CGI-43 protein
6153	GCTTTCATTGG	5,00	1,25	Hs.250911	Homo sapiens clone 23967 unknown mRNA, partial cds
6154	TTGGAGATCTC	19,00	3,76	Hs.50098	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex,
6155	ACTGCTGAACC	3,00	0,83	Hs.200600	secretory carrier membrane protein 3
6156	CACTTGCCCTA	11,00	2,39	Hs.15977	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9
6157	GCCAAGATGCC	4,00	1,06	Hs.83135	p53-responsive gene 6
6158	CCTGCCCCCCT	3,00	0,84	Hs.861	mitogen-activated protein kinase 3
6159	ACACTTCTTTC	2,00	0,60	Hs.83381	guanine nucleotide binding protein 11
6160	GCTAGGTCTGG	2,00	0,60	Hs.75354	GCN1 (general control of amino-acid synthesis 1, yea
6161	TCCATCCCTTG	2,00	0,60	Hs.7527	small fragment nuclease
6162	AGGCCTGGCTA	2,00	0,60	Hs.5011	RNA binding motif protein 9
6163	GAGAGCCTGCC	2,00	0,60	Hs.31305	transducin-like enhancer of split 3, homolog of Dros
6164	GTTTAAAAAGA	1,00	0,30	Hs.90005	superiorcervical ganglia, neural specific 10
6165	CCAAGGACTCT	1,00	0,30	Hs.79058	suppressor of Ty (S.cerevisiae) 4 homolog 1
6166	GAAAAGTTGCC	1,00	0,30	Hs.33122	KIAA1160 protein
6167	AATTATGACTT	1,00	0,30	Hs.2853	poly(rC)-binding protein 1
6168	TCAGTGCTCTC	1,00	0,30	Hs.284741	Human clone 23745 mRNA, complete cds
6169	CCTGTCTGCAC	1,00	0,30	Hs.25338	ESTs
6170	CGAATAAAATG	1,00	0,30	Hs.20815	erythroblast macrophage protein
6171	TTTGGACAATA	1,00	0,30	Hs.173685	Human DNA sequence from clone 30M3

					on chromosome 6p2
5	6172	GACGACTGACC	1,00	0,30	Hs.155530 interferon, gamma-inducible protein 16
	6173	CCCTATCACAA	1,00	0,30	Hs.150826 CATX-8 protein
	6174	GTGAATAAACA	1,00	0,30	Hs.143601 Homo sapiens cDNA FLJ20678 fis, clone KAIA4163
10	6175	GTGGGACCATT	1,00	0,30	Hs.11774 protein (peptidyl-prolyl cis/trans isomerase) NIMA-i
	6176	CTCAGGAAATA	7,00	1,67	Hs.284292 ubiquinol-cytochrome c reductase complex (7.2 kD)
	6177	ACCAAGGAGGA	5,00	1,27	Hs.283547 HSVI binding protein
15	6178	TCTCTACCCAC	8,00	1,87	Hs.64797 amyloid beta (A4) precursor-like protein 2
	6179	CAGTCTCTCAA	10,00	2,25	Hs.76230 ribosomal protein S10
	6180	CCTTGAGTACA	4,00	1,09	Hs.155247 aldolase C, fructose-bisphosphate
20	6181	TGCAGACCCAT	2,00	0,61	Hs.5437 Tax1 (human T-cell leukemia virus type I) binding pr
	6182	GGGCCAAAACC	1,00	0,31	Hs.9142 ESTs, Weakly similar to FLDED-1 [H.sapiens]
25	6183	GTCCTTCAGAA	1,00	0,31	Hs.82712 fragile X mental retardation, autosomal homolog 1
	6184	CAGTCTGGGAG	1,00	0,31	Hs.285115 interleukin 13 receptor, alpha 1
	6185	CGCCGCTTCTT	1,00	0,31	Hs.277401 bromodomain adjacent to zinc finger domain, 2A
30	6186	GCTTGGCCTGG	1,00	0,31	Hs.200586 brain-specific angiogenesis inhibitor 2
	6187	AGAACCTGCAA	1,00	0,31	Hs.154196 E4F transcription factor 1
	6188	AGGGCCACCTC	1,00	0,31	Hs.124015 ESTs, Weakly similar to GLO2_HUMAN HYDROXYACYLGLUTAT
35	6189	GGTCTGTTC	1,00	0,31	Hs.11081 ESTs, Weakly similar to S57447 HPBR11-7 protein - hu
	6190	GGCCAGCCCTT	6,00	1,51	Hs.155455 phosphofructokinase, liver
40	6191	GGGGGTGGATG	3,00	0,87	Hs.75087 Fas-activated serine/threonine kinase
	6192	AAGAAGACTTC	6,00	1,53	Hs.7719 GABA(A) receptor-associated protein
	6193	ACCTGCTGGTG	2,00	0,62	Hs.5807 hypothetical protein
	6194	GGGAAGGCACT	2,00	0,62	Hs.13144 HSPC160 protein
45	6195	ACTCAGCCCGG	2,00	0,62	Hs.101382 tumor necrosis factor, alpha-induced protein 2
	6196	TCTTAATGAAG	5,00	1,32	Hs.173912 eukaryotic translation initiation factor 4A, isoform
	6197	CAGGAGGAGTT	8,00	1,94	Hs.183760 glucose regulated protein, 58kD
50	6198	CGCCGGAACAC	39,00	7,60	Hs.286 ribosomal protein L4
	6199	CGGCTGGTGAA	6,00	1,53	Hs.75748 proteasome (prosome, macropain) subunit, beta type,
	6200	CACTTCAAGGG	9,00	2,14	Hs.77667 lymphocyte antigen 6 complex, locus E
55	6201	GACAGGCTGGC	2,00	0,62	Hs.78409 collagen, type XVIII, alpha 1
	6202	AACTCCCAGTT	2,00	0,62	Hs.110571 growth arrest and DNA-damage-inducible, beta
	6203	GAGCCATAGAA	1,00	0,32	Hs.82669 ESTs
60	6204	ATTAAAGTCAG	1,00	0,32	Hs.78748 KIAA0237 gene product
	6205	GTAGAGTTGGG	1,00	0,32	Hs.77897 splicing factor 3a, subunit 3, 60kD
	6206	AATCCAAAGGC	1,00	0,32	Hs.771 phosphorylase, glycogen; liver (Hers

					disease, glycog
6207	TGGTCTGGAGG	1,00	0,32	Hs.75822	TGFB1-induced anti-apoptotic factor 1
6208	TTACTTCAACT	1,00	0,32	Hs.6236	ESTs
6209	TGTCTGCCTGA	1,00	0,32	Hs.237617	Homo sapiens chromosome 19, cosmid R26894
6210	ATTTCCCAAAT	1,00	0,32	Hs.178112	DNA segment, single copy probe LNS-CAI/LNS-CAII (del
6211	CAGATAAACCA	1,00	0,32	Hs.168481	minichromosome maintenance deficient (S. cerevisiae)
6212	TCACAAAAGAG	1,00	0,32	Hs.12646	Homo sapiens mRNA; cDNA DKFZp434B1813 (from clone DK
6213	GGGGGCTGCTC	1,00	0,32	Hs.115960	ESTs
6214	GCCCCGCTTGT	5,00	1,34	Hs.80475	polymerase (RNA) II (DNA directed) polypeptide J (13
6215	AGGTTTCCTCC	2,00	0,63	Hs.9736	proteasome (prosome, macropain) 26S subunit, non-ATP
6216	GGAGCCATTCT	2,00	0,63	Hs.272630	vacuolar proton pump delta polypeptide
6217	TGCCCCCCTAG	2,00	0,63	Hs.134707	ESTs, Weakly similar to GEF-2 protein [H.sapiens]
6218	TTAAAGATTTA	4,00	1,13	Hs.77899	tropomyosin 1 (alpha)
6219	GTGACAGAAGA	15,00	3,38	Hs.129673	eukaryotic translation initiation factor 4A, isoform
6220	CCCCCGTGAAG	5,00	1,36	Hs.182018	interleukin-1 receptor-associated kinase 1
6221	TCTTCCAGGAG	6,00	1,58	Hs.74267	ribosomal protein L15
6222	CATTAAATTCA	2,00	0,64	Hs.31053	cytoskeleton-associated protein 1
6223	TTTTCAGCAGGA	2,00	0,64	Hs.146393	KIAA0025 gene product; MMS-inducible gene
6224	GGGGCTGTATT	2,00	0,64	Hs.1103	transforming growth factor, beta 1
6225	TGGAGGCCAGG	3,00	0,90	Hs.250581	SWI/SNF related, matrix associated, actin dependent
6226	TGTGGGTGCTG	4,00	1,14	Hs.194657	cadherin 1, E-cadherin (epithelial)
6227	GGGAGGATTAA	1,00	0,32	Hs.90753	Tat-interacting protein (30kD)
6228	GTGTGATGCTG	1,00	0,32	Hs.89519	KIAA1046 protein
6229	AATGTGATTTC	1,00	0,32	Hs.75693	prolylcarboxypeptidase (angiotensinase C)
6230	ACATCATACTG	1,00	0,32	Hs.61790	ESTs, Weakly similar to T01239 hypothetical protein
6231	TGATGTTTGCA	1,00	0,32	Hs.4552	ubiquilin 2
6232	CTTCTGTTTTT	1,00	0,32	Hs.280666	Homo sapiens chromosome 19, cosmid R32184
6233	GTTGGATAGGG	1,00	0,32	Hs.27184	growth factor, erv1 (S. cerevisiae)-like (augmenter
6234	CACTCTATCCG	1,00	0,32	Hs.258551	aspartyl aminopeptidase
6235	AATTCTGTAAA	1,00	0,32	Hs.241575	Human DNA sequence from clone 316G12 on chromosome 1
6236	CTGAAAACCAC	1,00	0,32	Hs.170279	tissue factor pathway inhibitor (lipoprotein-associa
6237	TGCTGAGGAAG	1,00	0,32	Hs.168350	KIAA0554 protein
6238	GGTACACTGCG	1,00	0,32	Hs.157145	tetracycline transporter-like protein
6239	TACATATGGAA	1,00	0,32	Hs.155499	golgi-specific brefeldin A resistance

					factor 1
5	6240	TCTGCTTTTGA	1,00	0,32	Hs.144504 hypothetical protein FLJ10624
	6241	ACAGCCAAGAG	1,00	0,32	Hs.14142 nudix (nucleoside diphosphate linked moiety X)-type
	6242	GGCTTGCTGAC	1,00	0,32	Hs.1369 decay accelerating factor for complement (CD55, Crom
10	6243	GATTACCTGTG	1,00	0,32	Hs.119403 hexosaminidase A (alpha polypeptide)
	6244	TCCGTGGTTGG	7,00	1,81	Hs.79516 brain acid-soluble protein 1
	6245	CAGCCTTGGAC	3,00	0,91	Hs.65648 RNA binding motif protein 8
	6246	ACAGGGTGACC	10,00	2,48	Hs.174050 endothelial differentiation-related factor 1
15	6247	TCCCTGTACAT	5,00	1,40	Hs.89563 nuclear cap binding protein subunit 1, 80kD
	6248	TTATGGATCTC	5,00	1,40	Hs.5662 guanine nucleotide binding protein (G protein), beta
20	6249	ACTCTGCCAAG	2,00	0,65	Hs.241543 DKFZP586F1524 protein
	6250	CAAATGAGGAG	14,00	3,32	Hs.69855 NRAS-related gene
	6251	TCCTCGGGCA	1,00	0,33	Hs.83081 GTP cyclohydrolase I feedback regulatory protein
25	6252	TTAAATGCAAA	1,00	0,33	Hs.7935 KIAA0952 protein
	6253	TCTGGACCGGC	1,00	0,33	Hs.78979 Golgi apparatus protein 1
	6254	ATTGATGACGG	1,00	0,33	Hs.7733 tetratricopeptide repeat domain 1
	6255	ACCTTATCAAC	1,00	0,33	Hs.75659 MpV17 transgene, murine homolog, glomerulosclerosis
30	6256	CCTGGGGGTGC	1,00	0,33	Hs.75196 ankyrin repeat-containing protein
	6257	ACAGCGTCTGC	1,00	0,33	Hs.63128 KIAA1292 protein
	6258	GCACAGAGCCG	1,00	0,33	Hs.5105 hypothetical protein FLJ10569
	6259	GGGATGGAGAA	1,00	0,33	Hs.28726 RAB9, member RAS oncogene family
35	6260	TTTGTTGCTTT	1,00	0,33	Hs.279882 PC326 protein
	6261	GATTTTCTACT	1,00	0,33	Hs.17969 KIAA0663 gene product
	6262	GGCTCAGGGCT	1,00	0,33	Hs.13014 ADP-ribosylation factor GTPase activating protein 1
40	6263	TACTTGGTCTT	1,00	0,33	Hs.11355 ESTs
	6264	TTCTATTTTGT	1,00	0,33	Hs.112058 CD27-binding (Siva) protein
	6265	AATAAAGGCTA	7,00	1,86	Hs.179735 ras homolog gene family, member C
45	6266	CTGTTGATTGC	16,00	3,77	Hs.249495 heterogeneous nuclear ribonucleoprotein A1
	6267	AAACCCGAAGA	2,00	0,66	Hs.3100 lysyl-tRNA synthetase
	6268	GAAATTTAAAG	6,00	1,66	Hs.274472 high-mobility group (nonhistone chromosomal) protein
50	6269	CGCAAGCTGGT	4,00	1,20	Hs.77886 lamin A/C
	6270	AAGGGAGGGTC	5,00	1,44	Hs.182248 sequestosome 1
	6271	GTCTACTCCTC	1,00	0,34	Hs.75199 protein phosphatase 2, regulatory subunit B (B56), b
55	6272	CGTCCCGGAGC	1,00	0,34	Hs.7345 MAD1 (mitotic arrest deficient, yeast, homolog)-like
	6273	GGACCAGGCTG	1,00	0,34	Hs.62771 Homo sapiens mRNA; cDNA DKFZp761E1423 (from clone DK
60	6274	CTTATTCCTTA	1,00	0,34	Hs.40323 BUB3 (budding uninhibited by benzimidazoles 3, yeast
	6275	CACTGCAAGGC	1,00	0,34	Hs.32060 ESTs

6276	GCAACACATCT	1,00	0,34	Hs.283109	hypothetical protein DKFZp762L1710
6277	GCTTCCGGCCC	1,00	0,34	Hs.19165	ESTs
6278	AAGATCATTGA	1,00	0,34	Hs.18894	adaptor-related protein complex 1, mu 2 subunit
6279	GTCACAACCTG	1,00	0,34	Hs.159608	aldehyde dehydrogenase 10 (fatty aldehyde dehydrogenase)
6280	AGTGACCGAAG	1,00	0,34	Hs.134342	TASP for testis-specific adriamycin sensitivity prot
6281	TAATTTTTCTA	1,00	0,34	Hs.107637	Homo sapiens clone 25107 mRNA sequence
6282	CAGTTCTCTGT	7,00	1,91	Hs.279921	HSPC035 protein
6283	GGCTGGTCTGG	4,00	1,20	Hs.17894	ESTs
6284	AGCCCTCCCTG	6,00	1,69	Hs.74111	RNA-binding protein (autoantigenic)
6285	CAGGCTTTTTG	2,00	0,67	Hs.83484	SRY (sex determining region Y)-box 4
6286	GAAAAGCCTTC	2,00	0,67	Hs.78619	gamma-glutamyl hydrolase (conjugase, folylpolygammag)
6287	GTTGAAACTCA	2,00	0,67	Hs.6179	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17 (72k)
6288	GTGCCTAGGAG	2,00	0,67	Hs.25999	Homo sapiens clone 23781 mRNA sequence
6289	GGCAACAAAAG	3,00	0,96	Hs.180446	karyopherin (importin) beta 1
6290	ATACATTTAGG	1,00	0,34	Hs.77324	eukaryotic translation termination factor 1
6291	CAATTTAAGTG	1,00	0,34	Hs.77324	eukaryotic translation termination factor 1
6292	CTCGCTCCAGG	1,00	0,34	Hs.72363	ESTs
6293	ATGGGTCAGAA	1,00	0,34	Hs.66151	Homo sapiens mRNA; cDNA DKFZp434A115 (from clone DKF
6294	AGTGGGTATTT	1,00	0,34	Hs.36237	CGI-34 protein
6295	GATTGGCGGCT	1,00	0,34	Hs.274350	actin-like 6
6296	GGAAGTGCAA	1,00	0,34	Hs.273186	hypothetical protein, clone Telethon(Italy B41) Stra
6297	GGATAATGCC	1,00	0,34	Hs.211608	nucleoporin 153kD
6298	TGTTTGCAATA	1,00	0,34	Hs.20313	protein tyrosine kinase 2 beta
6299	ATTCACCCCCT	1,00	0,34	Hs.173864	KIAA0561 protein
6300	CTTATAATAAG	1,00	0,34	Hs.129548	heterogeneous nuclear ribonucleoprotein K
6301	CTTTTTTCTGT	1,00	0,34	Hs.12013	ATP-binding cassette, sub-family E (OABP), member 1
6302	AAGCTCCCTGT	1,00	0,34	Hs.114416	transducin (beta)-like 3
6303	CAATCAGAATC	1,00	0,34	Hs.109052	chromosome 14 open reading frame 2
6304	CTGGCCCCGAG	1,00	0,34	Hs.100997	Human DNA sequence from clone RP1-18C9 on chromosome
6305	TACGTTGCAGC	3,00	0,96	Hs.21756	translation factor sui1 homolog
6306	AATGACTGAAT	2,00	0,68	Hs.93659	protein disulfide isomerase related protein (calcium
6307	CAGTGTTGGGG	2,00	0,68	Hs.272480	cell matrix adhesion regulator
6308	GTTTGCAAGTG	2,00	0,68	Hs.151787	U5 snRNP-specific protein, 116 kD
6309	GGTGAAGAGGA	3,00	0,97	Hs.233950	serine protease inhibitor, Kunitz type 1
6310	TGCTTCATCTG	5,00	1,49	Hs.10842	RAN, member RAS oncogene family
6311	CCCTCCTCCGT	2,00	0,69	Hs.81131	guanidinoacetate N-methyltransferase
6312	AGGTGCAGAGG	2,00	0,69	Hs.13501	pescadillo (zebrafish) homolog 1, con-

					taining BRCT do
5	6313	TGCTTTGCTTC	1,00	0,35	Hs.81875 growth factor receptor-bound protein 10
	6314	TTTTGTACTTG	1,00	0,35	Hs.4245 chromosome 11 hypothetical protein ORF3
	6315	AGAAGTACTGA	1,00	0,35	Hs.2934 ribonucleotide reductase M1 polypeptide
	6316	GGCGGCTGTGG	1,00	0,35	Hs.283476 peroxisomal acyl-CoA thioesterase
10	6317	GCCTGAGGGCC	1,00	0,35	Hs.239500 KIAA0273 gene product
	6318	TTGTGTGTACC	1,00	0,35	Hs.208985 ESTs, Weakly similar to plakophilin 2b [H.sapiens]
	6319	GAGAGAAAATT	1,00	0,35	Hs.181444 hypothetical protein
15	6320	AAATTGTTCCA	1,00	0,35	Hs.167106 proteasome (prosome, macropain) sub-unit, alpha type,
	6321	AACAGCTGGAA	1,00	0,35	Hs.13340 histone acetyltransferase 1
	6322	AATAAAAGACC	1,00	0,35	Hs.119178 cation-chloride cotransporter-interacting protein
20	6323	TCTGCTAAAGA	5,00	1,51	Hs.95958 solute carrier family 2 (facilitated glucose transpo
	6324	GA CTCTCTGTT	2,00	0,69	Hs.21635 tubulin, gamma 1
25	6325	AAAGGTTGGTT	2,00	0,69	Hs.182423 ES1 (zebrafish) protein, human homolog of
	6326	GCTTTTAAGGA	17,00	4,31	Hs.8102 ribosomal protein S20
	6327	AAGTCATTCAG	4,00	1,27	Hs.274416 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex,
30	6328	GTGCTTGTACT	2,00	0,70	Hs.151413 glia maturation factor, beta
	6329	AAGGATGCGGT	1,00	0,36	Hs.83126 TATA box binding protein (TBP)-associated factor, RN
35	6330	TTTTATGGGTA	1,00	0,36	Hs.79101 cyclin G1
	6331	CCTCCAGCAA	1,00	0,36	Hs.4200 hypothetical protein R32184_1
	6332	CTGTTTAAACT	1,00	0,36	Hs.3382 protein phosphatase 4, regulatory sub-unit 1
	6333	TAGTCATCAAG	1,00	0,36	Hs.281434 sialyltransferase
40	6334	GCAATGCAAAA	1,00	0,36	Hs.279937 KIAA1001 protein
	6335	TCTGCACTGAG	1,00	0,36	Hs.173789 Homo sapiens mRNA; cDNA DKFZp434J1313 (from clone DK
45	6336	GCCGGGCGCGG	1,00	0,36	Hs.155090 hypothetical protein
	6337	CACAAAATCTC	1,00	0,36	Hs.12372 KIAA0517 protein
	6338	GATTGTGCAAG	2,00	0,71	Hs.76666 C9orf10 protein
	6339	TTTTGAAGCAG	4,00	1,29	Hs.80464 hepatitis B virus x-interacting protein (9.6kD)
50	6340	GAGCAGCTGGA	2,00	0,72	Hs.166887 copine 1
	6341	TTTTTGATAAA	4,00	1,30	Hs.181165 eukaryotic translation elongation factor 1 alpha 1
55	6342	GCCGAGGAAGG	53,00	12,71	Hs.82148 ribosomal protein S12
	6343	GTTGTCTTTGG	6,00	1,84	Hs.284394 complement component 3
	6344	AGCAAGTCTCT	1,00	0,37	Hs.81548 2,4-dienoyl CoA reductase 1, mitochondrial
60	6345	CAGTGAATGAA	1,00	0,37	Hs.195614 splicing factor 3b, subunit 3, 130kD
	6346	CCTGAGGGTAC	1,00	0,37	Hs.178551 ribosomal protein L8
	6347	CAGCTCTGAGA	1,00	0,37	Hs.172865 cleavage stimulation factor, 3' pre-RNA, subunit 1,

65



6348	TGTAACAATAA	1,00	0,37	Hs.12600	Human DNA sequence from clone RP3-322G13 on chromoso	
6349	TATCTGTCTAC	5,00	1,58	Hs.145279	SET translocation (myeloid leukemia-associated)	5
6350	AAGCTGGAGGA	3,00	1,03	Hs.55682	eukaryotic translation initiation factor 3, subunit	
6351	GCCTCTGCCAG	2,00	0,72	Hs.106674	BRCA1 associated protein-1 (ubiquitin carboxy-termin	10
6352	ATGAAAAGAAA	3,00	1,04	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (from clone DK	
6353	TTGTTCTTTGT	2,00	0,74	Hs.91773	protein phosphatase 2 (formerly 2A), catalytic subun	15
6354	TCGTTGTTTAA	1,00	0,37	Hs.8054	CGI-68 protein	
6355	AGGCACTGGCC	1,00	0,37	Hs.8008	DNA methyltransferase 1-associated protein 1	
6356	CTGAGTTAGGT	1,00	0,37	Hs.72980	Protein P3	20
6357	CTCCCGGCGAT	1,00	0,37	Hs.72289	hypothetical protein FLJ20327	
6358	TCAGATCCGTC	1,00	0,37	Hs.57304	Ras-related GTP-binding protein	
6359	GGGCGAGAACA	1,00	0,37	Hs.278898	tumor necrosis factor alpha-inducible cellular prote	25
6360	AGGAATGTTAA	1,00	0,37	Hs.250904	zinc finger protein 258	
6361	ACATTCCAAGT	1,00	0,37	Hs.245188	tissue inhibitor of metalloproteinase 3 (Sorsby fund	
6362	AATACTTAAAT	1,00	0,37	Hs.241507	ribosomal protein S6	30
6363	CAGCACATTAT	1,00	0,37	Hs.184592	Human clone A9A2BRB5 (CAC)n/(GTG)n repeat-containing	
6364	CAGAGTGA CTG	1,00	0,37	Hs.172589	nuclear phosphoprotein similar to S. cerevisiae PWP1	35
6365	GAAATTAGGGA	1,00	0,37	Hs.167115	KIAA0830 protein	
6366	TTCTCTCCAAC	1,00	0,37	Hs.15087	KIAA0250 gene product	
6367	TTCTCCACCC	1,00	0,37	Hs.125743	ESTs	
6368	ATTTTCAAAAA	1,00	0,37	Hs.102497	paxillin	40
6369	GCACAGGCCAG	3,00	1,06	Hs.91481	NEU1 protein	
6370	ACCATTCTGCT	3,00	1,06	Hs.174195	interferon induced transmembrane protein 2 (1-8D)	
6371	GTTTATGGATA	2,00	0,75	Hs.75742	matrix Gla protein	45
6372	CTGTCATTGT	3,00	1,07	Hs.167460	splicing factor, arginine/serine-rich 3	
6373	CCTGGAAGAGG	12,00	3,49	Hs.75655	procollagen-proline, 2-oxoglutarate 4-dioxygenase (p	
6374	CTGTGCTCGGA	3,00	1,07	Hs.76394	enoyl Coenzyme A hydratase, short chain, 1, mitochon	50
6375	GATTAAGTGAG	2,00	0,75	Hs.95835	ESTs, Weakly similar to unnamed protein product [H.s	
6376	TGGGCGCCTTT	2,00	0,75	Hs.78601	uroporphyrinogen decarboxylase	55
6377	GAGGTGCCGGA	2,00	0,75	Hs.37003	v-Ha-ras Harvey rat sarcoma viral oncogene homolog	
6378	CTGCGGTGGCG	2,00	0,75	Hs.252831	reticulon 3	
6379	AAAACATCCAG	1,00	0,38	Hs.7763	vesicle docking protein p115	60
6380	GTTGGCCTGGT	1,00	0,38	Hs.74266	ESTs, Highly similar to similar to GTPase-activating	
6381	ACGAGCTGGAG	1,00	0,38	Hs.50267	putative GTP-binding protein similar to	

					RAY/RAB1C	
5	6382	GGCAGGCTGTG	1,00	0,38	Hs.33251	peptidylprolyl isomerase E (cyclophilin E)
	6383	GTGTTCCCAT	1,00	0,38	Hs.267120	Human DNA sequence from clone RP3-351K20 on chromoso
	6384	TTCATTAAAA	1,00	0,38	Hs.256309	Human beta-1D integrin mRNA, cytoplasmic domain, par
10	6385	GACATTTGTCC	1,00	0,38	Hs.184870	ESTs
	6386	CGGTTTGCAGA	1,00	0,38	Hs.15627	Nit protein 2
	6387	GCAAACAATCA	1,00	0,38	Hs.155489	NS1-associated protein 1
	6388	AACTCCTTCGT	1,00	0,38	Hs.137594	H2B histone family, member C
15	6389	TCTCAAGAAGC	1,00	0,38	Hs.100555	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 18 (Myc
	6390	GCCGTGTCCGC	38,00	10,00	Hs.241507	ribosomal protein S6
	6391	GGCTCCTGGCT	5,00	1,66	Hs.5215	integrin beta 4 binding protein
20	6392	TTCACAGTGGC	5,00	1,67	Hs.169992	hypothetical 43.2 Kd protein
	6393	TGGCTGTGTGG	4,00	1,39	Hs.25709	ESTs, Weakly similar to PSF_HUMAN PTB-ASSOCIATED SPL
	6394	TACAAAAGTGG	2,00	0,76	Hs.194662	calponin 3, acidic
25	6395	GGCAGGCGGGT	2,00	0,76	Hs.110906	Ets2 repressor factor
	6396	TGGCCCCAGGT	4,00	1,39	Hs.268571	apolipoprotein C-I
	6397	ATCAGTGGCTT	6,00	1,97	Hs.89545	proteasome (prosome, macropain) subunit, beta type,
30	6398	GCCTGCAGTCT	7,00	2,25	Hs.31439	serine protease inhibitor, Kunitz type, 2
	6399	GAAAGGTCTGG	3,00	1,10	Hs.118778	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein
	6400	AGGAATGCTTT	2,00	0,77	Hs.84131	threonyl-tRNA synthetase
35	6401	GCTGCTGGTGT	2,00	0,77	Hs.181391	hypothetical protein DKFZp761G2113
	6402	TGGAACAGGAT	1,00	0,39	Hs.90077	TG-interacting factor (TALE family homeobox)
	6403	CTACACCAGTT	1,00	0,39	Hs.71787	30S ribosomal protein S7 homolog
40	6404	CAGGATGACGC	1,00	0,39	Hs.66048	hypothetical protein FLJ10669
	6405	AGGGCAGTACT	1,00	0,39	Hs.265561	CD2-associated protein
	6406	CCCATCGTCTT	1,00	0,39	Hs.21490	hypothetical protein FLJ20302
	6407	CCTCCAGCAGC	1,00	0,39	Hs.17466	retinoic acid receptor responder (tazartene induced
45	6408	GAGTTCGACCT	1,00	0,39	Hs.145362	ESTs, Weakly similar to CHD2_HUMAN CHROMODOMAIN-HELI
	6409	CCCGACGTGCC	5,00	1,70	Hs.198269	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex,
50	6410	GCCTCTTGAAG	4,00	1,42	Hs.184326	CDC10 (cell division cycle 10, S. cerevisiae, homolo
	6411	CACACCCCTGA	2,00	0,77	Hs.90061	progesterone binding protein
55	6412	TAATAAAGCAT	2,00	0,77	Hs.4888	seryl-tRNA synthetase
	6413	GGGCAAGCCAG	2,00	0,77	Hs.110849	estrogen-related receptor alpha
	6414	TGGAAGGGCAC	3,00	1,11	Hs.132785	EAP30 subunit of ELL complex
	6415	CCTCCCCCGTC	4,00	1,43	Hs.268763	Breakpoint cluster region protein, uterine leiomyoma
60	6416	GAGGGGAAACG	2,00	0,78	Hs.81972	SHC (Src homology 2 domain-containing) transforming
	6417	GGAGGCAGGTG	2,00	0,78	Hs.206713	UDP-Gal:betaGlcNAc beta 1,4- galacto-

					syltransferase,
6418	ACAGACTGATA	1,00	0,40	Hs.98541	hypothetical protein
6419	TGGAAAGAGCC	1,00	0,40	Hs.9043	DKFZP564O092 protein
6420	CTTGGTAATTT	1,00	0,40	Hs.8768	hypothetical protein FLJ10849
6421	ACCTGTAATTG	1,00	0,40	Hs.284288	hqp0256 protein
6422	TTTCTGTAAA	1,00	0,40	Hs.12101	hypothetical protein
6423	GTTGCAGATAA	1,00	0,40	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) transferase (U)
6424	AGGTCCTAGCC	9,00	2,87	Hs.226795	glutathione S-transferase pi
6425	CAATGTGTTAT	6,00	2,03	Hs.74823	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex,
6426	CACAGGCAAAA	4,00	1,44	Hs.155291	KIAA0005 gene product
6427	CTGCACTTACT	4,00	1,45	Hs.77152	minichromosome maintenance deficient (S. cerevisiae)
6428	CGCATTAAGC	2,00	0,79	Hs.78793	protein kinase C, zeta
6429	AAGACTGGCTT	2,00	0,79	Hs.284296	Homo sapiens SURF-4 mRNA, complete cds
6430	GTGATCTCCGT	2,00	0,79	Hs.278554	heterochromatin-like protein 1
6431	GCCAAAACCTT	2,00	0,79	Hs.158287	KIAA0468 gene product
6432	TTCTGTGAATC	5,00	1,75	Hs.77870	ESTs
6433	TTACTTCCCCA	3,00	1,13	Hs.184641	delta-6 fatty acid desaturase
6434	CCCATCCGAAA	22,00	6,47	Hs.91379	ribosomal protein L26
6435	TTTCAGGGGAG	6,00	2,06	Hs.3804	DKFZP564C1940 protein
6436	GGCCCCGGACC	4,00	1,46	Hs.4742	anchor attachment protein 1 (Gaa1p, yeast) homolog
6437	CCAAGAAAGAA	2,00	0,80	Hs.169900	poly(A)-binding protein, cytoplasmic 4 (inducible fo
6438	GTGCTGGTGCT	1,00	0,40	Hs.9613	PPAR(gamma) angiopoietin related protein
6439	CCTTTGTAAAA	1,00	0,40	Hs.78465	v-jun avian sarcoma virus 17 oncogene homolog
6440	TTCTCAAGAAA	1,00	0,40	Hs.37189	similar to rat HREV107
6441	CTTTATGTGAT	1,00	0,40	Hs.3352	histone deacetylase 2
6442	TAGACTTCCTT	1,00	0,40	Hs.30011	ESTs
6443	ACATTTC AATT	1,00	0,40	Hs.285999	trinucleotide repeat containing 15
6444	CATTATCATC	1,00	0,40	Hs.227777	protein tyrosine phosphatase type IVA, member 1
6445	GATGGCTGCCT	1,00	0,40	Hs.18104	hypothetical protein FLJ11274
6446	TGGAAACTTTC	1,00	0,40	Hs.153834	KIAA0099 gene product
6447	CTGAAAAAAA	1,00	0,40	Hs.12142	hypothetical protein FLJ20563
6448	GCAGCTCCTGT	3,00	1,14	Hs.119257	ems1 sequence (mammary tumor and squamous cell carci
6449	GATGCTGCCAA	12,00	3,78	Hs.99914	ribosomal protein L22
6450	TGTGCTAATAT	3,00	1,15	Hs.183037	protein kinase, cAMP-dependent, regulatory, type I,
6451	TCCTGAAATAA	2,00	0,81	Hs.5636	Homo sapiens clone 23704 mRNA sequence
6452	CAGCATCTAAT	2,00	0,81	Hs.184062	putative Rab5-interacting protein
6453	GAGAGTAACAG	2,00	0,81	Hs.16003	retinoblastoma-binding protein 4
6454	TTTAATTGTGA	2,00	0,81	Hs.145279	SET translocation (myeloid leukemia-

					associated)
6455	GTGACCTCCTT	11,00	3,56	Hs.81097	cytochrome c oxidase subunit VIII
6456	GTTTTTGCTTC	4,00	1,48	Hs.79110	nucleolin
6457	AGGCATTGAAA	3,00	1,16	Hs.151734	nuclear transport factor 2 (placental protein 15)
6458	GAATGAGGACA	3,00	1,16	Hs.167791	reticulocalbin 1, EF-hand calcium binding domain
6459	GATCTCGCAAA	2,00	0,81	Hs.250773	signal sequence receptor, alpha (translocon-associated)
6460	CAGTGGGTGTT	2,00	0,81	Hs.220689	Ras-GTPase-activating protein SH3-domain-binding pro
6461	TGGACACAAGC	2,00	0,81	Hs.180832	arginyl-tRNA synthetase
6462	TGTGATCACAA	1,00	0,41	Hs.9661	proteasome (prosome, macropain) subunit, beta type,
6463	TGTGCTGTGCT	1,00	0,41	Hs.772	glycogen synthase 1 (muscle)
6464	GACAATGAGAA	1,00	0,41	Hs.75253	isocitrate dehydrogenase 3 (NAD+) gamma
6465	TTCCCTGCAAG	1,00	0,41	Hs.61628	calcium binding atopy-related autoantigen 1
6466	AAACAAATCAC	1,00	0,41	Hs.173714	MORF-related gene X
6467	GTTCACTGCAG	1,00	0,41	Hs.168383	intercellular adhesion molecule 1 (CD54), human rhin
6468	TTACACTAATA	1,00	0,41	Hs.159	tumor necrosis factor receptor superfamily, member 1
6469	GTAGGAAAGCT	1,00	0,41	Hs.132243	aminopeptidase puromycin sensitive
6470	GCGACGAGGCG	19,00	5,92	Hs.2017	ribosomal protein L38
6471	AAGTGATTCTG	3,00	1,19	Hs.180677	zinc finger protein 162
6472	GGCCTTTTTTT	4,00	1,52	Hs.109804	H1 histone family, member X
6473	AATATTGAGAA	4,00	1,52	Hs.106673	eukaryotic translation initiation factor 3, subunit
6474	TCATTGTAATG	2,00	0,83	Hs.283722	GTT1 protein
6475	GTGGCCACGGC	2,00	0,83	Hs.112405	S100 calcium-binding protein A9 (calgranulin B)
6476	AGACAGAGTGG	2,00	0,83	Hs.103833	ESTs, Weakly similar to AF151869_1 CGI-111 protein [
6477	ATGCAAGAGAG	1,00	0,42	Hs.78521	ESTs
6478	GGAGGAATTC	1,00	0,42	Hs.78056	cathepsin L
6479	GCGGGAGCGGG	1,00	0,42	Hs.78054	KIAA0224 gene product
6480	AGGATTAAAAA	1,00	0,42	Hs.72531	ESTs, Weakly similar to unknown [D.melanogaster]
6481	AAGAGCTAATG	1,00	0,42	Hs.55921	glutamyl-prolyl-tRNA synthetase
6482	GGAAGAGAAGG	1,00	0,42	Hs.40500	similar to S. cerevisiae RER1
6483	GGCTCCTTGAG	1,00	0,42	Hs.283741	exosome component Rrp46
6484	TGCCTCGTGAA	1,00	0,42	Hs.27160	ESTs
6485	AGAAGGCCTTG	1,00	0,42	Hs.239114	mannosidase, alpha, class 1A, member 2
6486	CTTGGGAGGCG	1,00	0,42	Hs.226223	KIAA0618 gene product
6487	CCCGGTGTGTG	1,00	0,42	Hs.20950	ESTs, Weakly similar to predicted using Genefinder [
6488	CCCGGCTCTTA	1,00	0,42	Hs.184544	ESTs

6489	GGTACCCATTT	1,00	0,42	Hs.180383	dual specificity phosphatase 6	
6490	GGTACAAATAA	1,00	0,42	Hs.173422	cAMP responsive element binding protein 3 (human)	
6491	CTTCTGCAAAT	1,00	0,42	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (from clone DKF	5
6492	ACCCAGCGGGC	1,00	0,42	Hs.126705	ESTs	
6493	GGAGCACTGTG	1,00	0,42	Hs.10362	ESTs	
6494	GAGAATTAATC	1,00	0,42	Hs.101025	basic transcription factor 3	10
6495	GAAAAAAAAAA	12,00	3,99	Hs.14839	polymerase (RNA) II (DNA directed) polypeptide G	
6496	GTGGGTGTCCT	2,00	0,84	Hs.27633	DKFZP586B0519 protein	
6497	ACCCACCCAG	2,00	0,84	Hs.240534	1-acylglycerol-3-phosphate O-acyltransferase 1 (lyso	15
6498	GCCAAGCCTGA	2,00	0,84	Hs.118796	annexin A6	
6499	AAAGGAAAGTC	2,00	0,84	Hs.109706	HN1 protein	
6500	GGGGTAAGAAA	8,00	2,81	Hs.80423	prostatic binding protein	20
6501	TGTCATCACAG	2,00	0,84	Hs.83354	lysyl oxidase-like 2	
6502	GAGAACGGGGA	2,00	0,84	Hs.6191	hypothetical protein DKFZp7621166	
6503	GACTCTGGGAT	2,00	0,84	Hs.11282	ESTs, Weakly similar to cleft lip and palate transme	25
6504	AAAGGGGGCAG	3,00	1,21	Hs.249247	heterogeneous nuclear protein similar to rat helix d	
6505	GTGTAATAAGA	7,00	2,52	Hs.75598	heterogeneous nuclear ribonucleoprotein A2/B1	30
6506	TGTATTACAGT	1,00	0,43	Hs.92909	SON DNA binding protein	
6507	CCTGAAGAAGT	1,00	0,43	Hs.78948	Rab geranylgeranyltransferase, beta subunit	
6508	CACGTTCCCTA	1,00	0,43	Hs.74579	KIAA0263 gene product	35
6509	AGGGATGGCCC	1,00	0,43	Hs.54411	putative T1/ST2 receptor binding protein	
6510	CTCTCAATATA	1,00	0,43	Hs.279518	amyloid precursor protein homolog HSD-2	
6511	TAAACTTTGTA	1,00	0,43	Hs.227891	ESTs, Weakly similar to Y167_HUMAN HYPOTHETICAL PROT	40
6512	CTATGGGATTT	1,00	0,43	Hs.179574	protein phosphatase 2 (formerly 2A), regulatory subu	
6513	TACTGTAGTCA	1,00	0,43	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT2RP2000369	45
6514	CTGGAGGCTGC	1,00	0,43	Hs.149152	ESTs, Weakly similar to rhophilin [M.musculus]	
6515	GCCCCTGAAGG	1,00	0,43	Hs.117582	CGI-43 protein	50
6516	GAGTCTGAGGG	2,00	0,85	Hs.174051	small nuclear ribonucleoprotein 70kD polypeptide (RN	
6517	GTGCGCTAGGG	8,00	2,86	Hs.9408	IKK-related kinase epsilon; inducible IkappaB kinase	55
6518	GAAAAGGGTTT	2,00	0,86	Hs.284287	putative integral membrane transporter	
6519	TGTTAATGTTA	2,00	0,86	Hs.261828	Homo sapiens mRNA; cDNA DKFZp434N0211 (from clone DK	
6520	TTCAGTGCCCA	1,00	0,43	Hs.74649	cytochrome c oxidase subunit VIc	60
6521	GGCAGCCTGGT	1,00	0,43	Hs.6430	protein with polyglutamine repeat; calcium (ca2+) ho	
6522	ACTACAGCACG	1,00	0,43	Hs.59745	NADH dehydrogenase (ubiquinone)	

					flavoprotein 3 (10kD
6523	GACTTCTGAGC	1,00	0,43	Hs.274317	DEAD-box protein abstrakt
6524	TTGGTGCTTGG	1,00	0,43	Hs.26343	ESTs
6525	ACTGGAACGAA	1,00	0,43	Hs.11223	isocitrate dehydrogenase 1 (NADP+), soluble
6526	GCTTGATGTGA	1,00	0,43	Hs.108548	hypothetical protein
6527	AAGCTGCTGGA	3,00	1,24	Hs.9822	HCNP protein
6528	CTGGGACTGAC	3,00	1,24	Hs.76719	U6 snRNA-associated Sm-like protein
6529	TGGGTGGGGGG	2,00	0,87	Hs.25197	STIP1 homology and U-Box containing protein 1
6530	GACCCTGCCCT	11,00	3,89	Hs.173464	FK506-binding protein 8 (38kD)
6531	GTTCGTGCCAA	20,00	6,71	Hs.179666	ribosomal protein L35a
6532	GACCAGAAAAA	5,00	1,95	Hs.180714	cytochrome c oxidase subunit VIa polypeptide 1
6533	GTGAAGGCAGT	33,00	10,73	Hs.77039	ribosomal protein S3A
6534	CAGATCTTTGT	9,00	3,29	Hs.119502	ubiquitin A-52 residue ribosomal protein fusion prod
6535	TGGGCTCTGAA	1,00	0,44	Hs.85963	CD36 antigen (collagen type I receptor, thrombospond
6536	CTTCGCGATGG	1,00	0,44	Hs.78871	KIAA0081 protein
6537	GAGGTCCTTCG	1,00	0,44	Hs.6453	inositol 1,3,4-triphosphate 5/6 kinase
6538	GTACATTGTAA	1,00	0,44	Hs.39122	ESTs
6539	GTTAATTGCTA	1,00	0,44	Hs.32148	AD-015 protein
6540	GCTTATAAAAA	1,00	0,44	Hs.256697	histidine triad nucleotide-binding protein
6541	CATACACACAC	1,00	0,44	Hs.254279	EST
6542	TTTCTCTCCCT	1,00	0,44	Hs.236030	SWI/SNF related, matrix associated, actin dependent
6543	CCCAATAAACT	1,00	0,44	Hs.233765	amida, partner of the E2A
6544	TAACAGTTGTG	1,00	0,44	Hs.155560	calnexin
6545	CTGCCATAACT	2,00	0,88	Hs.110445	CGI-97 protein
6546	TTCTCTCCCCA	2,00	0,88	Hs.106909	DKFZP566D193 protein
6547	CCCAGGGAGAA	3,00	1,27	Hs.79150	chaperonin containing TCP1, subunit 4 (delta)
6548	TGGCCTGCCCA	3,00	1,27	Hs.181002	MLL septin-like fusion (NOTE: non-standard symbol an
6549	TTACCTCCTTC	9,00	3,34	Hs.3343	phosphoglycerate dehydrogenase
6550	GCCAGCCCAGC	7,00	2,68	Hs.228059	KRAB-associated protein 1
6551	ATCTCTATCCC	1,00	0,45	Hs.75102	alanyl-tRNA synthetase
6552	CACCGGACACT	1,00	0,45	Hs.74649	cytochrome c oxidase subunit VIc
6553	GAATTTGTGTA	1,00	0,45	Hs.28707	signal sequence receptor, gamma (translocon-associat
6554	AAATTAAAACA	1,00	0,45	Hs.198307	von Hippel-Lindau binding protein 1
6555	TTTTTCAATCA	1,00	0,45	Hs.169387	KIAA0036 gene product
6556	CCTCTGGAGGC	1,00	0,45	Hs.167246	P450 (cytochrome) oxidoreductase
6557	CCTCCCCTGCA	1,00	0,45	Hs.14068	ESTs
6558	CATCCAAAACA	3,00	1,28	Hs.245710	heterogeneous nuclear ribonucleoprotein H1 (H)
6559	GTCTCATTTGA	2,00	0,89	Hs.92381	nudix (nucleoside diphosphate linked moiety X)-type
6560	ACACCTCTAAA	2,00	0,89	Hs.273230	hypothetical protein FLJ10830

6561	ATGGAGACTTC	2,00	0,89	Hs.239760	citrate synthase
6562	TGATCACCTAT	2,00	0,89	Hs.177861	CGI-110 protein
6563	GGAATAAATTA	4,00	1,65	Hs.697	cytochrome c-1
6564	AACTGTCCTTC	3,00	1,30	Hs.194673	phosphoprotein enriched in astrocytes 15
6565	ATCTTGTTACT	9,00	3,40	Hs.118162	fibronectin 1
6566	ATGGCTGGTAT	61,00	20,14	Hs.182426	ribosomal protein S2
6567	TTCTCTTCTCC	1,00	0,46	Hs.6106	RNA binding motif protein 4
6568	TACACTGCTTT	1,00	0,46	Hs.284233	NICE-5 protein
6569	ATGGATGCACT	1,00	0,46	Hs.24983	hypothetical protein from EUROIMAGE 2021883
6570	ACAAACAAAAG	1,00	0,46	Hs.23964	sin3-associated polypeptide, 18kD
6571	GCTCCAGCCAT	1,00	0,46	Hs.1706	interferon-stimulated transcription factor 3, gamma
6572	ACCTCTGGCTT	1,00	0,46	Hs.155606	paired mesoderm homeo box 1
6573	GGATGTAGAGA	1,00	0,46	Hs.155485	huntingtin interacting protein 2
6574	CTTTCAGATGT	4,00	1,69	Hs.99910	phosphofructokinase, platelet
6575	GAGGGTGCCAA	2,00	0,91	Hs.8986	complement component 1, q subcomponent, beta polypep
6576	GCTTCCATCTT	3,00	1,32	Hs.55296	HLA-B associated transcript-1
6577	GCACCTCAGCC	3,00	1,32	Hs.10702	hypothetical protein DKFZp761H221
6578	CCTACAGATAA	1,00	0,47	Hs.79037	heat shock 60kD protein 1 (chaperonin)
6579	AAGGAGCGGGA	1,00	0,47	Hs.43543	suppressor of white apricot homolog 2
6580	CCAAGGAATGG	1,00	0,47	Hs.271934	Homo sapiens mRNA; cDNA DKFZp434M162 (from clone DKF
6581	ATTCAGCCACG	1,00	0,47	Hs.26229	KIAA1366 protein
6582	AGTTTTATTTG	1,00	0,47	Hs.236494	RAB10, member RAS oncogene family
6583	TGAGGAAGACA	1,00	0,47	Hs.159627	death associated protein 3
6584	AGGTCCCTGTC	1,00	0,47	Hs.109571	translocase of inner mitochondrial membrane 10 (yeas
6585	CGCTTTGCGCG	1,00	0,47	Hs.106357	valosin-containing protein
6586	AAGAAGATAGA	16,00	5,89	Hs.184776	ribosomal protein L23a
6587	CTGAGACAAAG	8,00	3,16	Hs.101025	basic transcription factor 3
6588	GAAACAAGATG	6,00	2,45	Hs.78771	phosphoglycerate kinase 1
6589	GTGCGCTGAGC	6,00	2,45	Hs.277477	major histocompatibility complex, class I, C
6590	TGTGATCAGAC	13,00	4,90	Hs.107476	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1F0, s
6591	GTGATGGTGTA	6,00	2,46	Hs.197345	thyroid autoantigen 70kD (Ku antigen)
6592	TTTTGTGTGAA	3,00	1,34	Hs.182698	hypothetical protein FLJ10024
6593	GAGTGAGTGAG	2,00	0,93	Hs.10463	ESTs, Weakly similar to C44C1.2 gene product [C.eleg
6594	GGAGGGATCAG	3,00	1,34	Hs.6196	integrin-linked kinase
6595	GTAACTGGGA	1,00	0,47	Hs.48295	RNA helicase family
6596	GCAGGAACAGC	1,00	0,47	Hs.4770	KIAA1068 protein
6597	TAAGTTCCTTC	1,00	0,47	Hs.237971	ESTs
6598	TGTACATTCTG	1,00	0,47	Hs.1624	ephrin-A1
6599	CGGGATGCAGA	1,00	0,47	Hs.155560	calnexin
6600	AAGATTGGGGT	2,00	0,94	Hs.169610	CD44 antigen (homing function and Indian blood group
6601	GACTCACTTTT	13,00	4,99	Hs.699	peptidylprolyl isomerase B (cyclophilin B)

6602	GTGGTACAGGA	6,00	2,50	Hs.31731	peroxiredoxin 5
6603	CCAAGTTTTTT	4,00	1,75	Hs.75914	coated vesicle membrane protein
6604	CCTTGACCAAT	2,00	0,95	Hs.8148	selenoprotein T
6605	GAATCATTTTG	2,00	0,95	Hs.75249	ADP-ribosylation factor-like 6 interacting protein
6606	CGCTGTGGGGT	2,00	0,95	Hs.7486	protein expressed in thyroid
6607	CGGGGAGATGA	2,00	0,95	Hs.243960	N-myc downstream-regulated gene 2
6608	TCCGCGAGAAG	5,00	2,15	Hs.1665	zinc finger protein homologous to Zfp-36 in mouse
6609	TACAATAATTT	2,00	0,95	Hs.2730	heterogeneous nuclear ribonucleoprotein L
6610	CTGACCCCCTT	2,00	0,95	Hs.26492	beta-1,3-glucuronyltransferase 3 (glucuronosyltransf
6611	CTTTCCCCTTT	2,00	0,95	Hs.183800	Ran GTPase activating protein 1
6612	GGGCCCTTCCT	2,00	0,95	Hs.168073	DKFZP727M231 protein
6613	AACCAGTTTGT	2,00	0,95	Hs.15591	COP9 subunit 6 (MOV34 homolog, 34 kD)
6614	GAAGTCAGGCC	1,00	0,48	Hs.83634	host cell factor C1 (VP16-accessory protein)
6615	CTGAGGCCTGG	1,00	0,48	Hs.82109	syndecan 1
6616	TTAGTTACCTT	1,00	0,48	Hs.77273	ras homolog gene family, member A
6617	GGTAGCCACG	1,00	0,48	Hs.56828	trinucleotide repeat containing 5
6618	ACAGCTTTGTA	1,00	0,48	Hs.21229	f-box and WD-40 domain protein 1B
6619	TTCAGGGCTTC	1,00	0,48	Hs.184242	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase)
6620	GGAATGTACGT	9,00	3,64	Hs.429	ATP synthase, H+ transporting, mitochondrial F0 comp
6621	TCTCCAGGAAC	4,00	1,77	Hs.237924	CGI-69 protein
6622	AAGTGAGGAGA	4,00	1,77	Hs.231840	WW domain binding protein 2
6623	CTGGCGCCGAT	3,00	1,38	Hs.183180	hypothetical protein
6624	GTGTGGTGGTG	2,00	0,97	Hs.56845	GDP dissociation inhibitor 2
6625	TGGAAGGGCTC	2,00	0,97	Hs.31334	putative mitochondrial outer membrane protein import
6626	TAGTAAGTCAT	1,00	0,49	Hs.99914	ribosomal protein L22
6627	TCTCCCTTCAA	1,00	0,49	Hs.82906	CDC20 (cell division cycle 20, S. cerevisiae, homolo
6628	GGCAGATAGGT	1,00	0,49	Hs.285785	Homo sapiens cDNA FLJ20115 fis, clone COL05594
6629	CAGATTGTGAA	1,00	0,49	Hs.142653	ret finger protein
6630	GACCTGGGGA	1,00	0,49	Hs.116708	ESTs, Weakly similar to Y063_HUMAN HYPOTHETICAL PROT
6631	TGGCGGAGTCC	1,00	0,49	Hs.10915	ESTs, Weakly similar to F-box protein FBL9 [H.sapien
6632	GATGGTCAGTC	1,00	0,49	Hs.108779	DKFZP586E1519 protein
6633	GGCTTGGTTTA	1,00	0,49	Hs.107362	KIAA0909 protein
6634	TAGCTCTATGG	4,00	1,81	Hs.190703	ATPase, Na+/K+ transporting, alpha 1 polypeptide
6635	GAATTTTATAA	4,00	1,82	Hs.202	benzodiazapine receptor (peripheral)
6636	CGGCTGAATTC	3,00	1,42	Hs.75888	phosphogluconate dehydrogenase
6637	TGGGTGAGCCA	7,00	3,01	Hs.249982	cathepsin B



6638	GAAGGCATCCT	3,00	1,42	Hs.250758	proteasome (prosome, macropain) 26S subunit, ATPase,	
6639	GGGCCCCGCAG	2,00	0,99	Hs.75353	KIAA0123 protein	5
6640	GCCCGCAGGGT	2,00	0,99	Hs.74375	dishevelled 1 (homologous to Drosophila dsh)	
6641	GACAGATGGAC	1,00	0,50	Hs.83575	KIAA1533 protein	
6642	GAGTAGAGGCC	1,00	0,50	Hs.77813	sphingomyelin phosphodiesterase 1, acid lysosomal (a	10
6643	GCAGCCCGCGG	1,00	0,50	Hs.71472	ESTs, Highly similar to unnamed protein product [H.s	
6644	GTGATTGTTCA	1,00	0,50	Hs.6727	Ras-GTPase activating protein SH3 domain-binding pro	15
6645	CTCCTGAAGGC	1,00	0,50	Hs.4890	ubiquitin-conjugating enzyme E2E 3 (homologous to ye	
6646	GATAGGTCGGG	1,00	0,50	Hs.154721	aconitase 1, soluble	
6647	TTGTTTGTAAG	1,00	0,50	Hs.15020	homolog of mouse quaking QKI (KH domain RNA binding	20
6648	GTATAATTTGT	1,00	0,50	Hs.107979	small membrane protein 1	
6649	AAAAATAAAGG	7,00	3,02	Hs.155101	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 comp	25
6650	GCCTGTATGAG	26,00	10,09	Hs.180450	ribosomal protein S24	
6651	TTTCTGTATGT	2,00	1,00	Hs.180877	H3 histone, family 3B (H3.3B)	
6652	TCTTGTGCATA	8,00	3,45	Hs.2795	lactate dehydrogenase A	
6653	TCATCTTCAAC	2,00	1,00	Hs.75525	calreticulin	30
6654	TCACTTTCTTT	1,00	0,51	Hs.78865	TATA box binding protein (TBP)-associated factor, RN	
6655	TGGAGGGGCCA	1,00	0,51	Hs.74362	ClpP (caseinolytic protease, ATP-dependent, proteoly	35
6656	ATTGTGAACAA	1,00	0,51	Hs.55043	ESTs	
6657	TCTGTTTCCAG	1,00	0,51	Hs.155227	EphB4	
6658	TGGAATGAGCG	1,00	0,51	Hs.153998	creatine kinase, mitochondrial 1 (ubiquitous)	40
6659	GCTGGAGCGCC	1,00	0,51	Hs.12284	ESTs, Weakly similar to HS6B_DROME HEAT SHOCK PROTEI	
6660	GCTTTTTAGAA	7,00	3,10	Hs.251064	high-mobility group (nonhistone chromosomal) protein	45
6661	AAGTTTCCAAT	2,00	1,01	Hs.2903	protein phosphatase 4 (formerly X), catalytic subuni	
6662	TTTCCTTCCTT	2,00	1,01	Hs.104143	clathrin, light polypeptide (Lca)	
6663	CCTTCCAAATT	4,00	1,91	Hs.111076	malate dehydrogenase 2, NAD (mitochondrial)	50
6664	TCCTCTTTCCA	1,00	0,52	Hs.943	natural killer cell transcript 4	
6665	TGTCCTGGTTG	1,00	0,52	Hs.93765	lipoma HMGIC fusion partner	
6666	GTGGAAGACGA	1,00	0,52	Hs.80395	mal, T-cell differentiation protein	55
6667	ATTTGCCTCTG	1,00	0,52	Hs.7393	Homo sapiens mRNA full length insert cDNA clone EURO	
6668	CTGGGCCTCTG	1,00	0,52	Hs.50868	solute carrier family 22 (organic cation transporter	60
6669	TCTGAATCGGG	1,00	0,52	Hs.4316	trinucleotide repeat containing 12	
6670	GTGTGAAATAA	1,00	0,52	Hs.199179	RAN binding protein 2	
6671	CACGGACTCGT	1,00	0,52	Hs.170195	bone morphogenetic protein 7 (osteoge-	65

					nic protein 1)
5	6672	GCAGCAGGAAG	1,00	0,52	Hs.165743 tumor suppressing subtransferable candidate 4
	6673	CGGGTAGTATT	1,00	0,52	Hs.1437 glucosidase, alpha; acid (Pompe disease, glycogen st
	6674	AAAATATTTTA	1,00	0,52	Hs.119000 actinin, alpha 1
10	6675	TTTGTTAATTC	3,00	1,48	Hs.278857 heterogeneous nuclear ribonucleoprotein H2 (H')
	6676	GTGCTGAATGG	27,00	10,97	Hs.77385 myosin, light polypeptide 6, alkali, smooth muscle a
15	6677	GGCACCTCTGC	2,00	1,03	Hs.3763 amyloid beta (A4) precursor protein-binding, family
	6678	GGTGCTGGAGA	2,00	1,03	Hs.155020 putative methyltransferase
	6679	AATGCTTTGTT	10,00	4,38	Hs.272897 Tubulin, alpha, brain-specific
20	6680	CGGAGTCCATT	4,00	1,94	Hs.155595 neural precursor cell expressed, developmentally down
	6681	CGATGGTCCCC	3,00	1,50	Hs.7771 B-cell associated protein
	6682	CAGCTCCGCTT	2,00	1,04	Hs.82113 dUTP pyrophosphatase
	6683	ATAAAAAAAAAA	1,00	0,52	Hs.83942 cathepsin K (pseudodysostosis)
25	6684	GGACCTGCGCC	1,00	0,52	Hs.8297 ribonuclease 6 precursor
	6685	GAAACCCTCAC	1,00	0,52	Hs.75859 chromosome 11 open reading frame 4
	6686	GCAACCACGAC	1,00	0,52	Hs.182986 CGI-36 protein
	6687	GGATGCATTAG	1,00	0,52	Hs.172635 ESTs
30	6688	GCCAGCGTCAT	1,00	0,52	Hs.13386 gamma-tubulin complex protein 2
	6689	CCAAACGTGTA	12,00	5,24	Hs.181307 H3 histone, family 3A
	6690	TTCACAAAGGA	2,00	1,05	Hs.76913 proteasome (prosome, macropain) subunit, alpha type,
35	6691	GGTTTGGCTTA	7,00	3,25	Hs.73818 ubiquinol-cytochrome c reductase hinge protein
	6692	GGTTGGCAGGG	5,00	2,41	Hs.3745 milk fat globule-EGF factor 8 protein
	6693	TATAATCTTTA	1,00	0,53	Hs.923 single-stranded DNA-binding protein
40	6694	TAAAATTGCTG	1,00	0,53	Hs.75257 Hairpin binding protein, histone
	6695	CCGGAATGTGG	1,00	0,53	Hs.54702 xylosylprotein beta1,4-galactosyltransferase, polype
	6696	TTGTATTCCAG	1,00	0,53	Hs.3631 immunoglobulin (CD79A) binding protein 1
45	6697	GTACGTCTGGC	1,00	0,53	Hs.279754 pilin-like transcription factor
	6698	AAAACCTTTGTC	1,00	0,53	Hs.272458 protein phosphatase 3 (formerly 2B), catalytic subun
50	6699	GGGAGTAATAG	1,00	0,53	Hs.26045 protein tyrosine phosphatase, receptor type, A
	6700	TTTAATTTGTA	1,00	0,53	Hs.182793 golgi membrane protein GP73
	6701	AATACTTTTGT	1,00	0,53	Hs.165998 DKFZP564M2423 protein
	6702	CATTTACAGAGA	1,00	0,53	Hs.15259 BCL2-associated athanogene 3
55	6703	TCAATAAAGGA	1,00	0,53	Hs.118797 ubiquitin-conjugating enzyme E2D 3 (homologous to ye
	6704	GGAACCTTTAG	3,00	1,53	Hs.43857 similar to glucosamine-6-sulfatases
	6705	GGGGCAGGGCC	12,00	5,35	Hs.119140 eukaryotic translation initiation factor 5A
60	6706	TTCTAACATAT	2,00	1,06	Hs.78629 ATPase, Na <sup>+</sup> /K <sup>+</sup> transporting, beta 1 polypeptide

6707	GGGAGGGAAGA	2,00	1,06	Hs.75243	bromodomain-containing 2	
6708	AAGATCCCCGC	5,00	2,43	Hs.107187	divalent cation tolerant protein CUTA	
6709	GTATTGGCCTT	2,00	1,07	Hs.28757	transmembrane 9 superfamily member 2	5
6710	TTCTCCCGCTT	2,00	1,07	Hs.118126	protective protein for beta-galactosidase (galactosi	
6711	GAGTAAAAAAT	1,00	0,54	Hs.944	glucose phosphate isomerase	
6712	TACAATAAACC	1,00	0,54	Hs.9071	progesterone membrane binding protein	10
6713	TTGACCCTGGG	1,00	0,54	Hs.8128	phosphatidylserine decarboxylase	
6714	AGCCTGACTGC	1,00	0,54	Hs.80206	glucose-6-phosphate dehydrogenase	
6715	GAGGATTTGGG	1,00	0,54	Hs.43549	uncharacterized hematopoietic stem/progenitor cells	
6716	TGCTTTCAAAA	1,00	0,54	Hs.31439	serine protease inhibitor, Kunitz type, 2	15
6717	AAAGCAGTTTA	1,00	0,54	Hs.262962	ESTs	
6718	CTGTACTAGGT	1,00	0,54	Hs.226499	nesca protein	
6719	TGGGAGAAGTG	1,00	0,54	Hs.184544	ESTs	
6720	TCCTTGTTGGC	1,00	0,54	Hs.155742	glyoxylate reductase/hydroxypyruvate reductase	20
6721	GAGACTGCTTC	1,00	0,54	Hs.118078	ESTs	
6722	ACAACCTCAATA	4,00	2,01	Hs.75922	brain protein I3	
6723	CGCTTTTGTAG	2,00	1,08	Hs.5297	DKFZP564A2416 protein	25
6724	GAGGTCCCTGG	5,00	2,48	Hs.74077	proteasome (prosome, macropain) subunit, alpha type,	
6725	ATTGTTTATGG	12,00	5,52	Hs.181163	high-mobility group (nonhistone chromosomal) protein	30
6726	CTGAGGCGCTT	1,00	0,55	Hs.78769	thimet oligopeptidase 1	
6727	TTCATTTGTCT	1,00	0,55	Hs.78452	solute carrier family 20 (phosphate transporter), me	
6728	GAGAGCACCTT	1,00	0,55	Hs.273237	postmeiotic segregation increased 2-like 8	35
6729	AGTGGCTGCC	1,00	0,55	Hs.24435	ESTs	
6730	CCCTTCACTGG	1,00	0,55	Hs.22557	ESTs, Highly similar to unnamed protein product [H.s	40
6731	GCCTGGGACTC	3,00	1,58	Hs.98057	ESTs, Weakly similar to I68667 transcription factor	
6732	CACTCAGTGTG	2,00	1,10	Hs.75379	solute carrier family 1 (glial high affinity glutama	45
6733	TTTCTAGGGGT	3,00	1,59	Hs.108969	PTD008 protein	
6734	TCCAAGGAAGG	2,00	1,10	Hs.15250	peroxisomal D3,D2-enoyl-CoA isomerase	
6735	GCAAAACCAGC	3,00	1,60	Hs.15071	chaperonin containing TCP1, subunit 8 (theta)	50
6736	GCTGTTTTGTT	1,00	0,56	Hs.92186	Leman coiled-coil protein	
6737	GAGCTGTTGGT	1,00	0,56	Hs.851	integrin, alpha E (antigen CD103, human mucosal lymph	55
6738	CATAGAGCCAC	1,00	0,56	Hs.6118	hypothetical protein FLJ10968	
6739	AAACCTCTCAA	1,00	0,56	Hs.22981	DKFZP586M1523 protein	
6740	GAGGTGCTCTA	1,00	0,56	Hs.181385	uncharacterized hematopoietic stem/progenitor cells	60
6741	AGCCCGCCGCG	1,00	0,56	Hs.154036	tumor suppressing subtransferable candidate 3	

6742	CTAACTTCGTT	1,00	0,56	Hs.14838	hypothetical protein FLJ10773
6743	GGCTTTACCT	9,00	4,33	Hs.119140	eukaryotic translation initiation factor 5A
5 6744	CATCTGTGAGC	2,00	1,11	Hs.75189	death-associated protein
6745	CCCCCAATTCT	2,00	1,11	Hs.194534	vesicle-associated membrane protein 2 (synaptobrevin)
6746	AATTTCTATTT	2,00	1,12	Hs.5322	guanine nucleotide binding protein (G protein), gamma
10 6747	GCGATTCCGGA	2,00	1,12	Hs.283724	ESTs, Weakly similar to HYA22 [H.sapiens]
6748	TCAGTTTGGAG	3,00	1,63	Hs.3873	palmitoyl-protein thioesterase 1 (ceroid-lipofusino)
15 6749	TGTCAGAGATG	1,00	0,57	Hs.73957	RAB5A, member RAS oncogene family
6750	ATTGCTTTTGA	1,00	0,57	Hs.40500	similar to S. cerevisiae RER1
6751	GCTAGTGATGT	1,00	0,57	Hs.284162	60S ribosomal protein L30 isolog
6752	CCGGCGCGTGT	1,00	0,57	Hs.107387	CGI-20 protein
20 6753	TGCACCACAGA	2,00	1,13	Hs.9534	signal peptidase complex (18kD)
6754	ATGGCCAACTT	2,00	1,13	Hs.227835	KIAA1049 protein
6755	GTGTCTCATCT	2,00	1,13	Hs.144904	nuclear receptor co-repressor 1
6756	ATGAGCTATGA	1,00	0,57	Hs.8752	transmembrane protein 4
25 6757	GTCAGAACTTG	1,00	0,57	Hs.82101	pleckstrin homology-like domain, family A, member 1
6758	CTGAAATTCGG	1,00	0,57	Hs.79658	casein kinase 1, epsilon
6759	ACAAATTATGA	1,00	0,57	Hs.78902	voltage-dependent anion channel 2
30 6760	TTTGCAATTAT	1,00	0,57	Hs.75137	KIAA0193 gene product
6761	GGGCTGGGGTA	2,00	1,14	Hs.90436	sperm associated antigen 7
6762	GTGGGGCTAGG	2,00	1,15	Hs.75180	protein phosphatase 5, catalytic subunit
6763	GTGTGTAAAAA	2,00	1,15	Hs.181373	accessory proteins BAP31/BAP29
35 6764	AATGGATTACC	1,00	0,58	Hs.82202	ribosomal protein L17
6765	CTTGTAACAGA	1,00	0,58	Hs.82124	laminin, beta 1
6766	GAAGGCATCTT	1,00	0,58	Hs.71377	p138-tox
6767	GGGGGCCCGT	1,00	0,58	Hs.5809	putative transmembrane protein
40 6768	TGATGCGCGCT	1,00	0,58	Hs.25664	tumor suppressor deleted in oral cancer-related 1
6769	TCTGTGACCTT	1,00	0,58	Hs.198793	KIAA0750 gene product
6770	AGACAAGTTTA	1,00	0,58	Hs.120874	ESTs
45 6771	TTCCTGACTAC	1,00	0,58	Hs.10098	putative nucleolar RNA helicase
6772	GCAATAAATGG	2,00	1,16	Hs.89434	drebrin 1
6773	AGGAGCGGGGT	2,00	1,16	Hs.252189	syndecan 4 (amphiglycan, ryudocan)
50 6774	TCAGAAGTTTT	2,00	1,16	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HEP08257
6775	GCGGGGTACCC	4,00	2,18	Hs.227823	pM5 protein
6776	GCGGGAGGGCT	3,00	1,68	Hs.154162	ADP-ribosylation factor-like 2
6777	AAAGCAAACCA	2,00	1,16	Hs.161554	hypothetical protein FLJ20159
55 6778	GCACCCTCAGA	1,00	0,59	Hs.82294	regulator of G-protein signalling 3
6779	ATCTTTTAAAA	1,00	0,59	Hs.75867	solute carrier family 20 (phosphate transporter), me
6780	GGGCAGAATTG	1,00	0,59	Hs.70500	KIAA0370 protein
60 6781	ACTTTTTAAAA	1,00	0,59	Hs.226483	diaphanous (Drosophila, homolog) 2
6782	TATTCTCAATA	1,00	0,59	Hs.181311	asparaginyl-tRNA synthetase
6783	CGCTGTGTGCT	1,00	0,59	Hs.181246	glucosidase, beta; acid, pseudogene

6784	TCTGGACTCGG	1,00	0,59	Hs.153612	ATP-binding cassette, sub-family F (GCN20), member 2
6785	TTTCGTAGATG	1,00	0,59	Hs.107747	DKFZP566C243 protein
6786	ACAAATCCTTG	3,00	1,70	Hs.752	FK506-binding protein 1A (12kD)
6787	GTCTTAACTCA	2,00	1,17	Hs.5074	similar to S. pombe dim1+
6788	GAGTTATGTTG	2,00	1,17	Hs.279915	translocase of inner mitochondrial membrane 8 (yeast
6789	GAGTAGAGAAA	3,00	1,71	Hs.145279	SET translocation (myeloid leukemia-associated)
6790	ATAGGTCAGAA	4,00	2,23	Hs.29665	KIAA0911 protein
6791	TAATGGTAACT	4,00	2,24	Hs.181028	cytochrome c oxidase subunit Va
6792	GCAGTGGCCTC	2,00	1,19	Hs.184276	solute carrier family 9 (sodium/hydrogen exchanger),
6793	AACATTCTAAG	1,00	0,60	Hs.8813	syntaxin binding protein 3
6794	TGAGAGACATC	1,00	0,60	Hs.8164	Mulibrey nanism
6795	TGCTGCCTGTT	3,00	1,74	Hs.118110	bone marrow stromal cell antigen 2
6796	TGGATCCTAGA	3,00	1,75	Hs.5273	NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30kD
6797	GATCACAGTTT	3,00	1,75	Hs.234489	lactate dehydrogenase B
6798	AATGGAAATCG	1,00	0,61	Hs.4943	hepatocellular carcinoma associated protein; breast
6799	TTAATATATGC	1,00	0,61	Hs.237955	hypothetical protein PRO2706
6800	TTTTAACTTG	1,00	0,61	Hs.226770	DKFZP566C0424 protein
6801	CCCCAGTCGGC	1,00	0,61	Hs.171596	EphA2
6802	CTGGGTGAAGT	1,00	0,61	Hs.169388	ESTs
6803	ATCAAGAATCC	1,00	0,61	Hs.14623	interferon, gamma-inducible protein 30
6804	TAATAAATGCT	1,00	0,61	Hs.118463	(Manual assignment) MEMOREC GS2L1 putative phospholi
6805	ATTATTTTTCT	7,00	3,79	Hs.153	ribosomal protein L7
6806	ATTCCAATCTT	2,00	1,22	Hs.178710	clathrin, heavy polypeptide (Hc)
6807	ACTGGGTCTAT	10,00	5,34	Hs.275163	non-metastatic cells 2, protein (NM23B) expressed in
6808	TTAAGAGGGGG	2,00	1,22	Hs.243886	nuclear autoantigenic sperm protein (histone-binding
6809	CAAAGACAATT	1,00	0,62	Hs.23528	HSPC038 protein
6810	ACCCTCTCCCT	1,00	0,62	Hs.19122	eukaryotic translation initiation factor 4E-like 3
6811	TGGACCAGGCG	1,00	0,62	Hs.167641	hypothetical protein from EUROIMAGE 1703145
6812	ATGGTGCTGAC	1,00	0,62	Hs.166	sterol regulatory element binding transcription fact
6813	CTTTGATCAGG	1,00	0,62	Hs.118249	brefeldin A-inhibited guanine nucleotide-exchange pr
6814	GATGACGACTC	1,00	0,62	Hs.107019	sympleskin; Huntingtin interacting protein I
6815	ACAACTTAGG	6,00	3,36	Hs.177656	calmodulin 1 (phosphorylase kinase, delta)
6816	TCTTTACTTGA	2,00	1,23	Hs.6895	actin related protein 2/3 complex, subunit 3 (21 kD)
6817	AGTTGAAATTC	2,00	1,23	Hs.180428	KIAA1181 protein
6818	TCCGGCCGCGA	4,00	2,35	Hs.171774	hypothetical protein

	6819	ATGCGAAAGGC	2,00	1,24	Hs.89466	dodecenoyl-Coenzyme A delta isom- erase (3,2 trans-eno
5	6820	AAATAAGAAT	2,00	1,24	Hs.790	microsomal glutathione S-transferase 1
	6821	GTGCCTGTGCT	1,00	0,63	Hs.8888	Homo sapiens mRNA; cDNA DKFZp434C2019 (from clone DK
	6822	TAGGACCCTGC	1,00	0,63	Hs.76873	hyaluronoglucosaminidase 2
10	6823	GTAATGAAGCA	1,00	0,63	Hs.5011	RNA binding motif protein 9
	6824	CCGAAAAAGTG	1,00	0,63	Hs.24763	RAN binding protein 1
	6825	CTTCAGGACCT	1,00	0,63	Hs.239356	syntaxin binding protein 1
	6826	GACACAGGCAG	1,00	0,63	Hs.143641	low density lipoprotein receptor-related protein 3
15	6827	CAAATAAAAAG	1,00	0,63	Hs.1116	lymphotoxin beta receptor (TNFR super- family, member
	6828	GTGAAAAAAA	2,00	1,25	Hs.181373	accessory proteins BAP31/BAP29
20	6829	GCAGCTCAGGC	3,00	1,82	Hs.79572	cathepsin D (lysosomal aspartyl prote- ase)
	6830	TTGACACTTTC	3,00	1,82	Hs.26136	ESTs
	6831	AACTAATACTA	7,00	3,97	Hs.118724	DR1-associated protein 1 (negative cofactor 2 alpha)
25	6832	GGTGATGAGGA	2,00	1,26	Hs.12107	putative breast adenocarcinoma marker (32kD)
	6833	TAAGTTTAATT	1,00	0,64	Hs.75760	sterol carrier protein 2
	6834	AGACCATATTA	1,00	0,64	Hs.23964	sin3-associated polypeptide, 18kD
30	6835	TGGGCAGCTGG	1,00	0,64	Hs.180920	ribosomal protein S9
	6836	ATATTTTCCTG	1,00	0,64	Hs.128866	Novel human gene mapping to chomo- some 1
	6837	ATGCCCCTGAG	1,00	0,64	Hs.118223	microfibrillar-associated protein 4
35	6838	AGCTCTTGGAG	3,00	1,85	Hs.7833	selenium binding protein 1
	6839	GGCCAAAGGCC	2,00	1,28	Hs.278569	KIAA0064 gene product
	6840	ATCTGAAGCAA	2,00	1,28	Hs.256311	granin-like neuroendocrine peptide pre- cursor
40	6841	TAGCATTTTAA	1,00	0,64	Hs.77665	KIAA0102 gene product
	6842	ATGTGGCACAT	1,00	0,64	Hs.67776	ESTs
	6843	AGTTTCTTGTC	1,00	0,64	Hs.246381	CD68 antigen
45	6844	AAGTATTGTGT	1,00	0,64	Hs.100688	Homo sapiens cDNA FLJ11279 fis, clone PLACE1009444,
	6845	TTTTGGGGGCT	2,00	1,29	Hs.26683	ESTs, Weakly similar to lamin B receptor homolog TM7
	6846	AGTGTCTGTGA	3,00	1,88	Hs.8867	cysteine-rich, angiogenic inducer, 61
50	6847	TCACCCACACC	26,00	13,97	Hs.234518	ribosomal protein L23
	6848	AAGATTGGTGG	5,00	3,00	Hs.1244	CD9 antigen (p24)
	6849	TAGTTGAAGTC	6,00	3,55	Hs.131255	ubiquinol-cytochrome c reductase bind- ing protein
55	6850	ATACTTTAATC	2,00	1,29	Hs.79274	annexin A5
	6851	ATGGCTGGGCT	1,00	0,65	Hs.752	FK506-binding protein 1A (12kD)
	6852	TTCGCTTCCTG	1,00	0,65	Hs.6120	Homo sapiens mRNA; cDNA DKFZp434E146 (from clone DKF
60	6853	GAATGTAAGTA	1,00	0,65	Hs.6113	staufer (Drosophila, RNA-binding prote- in)
	6854	CTTTGCTGTGT	1,00	0,65	Hs.138617	thyroid hormone receptor interactor 12

6855	CCTGACGCTCC	1,00	0,65	Hs.11747	hypothetical protein FLJ20391	
6856	GGGCCTGACAT	1,00	0,65	Hs.11039	Homo sapiens clone 24804 mRNA sequence	5
6857	GGAAGCACGGA	4,00	2,46	Hs.148495	proteasome (prosome, macropain) 26S subunit, non-ATP	
6858	TCCTTCTCCAC	3,00	1,89	Hs.119000	actinin, alpha 1	
6859	AAATAGATCCA	2,00	1,30	Hs.171271	catenin (cadherin-associated protein), beta 1 (88kD)	10
6860	CAGCCCCTCTT	2,00	1,31	Hs.82503	H.sapiens mRNA for 3'UTR of unknown protein	
6861	AATACCTCGTG	2,00	1,31	Hs.24220	hypothetical protein	15
6862	CTGGTCCTCCT	1,00	0,66	Hs.9739	ESTs	
6863	ATCAAGTGGAC	1,00	0,66	Hs.79077	KIAA0233 gene product	
6864	GCTTATGTAA	1,00	0,66	Hs.75187	translocase of outer mitochondrial membrane 20 (yeas)	20
6865	AGCTTATTGAG	1,00	0,66	Hs.273077	Human DNA sequence from clone RP3-417M14 on chromoso	
6866	GGCTTCCTGGG	1,00	0,66	Hs.253041	EST	
6867	GACATCGAGGC	1,00	0,66	Hs.252574	ribosomal protein L10a	25
6868	TGATGTCTGGT	2,00	1,32	Hs.83883	PMEPA1 protein	
6869	GCTAAGGAGAT	5,00	3,08	Hs.286250	ras-related C3 botulinum toxin substrate 1 (rho fami	
6870	GCTGTTGCGCG	7,00	4,20	Hs.8102	ribosomal protein S20	30
6871	GCAGGGTGGGG	2,00	1,33	Hs.182278	calmodulin 2 (phosphorylase kinase, delta)	
6872	GGCTGCCCTGG	3,00	1,94	Hs.74566	dihydropyrimidinase-like 3	
6873	CAGTGAACAAG	1,00	0,67	Hs.9825	CGI-128 protein	35
6874	GTGGCCC GCAG	1,00	0,67	Hs.96200	neighbor of A-kinase anchoring protein 95	
6875	CTGCAGTTAGC	1,00	0,67	Hs.9614	ESTs, Weakly similar to Ps 2	
6876	GAAAGGATTTT	1,00	0,67	Hs.84318	replication protein A1 (70kD)	40
6877	TGCATATCATC	1,00	0,67	Hs.79090	exportin 1 (CRM1, yeast, homolog)	
6878	TGCGTCACCGT	1,00	0,67	Hs.78202	SWI/SNF related, matrix associated, actin dependent	
6879	TCTTGATTTAC	1,00	0,67	Hs.74561	alpha-2-macroglobulin	45
6880	GTGATGGGGCC	1,00	0,67	Hs.62620	chromosome 6 open reading frame 1	
6881	GGTGTGGGTGA	1,00	0,67	Hs.285363	ESTs	
6882	GGCCACTCTAG	1,00	0,67	Hs.23111	phenylalanine-tRNA synthetase-like	
6883	CTCCCTTGCCC	1,00	0,67	Hs.181271	CGI-120 protein	50
6884	GGCCCTGGTGT	1,00	0,67	Hs.153227	cyclin G associated kinase	
6885	AGGTTCTGCCT	1,00	0,67	Hs.102469	putative nuclear protein	
6886	TGATAATTCAA	5,00	3,14	Hs.100688	Homo sapiens cDNA FLJ11279 fis, clone PLACE1009444,	55
6887	TTTTCTGCATA	1,00	0,68	Hs.77318	platelet-activating factor acetylhydrolase, isoform	
6888	TGTTAGATTTC	1,00	0,68	Hs.77254	chromobox homolog 1 (Drosophila HP1 beta)	60
6889	TGGAAGAACT	1,00	0,68	Hs.37810	ESTs	
6890	GCCAGGTGGAA	1,00	0,68	Hs.29203	Homo sapiens G protein beta subunit mRNA, partial cd	

6891	TTTTGTTTTG	1,00	0,68	Hs.183418	cell division cycle 2-like 1 (PITSLRE proteins)
6892	TTAAGAGGGAC	1,00	0,68	Hs.178137	transducer of ERBB2, 1
6893	TTGGCAACATT	1,00	0,68	Hs.11463	UMP-CMP kinase
6894	TCGAAGAACCG	2,00	1,36	Hs.76294	CD63 antigen (melanoma 1 antigen)
6895	CACTTTTGGGC	2,00	1,37	Hs.75080	LIM and SH3 protein 1
6896	TTTCTGCACTT	1,00	0,69	Hs.270876	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ
6897	CAGGGCGGGTT	1,00	0,69	Hs.23978	scaffold attachment factor B
6898	TAACCTGCTAT	1,00	0,69	Hs.14541	cullin 1
6899	TACCATCAATA	41,00	23,35	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase
6900	ACTGAGGTGCC	2,00	1,38	Hs.284159	FIBP-1 protein
6901	GCCATATTATG	1,00	0,70	Hs.19280	cysteine-rich repeat-containing protein S52 precursor
6902	ATTTTAGAATT	1,00	0,70	Hs.179662	nucleosome assembly protein 1-like 1
6903	TTCAAAAAA	1,00	0,70	Hs.12677	CGI-147 protein
6904	AGGAGCTGCTG	4,00	2,63	Hs.90443	NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD)
6905	GGGGGTCACCG	4,00	2,63	Hs.80986	ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 comp
6906	CTGTAGTGTG	4,00	2,65	Hs.75375	malate dehydrogenase 1, NAD (soluble)
6907	CGCCGACGATG	11,00	6,80	Hs.265827	interferon, alpha-inducible protein (clone IFI-6-16)
6908	AAAAGGTTATG	1,00	0,71	Hs.75283	sorting nexin 1
6909	TAAACCTGTCT	1,00	0,71	Hs.70333	hypothetical protein
6910	GCTGTGCCTGG	1,00	0,71	Hs.58247	protease, serine, 4 (trypsin 4, brain)
6911	TGCCCACTCAT	1,00	0,71	Hs.31130	transmembrane 7 superfamily member 2
6912	CGGGATTCTC	1,00	0,71	Hs.118126	protective protein for beta-galactosidase (galactosi
6913	TTGATGTACAG	1,00	0,71	Hs.11482	splicing factor, arginine/serine-rich 11
6914	TTTGGAATCA	1,00	0,71	Hs.110803	CGI-99 protein
6915	TTTTATTGGAA	1,00	0,71	Hs.106242	cytochrome P450, subfamily IVF, polypeptide 3 (leuko
6916	GGTAGCCTGGG	3,00	2,05	Hs.108327	damage-specific DNA binding protein 1 (127kD)
6917	ATGCAGCCATA	2,00	1,40	Hs.75212	ornithine decarboxylase 1
6918	AATTTTATTTT	2,00	1,40	Hs.2853	poly(rC)-binding protein 1
6919	CTTAAGGATTC	2,00	1,40	Hs.165998	DKFZP564M2423 protein
6920	ACTGAGGAAAG	3,00	2,06	Hs.77326	insulin-like growth factor binding protein 3
6921	TTTTCTGAAAA	4,00	2,70	Hs.76136	thioredoxin
6922	GCTGCACCGGT	1,00	0,72	Hs.70582	ESTs, Moderately similar to AF144056_1 apoptosis rel
6923	TACACGTGAGG	2,00	1,42	Hs.11156	hypothetical protein
6924	CTGGGCCTGGC	4,00	2,72	Hs.74573	similar to vaccinia virus HindIII K4L ORF
6925	TTTGTAGATGG	2,00	1,43	Hs.3069	heat shock 70kD protein 9B (mortalin-2)
6926	GGGGGTTGGTT	1,00	0,72	Hs.4779	KIAA1150 protein
6927	TCCTGCAGCTG	1,00	0,72	Hs.283111	HCDI protein
6928	ATGTTAGGGAT	1,00	0,72	Hs.169206	vesicle-associated soluble NSF attach-



					ment protein re
6929	GGGTCTGCGGG	1,00	0,72	Hs.146219	copine VII
6930	AACTTGATACG	1,00	0,72	Hs.119597	stearoyl-CoA desaturase (delta-9-desaturase)
6931	TGCATTAAGTG	1,00	0,73	Hs.7351	cyclic AMP phosphoprotein, 19 kD
6932	TTAAACTCCAA	1,00	0,73	Hs.273369	uncharacterized hematopoietic stem/progenitor cells
6933	ACCTGCCGACA	1,00	0,73	Hs.25664	tumor suppressor deleted in oral cancer-related 1
6934	AAGGAGCTGGC	1,00	0,73	Hs.155165	zinc finger protein-like 1
6935	CAGGGTCCCCA	1,00	0,73	Hs.144391	hypothetical protein FLJ10647
6936	TCCGAGCCCCC	1,00	0,73	Hs.12971	thioredoxin reductase beta
6937	TTAGATAAGCA	2,00	1,47	Hs.82916	chaperonin containing TCP1, subunit 6A (zeta 1)
6938	GTTACAACTA	1,00	0,74	Hs.75248	topoisomerase (DNA) II beta (180kD)
6939	TTGGGAGTGAG	1,00	0,74	Hs.26285	imidazoline receptor candidate
6940	CTGGTGATGGC	1,00	0,74	Hs.242463	keratin 8
6941	TACGTACTGCC	1,00	0,74	Hs.23410	translocase of inner mitochondrial membrane 13 (yeas
6942	GATGCCTCTGC	1,00	0,74	Hs.145061	ESTs, Weakly similar to TBP-associated factor [H.sap
6943	CTTCCAGCTAA	11,00	7,28	Hs.217493	annexin A2
6944	TTGTTGTTGAA	6,00	4,14	Hs.182278	calmodulin 2 (phosphorylase kinase, delta)
6945	ACTGCTTGCCC	3,00	2,18	Hs.77502	methionine adenosyltransferase II, alpha
6946	GCTGGGGTGGG	1,00	0,75	Hs.86131	Fas (TNFRSF6)-associated via death domain
6947	GGCAGGCACAA	1,00	0,75	Hs.75105	emopamil-binding protein (sterol isomerase)
6948	CAGCCAAATAA	1,00	0,75	Hs.65709	F-box protein FBG2
6949	AATAGCTCAGG	1,00	0,75	Hs.4990	KIAA1089 protein
6950	AAGAAGCAAGA	1,00	0,75	Hs.2953	ribosomal protein S15a
6951	TGTTGTGCGCG	1,00	0,75	Hs.11364	potassium inwardly-rectifying channel, subfamily J, m
6952	CCTGTCCTTTC	1,00	0,76	Hs.5300	bladder cancer associated protein
6953	CCTATGTAAGG	1,00	0,76	Hs.146381	RNA binding motif protein, X chromosome
6954	CTGGGCGTGTC	5,00	3,58	Hs.161554	hypothetical protein FLJ20159
6955	TTTCCAATCTC	1,00	0,77	Hs.73793	vascular endothelial growth factor
6956	CTACCAGCACC	1,00	0,77	Hs.164256	hypothetical protein FLJ20657
6957	GGGCTGGGCCC	2,00	1,54	Hs.100071	6-phosphogluconolactonase
6958	AAAAGCAGAT	3,00	2,26	Hs.75428	superoxide dismutase 1, soluble (amyotrophic lateral
6959	TTTTACAGTAC	1,00	0,78	Hs.86347	hypothetical protein
6960	CTGTGTAAGCT	1,00	0,78	Hs.79137	protein-L-isoaspartate (D-aspartate) O-methyltransfe
6961	CGGCGCTCCCT	1,00	0,78	Hs.29285	ZYG homolog
6962	GCATCTGTTTA	1,00	0,78	Hs.250175	hypothetical protein dJ483K16.1
6963	CTCTGCTCGGC	1,00	0,78	Hs.241531	peflin
6964	TAGGTTCTGT	1,00	0,78	Hs.159604	cysteinyl-tRNA synthetase

6965	TGAAGTAACAA	3,00	2,28	Hs.150580	putative translation initiation factor
6966	GGGGAAATCGC	24,00	16,17	Hs.76293	thymosin, beta 10
6967	TTGCTAGAGGG	2,00	1,56	Hs.172791	ubiquitously-expressed transcript
6968	CAGACGCTCCG	1,00	0,79	Hs.83006	CGI-139 protein
6969	TGGTGCAGCAT	1,00	0,79	Hs.71787	30S ribosomal protein S7 homolog
6970	TCTGCAAATTA	1,00	0,79	Hs.274398	Homo sapiens cDNA FLJ10433 fis, clone NT2RP1000478,
6971	TGAATGGCCTA	1,00	0,79	Hs.20597	host cell factor homolog
6972	GAAATGATGAG	5,00	3,70	Hs.80686	prefoldin 5
6973	CGCCGCGGTGG	8,00	5,74	Hs.4835	eukaryotic translation initiation factor 3, subunit
6974	TTGTAAAAGGA	2,00	1,58	Hs.106357	valosin-containing protein
6975	AGCAGGGCTCC	5,00	3,73	Hs.100623	phospholipase C, beta 3, neighbor pseudogene
6976	TGAGCCTCGTG	2,00	1,59	Hs.254105	enolase 1, (alpha)
6977	GAAATACAGTG	1,00	0,80	Hs.67201	5'(3')-deoxyribonucleotidase
6978	GATAATTTTGT	1,00	0,80	Hs.6468	HSPC142 protein
6979	GGCGCCAAAAA	1,00	0,80	Hs.119324	kinesin-like 4
6980	CCAATAAAGTG	1,00	0,80	Hs.101850	retinol-binding protein 1, cellular
6981	ATCTTTCTGGC	4,00	3,05	Hs.75103	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase
6982	GCTGCGGTCCT	1,00	0,81	Hs.795	H2A histone family, member O
6983	CAATTACCTGC	1,00	0,81	Hs.284263	Homo sapiens clone H63 unknown mRNA
6984	CACGAAGATGC	1,00	0,81	Hs.10247	activated leucocyte cell adhesion molecule
6985	AGAACAAAACC	6,00	4,53	Hs.180909	peroxiredoxin 1
6986	GGTGCCCAAGT	2,00	1,62	Hs.75607	myristoylated alanine-rich protein kinase C substrate
6987	GAGAGTGTCTG	3,00	2,38	Hs.5831	tissue inhibitor of metalloproteinase 1 (erythroid p)
6988	GCACAAGAAGA	9,00	6,65	Hs.81634	ATP synthase, H+ transporting, mitochondrial F0 comp
6989	TTTTATCTGGT	1,00	0,82	Hs.64239	Human DNA sequence from clone RP5-1174N9 on chromoso
6990	TGTTTGGGGGC	1,00	0,82	Hs.61478	ESTs
6991	ACTGTCTCCAG	1,00	0,82	Hs.16611	tumor protein D52-like 1
6992	ATGGCCAGAAA	1,00	0,82	Hs.141011	calmodulin 3 (phosphorylase kinase, delta)
6993	TATTTTGTGTA	1,00	0,82	Hs.13046	thioredoxin reductase 1
6994	GGGGAGCTCGG	1,00	0,82	Hs.117582	CGI-43 protein
6995	ACTGCCCAAC	1,00	0,82	Hs.103147	ESTs, Weakly similar to similar to SP:YR40_BACSU [C.
6996	TGAATCTGGGT	2,00	1,63	Hs.145279	SET translocation (myeloid leukemia-associated)
6997	ACCTCTCTAAA	1,00	0,83	Hs.94392	LDL induced EC protein
6998	GAGAGCTACAT	1,00	0,83	Hs.169919	electron-transfer-flavoprotein, alpha polypeptide (g
6999	AGGTAAAAGAG	1,00	0,83	Hs.103042	microtubule-associated protein 1B
7000	GTGCTGCGTGA	2,00	1,64	Hs.4209	ribosomal protein, mitochondrial, L2

7001	GGGATGGCAGC	2,00	1,64	Hs.159637	valyl-tRNA synthetase 2	
7002	CCAAAAA	2,00	1,64	Hs.132071	hypothetical protein FLJ20455	
7003	GCCCCAGGTAG	1,00	0,84	Hs.78466	proteasome (prosome, macropain) 26S subunit, non-ATP	5
7004	AAACCTGGGAA	1,00	0,84	Hs.63788	propionyl Coenzyme A carboxylase, beta polypeptide	
7005	GGGGGAGGGAA	1,00	0,84	Hs.108530	hypothetical protein FLJ10856	10
7006	TGTAAGTCTGC	2,00	1,66	Hs.119537	GAP-associated tyrosine phosphoprotein p62 (Sam68)	
7007	ACGTGGTGATG	2,00	1,67	Hs.279945	HSPC023 protein	
7008	CAGGACAGTTT	1,00	0,84	Hs.78305	RAB2, member RAS oncogene family	15
7009	ACCGTATTCCA	1,00	0,84	Hs.198281	pyruvate kinase, muscle	
7010	GCCGATCCTCG	2,00	1,69	Hs.24930	tubulin-specific chaperone a	
7011	TTGTCTGCCTT	3,00	2,48	Hs.7788	Homo sapiens BAC clone CTB-122E10 from 7q11.23-q21.1	20
7012	GAGAGTGTACT	1,00	0,85	Hs.20716	translocase of inner mitochondrial membrane 17 (yeas	
7013	GGGGGAATTTT	1,00	0,85	Hs.129548	heterogeneous nuclear ribonucleoprotein K	25
7014	ATTTTTGGTGG	1,00	0,85	Hs.110	putative L-type neutral amino acid transporter	
7015	ATCCGGCGCCA	4,00	3,26	Hs.172772	transcription elongation factor B (SIII), polypeptid	30
7016	TCTGTCAAGAC	3,00	2,49	Hs.76572	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 comp	
7017	CGGACTCACTG	3,00	2,51	Hs.84700	similar to phosphatidylcholine transfer protein 2	35
7018	AAACCCCAATA	2,00	1,72	Hs.285501	Human rearranged immunoglobulin lambda light chain m	
7019	TCAACTTCTGG	1,00	0,86	Hs.7594	solute carrier family 2 (facilitated glucose transpo	40
7020	GACCAGCCCAT	1,00	0,86	Hs.75799	protease, serine, 8 (prostasin)	
7021	AGCAAGCCCCC	1,00	0,86	Hs.65588	DAZ associated protein 1	45
7022	TTGTGATGGG	1,00	0,86	Hs.55505	hypothetical protein FLJ20442	
7023	TACAGCACGGA	1,00	0,86	Hs.111811	microsomal glutathione S-transferase 3	
7024	GAAACCGAGGG	4,00	3,30	Hs.279813	hypothetical protein	50
7025	GTGTTAACCAG	15,00	11,62	Hs.74267	ribosomal protein L15	
7026	GTTGGTCTGTA	2,00	1,74	Hs.108258	actin binding protein; macrophin (micro-filament and	55
7027	TCTTTCCCAA	1,00	0,87	Hs.268557	pleckstrin homology-like domain, family A, member 3	
7028	GTCTTTCTTGG	3,00	2,57	Hs.151536	RAB13, member RAS oncogene family	60
7029	CTCAGACAGTG	3,00	2,57	Hs.108957	40S ribosomal protein S27 isoform	
7030	GAACACATCCA	16,00	12,51	Hs.75879	ribosomal protein L19	
7031	GGGTTTTTATT	4,00	3,37	Hs.74497	nuclease sensitive element binding protein 1	
7032	AGAACCTTTGC	1,00	0,88	Hs.74649	cytochrome c oxidase subunit VIc	
7033	GCCTGATTTTT	1,00	0,88	Hs.278721	HLA class II region expressed gene KE4	
7034	GAGAGGTTGAT	1,00	0,88	Hs.194709	paraneoplastic antigen MA1	
7035	TGTAGTTTGAG	4,00	3,38	Hs.182643	transcription elongation factor B (SIII),	

					polypeptid
7036	AAGGAGATGGG	23,00	17,88	Hs.184014	ribosomal protein L31
7037	AACGCTGCCTG	2,00	1,77	Hs.28914	adenine phosphoribosyltransferase
7038	CAGCCTCCCTG	1,00	0,89	Hs.75593	uroporphyrinogen III synthase (congenital erythropoi
7039	TTAATAGTGGG	1,00	0,89	Hs.18271	Homo sapiens mRNA; cDNA DKFZp434P1217 (from clone DK
7040	TGGCCCCACCC	12,00	9,68	Hs.198281	pyruvate kinase, muscle
7041	TGAAATAAAAC	9,00	7,37	Hs.173205	nucleophosmin (nucleolar phosphoprotein B23, numatri
7042	TCCCTGGCTGT	1,00	0,90	Hs.78575	prosaposin (variant Gaucher disease and variant meta
7043	TATACCAATCA	1,00	0,90	Hs.75866	dimethylarginine dimethylaminohydrolase 1
7044	CAGATAACATA	1,00	0,90	Hs.75187	translocase of outer mitochondrial membrane 20 (yeas
7045	TGGATCCTCGT	1,00	0,90	Hs.5268	hypothetical protein FLJ10479
7046	CCTATCAGTAA	1,00	0,90	Hs.183752	microseminoprotein, beta-
7047	AGGTCAGAGGG	1,00	0,90	Hs.181165	eukaryotic translation elongation factor 1 alpha 1
7048	CCTGCCCCCTTC	1,00	0,90	Hs.173255	small nuclear ribonucleoprotein polypeptide A
7049	GGTACTCGATG	1,00	0,90	Hs.121576	aspartate beta-hydroxylase
7050	TTTGGAATGTT	2,00	1,80	Hs.78825	matrin 3
7051	CTGGATCTGGG	2,00	1,80	Hs.75658	phosphorylase, glycogen; brain
7052	GTGCCATATTT	2,00	1,80	Hs.5337	isocitrate dehydrogenase 2 (NADP+), mitochondrial
7053	TACATCCGAAT	2,00	1,80	Hs.21321	Homo sapiens mRNA; cDNA DKFZp564E1363 (from clone DK
7054	GAAGTTATGAA	3,00	2,66	Hs.4112	t-complex 1
7055	TTTATTTCTAC	1,00	0,91	Hs.85963	CD36 antigen (collagen type I receptor, thrombospond
7056	TCAACGGTGTG	1,00	0,91	Hs.279886	novel centrosomal protein RanBPM
7057	CCTCTTCAGGC	1,00	0,91	Hs.173205	nucleophosmin (nucleolar phosphoprotein B23, numatri
7058	TCAGTTCTTGA	1,00	0,91	Hs.103804	heterogeneous nuclear ribonucleoprotein U (scaffold
7059	CCTTTCCTTTA	3,00	2,67	Hs.74576	GDP dissociation inhibitor 1
7060	ACCGCCGTGGT	4,00	3,52	Hs.68877	cytochrome b-245, alpha polypeptide
7061	GTAAAAGTTCT	1,00	0,92	Hs.75337	nucleolar phosphoprotein p130
7062	GTTTCAGGTAA	1,00	0,92	Hs.1526	ATPase, Ca++ transporting, cardiac muscle, slow twit
7063	TTCCAGACCTT	3,00	2,71	Hs.75722	ribophorin II
7064	TTATGGGATCT	13,00	10,88	Hs.5662	guanine nucleotide binding protein (G protein), beta
7065	GTGGGGGGGAGG	1,00	0,93	Hs.205736	HLA class II region expressed gene KE2
7066	TAATTTTGGAT	1,00	0,93	Hs.117582	CGI-43 protein
7067	GGGCAGATGCC	1,00	0,93	Hs.105894	Homo sapiens mRNA; cDNA DKFZp434G231 (from clone DKF
7068	GTTCTCCCACT	3,00	2,73	Hs.14038	sec61 homolog

7069	AAGCCAGCCCC	3,00	2,74	Hs.1432	protein kinase C substrate 80K-H	
7070	GGCCCCATTTT	1,00	0,94	Hs.88778	carbonyl reductase 1	
7071	TAATATTTTAA	1,00	0,94	Hs.182485	actinin, alpha 4	5
7072	GCGGGTGTGGA	1,00	0,95	Hs.78935	methionine aminopeptidase; eIF-2-associated p67	
7073	CCCAGATGATA	1,00	0,95	Hs.7854	zinc/iron regulated transporter-like	
7074	GGTTTGATTAC	1,00	0,95	Hs.69559	KIAA1096 protein	10
7075	TAATTACTCTT	1,00	0,95	Hs.44163	13kDa differentiation-associated protein	
7076	TGTACTACTTA	1,00	0,95	Hs.286114	Homo sapiens cDNA FLJ10301 fis, clone NT2RM2000032	
7077	AGGATGACCCC	1,00	0,95	Hs.25334	HSPC113 protein	15
7078	CTCTGTGTGGA	1,00	0,95	Hs.234279	microtubule-associated protein, RP/EB family, member	
7079	CTCTTATCACC	1,00	0,95	Hs.100043	ESTs, Weakly similar to PSF_HUMAN PTB-ASSOCIATED SPL	20
7080	ATAGACATAAA	2,00	1,90	Hs.78614	complement component 1, q subcomponent binding prote	
7081	TTTTCTGCTGG	2,00	1,90	Hs.204041	chromosome 14 open reading frame 3	
7082	GTCTCACGTGG	1,00	0,96	Hs.46975	Homo sapiens cDNA FLJ20187 fis, clone COLF0433	25
7083	CACACAATGTG	1,00	0,96	Hs.117582	CGI-43 protein	
7084	GATTGGGGATT	1,00	0,96	Hs.103834	ESTs, Weakly similar to unnamed protein product [H.s	
7085	GCCCCTCCGGC	5,00	4,56	Hs.180859	16.7Kd protein	30
7086	AAAAAACTCCA	1,00	0,97	Hs.82193	esterase D/formylglutathione hydrolase	
7087	CTCTTCAGGAG	1,00	0,97	Hs.30954	phosphomevalonate kinase	
7088	CAGAAGAGGCT	1,00	0,97	Hs.153910	DiGeorge syndrome critical region gene 6	35
7089	GGAACGGATGT	2,00	1,93	Hs.58589	glycogenin 2	
7090	GAGTGGGGGCT	2,00	1,93	Hs.14089	quiescent cell proline dipeptidase	
7091	GAATCGGTTAT	3,00	2,84	Hs.80595	NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD	40
7092	AATATGCTTTA	1,00	0,98	Hs.77805	ATPase, H+ transporting, lysosomal (vacuolar proton	
7093	GTGTCTCGCAG	1,00	0,98	Hs.75510	annexin A11	45
7094	CTTAAATATCA	1,00	0,98	Hs.184011	pyrophosphatase (inorganic)	
7095	GTGGAGCGGAG	1,00	0,99	Hs.281616	KIAA0890 protein	
7096	ACAAACTGTGG	3,00	2,89	Hs.90370	actin related protein 2/3 complex, subunit 1A (41 kD	
7097	TATTTTGTGAG	2,00	1,97	Hs.75607	myristoylated alanine-rich protein kinase C substrat	50
7098	TGCATCTGGTG	5,00	4,72	Hs.75410	heat shock 70kD protein 5 (glucose-regulated protein	
7099	GTGGCTGCTGT	1,00	1,00	Hs.41182	ESTs	55
7100	GAAAGAGCTGA	1,00	1,00	Hs.147097	H2A histone family, member X	
7101	GAGTCAGCATT	1,00	1,00	Hs.103804	heterogeneous nuclear ribonucleoprotein U (scaffold	
7102	ATTGGCTTAAA	2,00	2,00	Hs.75323	prohibitin	60
7103	TTTGTTTTTGA	1,00	1,01	Hs.170088	ESTs, Moderately similar to unnamed protein product	

7104	ACCATTGGATT	1,00	1,01	Hs.146360	interferon induced transmembrane protein 1 (9-27)
7105	AGGCGAGATCA	4,00	3,87	Hs.233952	proteasome (prosome, macropain) subunit, alpha type,
7106	GGATTGTCTGG	2,00	2,01	Hs.83753	small nuclear ribonucleoprotein polypeptides B and B
7107	GGCGCCTCCTT	2,00	2,02	Hs.77290	transaldolase 1
7108	AAAATGTACTG	1,00	1,02	Hs.24763	RAN binding protein 1
7109	TACTGTGGATC	1,00	1,02	Hs.21537	protein phosphatase 1, catalytic subunit, beta isofo
7110	ATGGTTAAAGG	1,00	1,02	Hs.142613	Homo sapiens cDNA FLJ10281 fis, clone HEMBB1001289
7111	CCAGCGTGGAA	1,00	1,02	Hs.129010	ESTs, Highly similar to KINN_HUMAN NEURONAL KINESIN
7112	TTGGACCTGGG	5,00	4,85	Hs.89761	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 comp
7113	TTGGACTGAGC	2,00	2,04	Hs.6518	ganglioside expression factor 2
7114	TGCCTTACTTT	1,00	1,03	Hs.80019	programmed cell death 6
7115	TTAGCAGTTGG	1,00	1,03	Hs.268555	5'-3' exoribonuclease 2
7116	TGCAGGCCTGG	2,00	2,05	Hs.82030	tryptophanyl-tRNA synthetase
7117	CCCCCTCGTGC	1,00	1,04	Hs.83636	adrenergic, beta, receptor kinase 1
7118	TAGTCTTAACA	1,00	1,04	Hs.75137	KIAA0193 gene product
7119	GCCACATCCG	2,00	2,07	Hs.84753	KIAA0246 protein
7120	TGAGAGGGTGT	2,00	2,07	Hs.74405	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase
7121	CCTTGGTGCCG	1,00	1,05	Hs.8375	TNF receptor-associated factor 4
7122	ATTGTGAGGCC	1,00	1,05	Hs.281434	sialyltransferase
7123	GAGAATCTGCT	1,00	1,05	Hs.23960	cyclin B1
7124	CCGGGCGTGGT	1,00	1,05	Hs.132898	delta-5 desaturase; delta-5 fatty acid desaturase
7125	ACTCCCTCCTT	1,00	1,06	Hs.76230	ribosomal protein S10
7126	TATCGTTGCCT	1,00	1,06	Hs.3887	proteasome (prosome, macropain) 26S subunit, non-ATP
7127	TGCTACTGGTA	1,00	1,06	Hs.3196	surfeit 1
7128	ATTCTTCGGAC	1,00	1,06	Hs.226372	DKFZP434J154 protein
7129	TACCAGCACAG	1,00	1,06	Hs.119908	nucleolar protein NOP5/NOP58
7130	AACTACATAGG	1,00	1,07	Hs.9527	apoptosis related protein APR-3
7131	TAAGTGGAGGA	1,00	1,07	Hs.82906	CDC20 (cell division cycle 20, S. cerevisiae, homolo
7132	CCTGAACTGGC	1,00	1,07	Hs.74441	chromodomain helicase DNA binding protein 4
7133	CCGTAGTGCCT	1,00	1,07	Hs.6891	splicing factor, arginine/serine-rich 6
7134	AACTGCGGCAG	1,00	1,07	Hs.63908	Homo sapiens HSPC316 mRNA, partial cds
7135	TGTTCTCCATT	1,00	1,07	Hs.182255	non-histone chromosome protein 2 (S. cerevisiae)-lik
7136	TGTTTTTATGT	1,00	1,08	Hs.3192	6-pyruvoyl-tetrahydropterin synthase/dimerization co
7137	CCTCCTCTGAC	1,00	1,08	Hs.28505	ubiquitin-conjugating enzyme E2H (homologous to yeas

7138	CCAAATGCTGG	1,00	1,08	Hs.178485	ESTs
7139	CCGGCCCCTCC	1,00	1,08	Hs.155524	peanut (Drosophila)-like 2
7140	CAAGTTAGTGG	1,00	1,08	Hs.117582	CGI-43 protein
7141	GGGGGCGCCTT	1,00	1,09	Hs.164280	solute carrier family 25 (mitochondrial carrier; ade
7142	ATATAGGTCGT	1,00	1,10	Hs.84981	X-ray repair complementing defective repair in Chine
7143	CTGCCTTCTTG	1,00	1,10	Hs.79081	protein phosphatase 1, catalytic subunit, gamma isof
7144	CGTACTGAGCG	1,00	1,10	Hs.180610	splicing factor proline/glutamine rich (polypyrimidi
7145	GACCCCTGTCA	1,00	1,11	Hs.6445	Homo sapiens (clone s153) mRNA frag-ment
7146	GCTTGTTCTCT	1,00	1,11	Hs.2699	glypican 1
7147	CTGCAGACCCA	1,00	1,11	Hs.196176	enoyl Coenzyme A hydratase 1, peroxi-somal
7148	CTGTGCATTTT	2,00	2,21	Hs.172207	non-POU-domain-containing, octamer-binding
7149	AGTTTCCCAAT	3,00	3,27	Hs.75854	sulfotransferase family, cytosolic, 1C, member 2
7150	GGGTGCTTGGT	1,00	1,12	Hs.6551	ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton
7151	AGCTGTGTAAA	1,00	1,12	Hs.279923	putative nucleotide binding protein, estradiol-induc
7152	CAAGATAAATT	1,00	1,12	Hs.177556	melanoma antigen, family D, 1
7153	ATAGAGGCAAT	2,00	2,22	Hs.173714	MORF-related gene X
7154	TGGTGACAGTT	2,00	2,23	Hs.9242	purine-rich element binding protein B
7155	CAGCTCATCTA	2,00	2,23	Hs.285634	Homo sapiens HSPC222 mRNA, com-plete cds
7156	GGGGTCTGGGC	1,00	1,13	Hs.33026	Human DNA sequence from clone RP3-402G11 on chromoso
7157	ACTGCGAGGAC	1,00	1,13	Hs.110477	dolichyl-phosphate mannosyltransferase polypeptide 3
7158	ACGCAGGCGCC	1,00	1,14	Hs.78103	nucleosome assembly protein 1-like 4
7159	GACTAAGAAAT	1,00	1,14	Hs.66713	hepatitis delta antigen-interacting protein A
7160	TGGGCTTGCCT	1,00	1,14	Hs.285163	ESTs
7161	CGCGCCCGGCC	1,00	1,14	Hs.248267	thiosulfate sulfurtransferase (rhodanese)
7162	GTGAAGCTGAT	1,00	1,14	Hs.106671	cleft lip and palate associated trans-membrane protei
7163	TGAAACTCATC	2,00	2,27	Hs.85844	neurotrophic tyrosine kinase, receptor, type 1
7164	CTGCCAACTTC	2,00	2,28	Hs.180370	cofilin 1 (non-muscle)
7165	TAGGATGGGGT	1,00	1,15	Hs.76941	ATPase, Na <sup>+</sup> /K <sup>+</sup> transporting, beta 3 polypeptide
7166	TACTTGTGTGT	1,00	1,15	Hs.6354	stromal cell derived factor receptor 1
7167	TCAGCTTCACC	1,00	1,15	Hs.28707	signal sequence receptor, gamma (trans-locon-associat
7168	CCTCCACCTAG	5,00	5,48	Hs.146354	peroxiredoxin 2
7169	CGGTTACTGTG	3,00	3,39	Hs.49767	NADH dehydrogenase (ubiquinone) Fe-S protein 6 (13kD

5	7170	GAGCCTTGGTG	2,00	2,31	Hs.183994	protein phosphatase 1, catalytic subunit, alpha isof
	7171	GGAGCTCTGTG	3,00	3,42	Hs.227750	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4
	7172	GGTTTGTGTGT	1,00	1,17	Hs.83954	hypothetical protein
10	7173	CGATATTCCCC	1,00	1,17	Hs.37616	Human D9 splice variant B mRNA, complete cds
	7174	GGAAGTTCAAA	1,00	1,17	Hs.237536	ESTs, Weakly similar to AF151067_1 HSPC233 [H.sapien
	7175	AATGGAATGGA	1,00	1,17	Hs.11365	ESTs
15	7176	TCTGCCTGGGG	2,00	2,34	Hs.24379	MUM2 protein
	7177	AGATCCTACTT	1,00	1,18	Hs.48876	farnesyl-diphosphate farnesyltransferase 1
	7178	GGAATCCAATC	1,00	1,18	Hs.252587	pituitary tumor-transforming 1
20	7179	CTTGCCTGAAG	1,00	1,20	Hs.193163	bridging integrator 1
	7180	GCCTGGCCATC	2,00	2,39	Hs.63042	DKFZp564J157 protein
	7181	TCCTGCTGCCG	2,00	2,40	Hs.239500	KIAA0273 gene product
	7182	CACCTTCCAGC	1,00	1,21	Hs.279869	melanoma-associated antigen recognised by cytotoxic
25	7183	TCCAATACTGC	1,00	1,22	Hs.84153	dynamitin (dynactin complex 50 kD subunit)
	7184	CAGCTGTAGTT	1,00	1,22	Hs.75824	KIAA0174 gene product
30	7185	AGAATATCAGT	1,00	1,22	Hs.31803	ESTs, Weakly similar to N-WASP [H.sapiens]
	7186	TCCTAGTAGGA	1,00	1,22	Hs.252831	reticulon 3
	7187	ACCAAGCTGGG	1,00	1,22	Hs.239307	tyrosyl-tRNA synthetase
35	7188	AAGAATTTGAA	1,00	1,22	Hs.183435	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1
	7189	GCCCCGAGCCC	1,00	1,22	Hs.178112	DNA segment, single copy probe LNS-CAI/LNS-CAII (del
40	7190	AAGGAAGATCC	1,00	1,22	Hs.11465	glutathione-S-transferase like; glutathione transfer
	7191	CAGTTTGTACA	1,00	1,22	Hs.1023	pyruvate dehydrogenase (lipoamide) alpha 1
45	7192	CGTGTTAATGG	3,00	3,60	Hs.2110	zinc finger protein 9 (a cellular retroviral nucleic
	7193	GCGGTTGTGGC	1,00	1,23	Hs.79356	Lysosomal-associated multispinning membrane protein-
	7194	AAAGTTCTCAG	1,00	1,23	Hs.284243	tetraspan NET-6 protein
50	7195	ATACAGAATAA	1,00	1,23	Hs.169228	delta-like homolog (Drosophila)
	7196	ACCTTTACTGT	1,00	1,24	Hs.77356	transferrin receptor (p90, CD71)
	7197	TGGGCCTGGCT	1,00	1,24	Hs.6351	cleavage and polyadenylation specific factor 4, 30kD
55	7198	CATAAAGTTTA	1,00	1,24	Hs.3642	DKFZP564B163 protein
	7199	TGTCCTGGTTC	2,00	2,47	Hs.179665	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
60	7200	CGGTTTGCATC	1,00	1,25	Hs.31547	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex,
	7201	TTCTGTGTCAC	1,00	1,25	Hs.111024	solute carrier family 25 (mitochondrial carrier; cit
65	7202	AAGTTCTGCGG	1,00	1,26	Hs.79411	replication protein A2 (32kD)



7203	TGCTCCTACCC	2,00	2,50	Hs.111732	Fc fragment of IgG binding protein
7204	GTTGCTGCCCT	1,00	1,27	Hs.9234	seven transmembrane domain protein
7205	AGGGTTGGAAG	1,00	1,27	Hs.15106	chromosome 14 open reading frame 1
7206	ATCCGGGGAGC	1,00	1,27	Hs.109752	putative c-Myc-responsive
7207	TTTTTGACAG	2,00	2,52	Hs.78040	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein
7208	TTTCAGAGAGA	4,00	4,92	Hs.75975	signal recognition particle 9kD
7209	GTTAACGTCCC	5,00	6,11	Hs.178391	ribosomal protein L44
7210	CTGATGGCAGA	1,00	1,28	Hs.75874	pregnancy-associated plasma protein A
7211	CCTTTGGCTAG	1,00	1,28	Hs.108957	40S ribosomal protein S27 isoform
7212	TAAGTGAATA	2,00	2,55	Hs.75103	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase
7213	GTGCTGGAGAA	3,00	3,79	Hs.53125	small nuclear ribonucleoprotein D2 polypeptide (16.5
7214	TAAGGAGCTGA	13,00	15,71	Hs.77904	ribosomal protein S26
7215	CACCCCTGATG	7,00	8,65	Hs.173724	creatine kinase, brain
7216	CCCCTCTGAGT	1,00	1,31	Hs.7957	adenosine deaminase, RNA-specific
7217	ACTACCTTCAC	1,00	1,31	Hs.279529	px19-like protein
7218	GGGCCAGGAG	1,00	1,31	Hs.118983	ESTs, Weakly similar to diaphanous 1 [H.sapiens]
7219	GGCCCTGAGCG	4,00	5,09	Hs.71618	polymerase (RNA) II (DNA directed) polypeptide L (7.
7220	TAACCAATCAG	2,00	2,61	Hs.479	RAB5C, member RAS oncogene family
7221	GCTGCCCTTGA	4,00	5,10	Hs.278242	tubulin, alpha, ubiquitous
7222	TTTGGGGCTGG	2,00	2,62	Hs.7476	ATPase, H+ transporting, lysosomal (vacuolar proton
7223	CCCCTCCCTCC	1,00	1,32	Hs.79410	solute carrier family 4, anion exchanger, member 2 (
7224	AATAAATGGAT	2,00	2,64	Hs.109052	chromosome 14 open reading frame 2
7225	GGAAAAA	7,00	8,81	Hs.177530	ATP synthase, H+ transporting, mitochondrial F1 comp
7226	GGAAAAGTGGT	1,00	1,33	Hs.75621	protease inhibitor 1 (anti-elastase), alpha-1-antitr
7227	TGGCTTGCTCA	1,00	1,33	Hs.3688	cisplatin resistance-associated overexpressed protei
7228	GCCCGTGCCAC	1,00	1,33	Hs.15760	ESTs, Weakly similar to similar to Yeast hypotheticala
7229	CCACCCCCACC	1,00	1,33	Hs.148101	serum constituent protein
7230	GGTGGCTTTGC	1,00	1,34	Hs.109760	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3
7231	AATGCTGGCAA	1,00	1,35	Hs.181195	MRJ gene for a member of the DNAJ protein family
7232	GACCGAGGTGG	1,00	1,35	Hs.129953	Ewing sarcoma breakpoint region 1
7233	CAGAGATGAAT	2,00	2,70	Hs.8997	heat shock 70kD protein 1A
7234	ATCTGAAGCAG	1,00	1,36	Hs.256311	granin-like neuroendocrine peptide precursor
7235	TGCAGCGCCTG	1,00	1,37	Hs.77573	uridine phosphorylase
7236	GCCAGGAAGCC	1,00	1,37	Hs.182281	hypothetical protein
7237	CTTTTCTTCTG	1,00	1,37	Hs.148027	polymerase (RNA) II (DNA directed) polypeptide B (14

7238	GCGCCGCCCA	1,00	1,37	Hs.108665	zinedin
7239	ATGGGGCAGGG	1,00	1,38	Hs.79226	fasciculation and elongation protein zeta 1 (zygin I)
7240	CATTCCTCCTT	1,00	1,38	Hs.2985	emerin (Emery-Dreifuss muscular dystrophy)
7241	ACAACGTCCAG	1,00	1,38	Hs.118893	p53-responsive gene 2
7242	CTCTTCGAGAA	3,00	4,08	Hs.76686	glutathione peroxidase 1
7243	GGCTCCCCTG	5,00	6,68	Hs.74335	heat shock 90kD protein 1, beta
7244	GTATCTTCACA	1,00	1,39	Hs.250899	heat shock factor binding protein 1
7245	CTTAAATCTGG	1,00	1,40	Hs.94	heat shock protein, DNAJ-like 2
7246	GATGCGCTTGT	1,00	1,40	Hs.184014	ribosomal protein L31
7247	TAGACTTATTG	1,00	1,40	Hs.170197	glutamic-oxaloacetic transaminase 2, mitochondrial (
7248	ACGATTGATGA	1,00	1,40	Hs.161554	hypothetical protein FLJ20159
7249	GCAACGGGCCC	1,00	1,41	Hs.8679	cytosolic acyl coenzyme A thioester hydrolase
7250	ATAAATTGGGT	1,00	1,41	Hs.81634	ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 comp
7251	TTTTAAATTAG	1,00	1,41	Hs.75598	heterogeneous nuclear ribonucleoprotein A2/B1
7252	CTCGGTGATGT	1,00	1,41	Hs.279903	Ras homolog enriched in brain 2
7253	AGATGTGTGGG	1,00	1,41	Hs.146812	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coen
7254	ACGGCTCCGAG	1,00	1,42	Hs.48563	ESTs
7255	CCTCTCCTCCC	1,00	1,43	Hs.85004	centromere protein B (80kD)
7256	TACATTCTGTG	1,00	1,44	Hs.86386	myeloid cell leukemia sequence 1 (BCL2-related)
7257	TGCTGACTCCC	1,00	1,45	Hs.29076	ESTs, Highly similar to NEST_HUMAN NESTIN[H.sapien
7258	CCGCTGCTTGT	1,00	1,46	Hs.77768	heat shock protein, neuronal DNAJ-like 1
7259	TAACATTAAAG	1,00	1,47	Hs.84981	X-ray repair complementing defective repair in China
7260	TGGAGCGCTAC	1,00	1,49	Hs.237924	CGI-69 protein
7261	CCCTCTTTGGA	1,00	1,50	Hs.181174	ESTs
7262	GTGCTGGACCT	2,00	3,03	Hs.179774	proteasome (prosome, macropain) activator subunit 2
7263	GCCACACCCCA	1,00	1,52	Hs.7718	ESTs, Weakly similar to KIAA1402 protein [H.sapiens]
7264	TAATTCTTCTC	2,00	3,09	Hs.1708	chaperonin containing TCP1, subunit 3 (gamma)
7265	GTGTGTGGTGC	1,00	1,56	Hs.151032	Homo sapiens clone 23856 unknown mRNA, partial cds
7266	GCAACAGCAAT	3,00	4,60	Hs.9950	Sec61 gamma
7267	GGTGTGGAAGT	1,00	1,57	Hs.9659	hypothetical protein DKFZp434E026
7268	GAGCGGGATGG	2,00	3,12	Hs.77060	proteasome (prosome, macropain) subunit, beta type,
7269	ACACTACGGGT	1,00	1,58	Hs.109494	secreted protein of unknown function.
7270	GCTGGAGCTAG	1,00	1,59	Hs.74635	dihydrolipoamide dehydrogenase (E3 component of pyru
7271	TAACCTGTGAC	2,00	3,18	Hs.118512	integrin, alpha V (vitronectin receptor, alpha polyp

7272	TAAGATTTC	1,00	1,61	Hs.15265	heterogeneous nuclear ribonucleoprotein R	
7273	ACAAGTACCCA	1,00	1,61	Hs.142827	P311 protein	5
7274	GGGCCCCAAAG	2,00	3,25	Hs.256301	ESTs	
7275	CATCCTGCTGC	2,00	3,26	Hs.74619	proteasome (prosome, macropain) 26S subunit, non-ATP	
7276	CCAGGGGAGAA	2,00	3,27	Hs.278613	interferon, alpha-inducible protein 27	10
7277	TGCTGTGTGCT	1,00	1,65	Hs.90606	15 kDa selenoprotein	
7278	TGAAAGTGTGG	1,00	1,65	Hs.36927	heat shock 105kD	
7279	AAACATTGGGG	1,00	1,66	Hs.8203	endomembrane protein emp70 precursor isolog	15
7280	TGGAACCTTGC	1,00	1,66	Hs.194625	dynein, cytoplasmic, light intermediate polypeptide	
7281	TGAAGAGAAGA	1,00	1,66	Hs.120	anti-oxidant protein 2 (non-selenium glutathione per	20
7282	CCTGTGACAGC	2,00	3,32	Hs.120	anti-oxidant protein 2 (non-selenium glutathione per	
7283	CAACTAATTCA	11,00	17,42	Hs.75106	clusterin (complement lysis inhibitor, SP-40,40, sul	25
7284	AAGGCCTTGTG	1,00	1,67	Hs.74649	cytochrome c oxidase subunit VIc	
7285	AGAGCCCTAGG	1,00	1,67	Hs.16297	COX17 (yeast) homolog, cytochrome c oxidase assembly	
7286	TTTTTACTGAT	1,00	1,68	Hs.111577	integral membrane protein 2C	30
7287	GCTGGCTGGCT	3,00	5,01	Hs.108809	chaperonin containing TCP1, subunit 7 (eta)	
7288	CGTTCCTGCGG	2,00	3,39	Hs.75424	inhibitor of DNA binding 1, dominant negative helix-	35
7289	CCATTTTTACC	1,00	1,71	Hs.59271	U2(RNU2) small nuclear RNA auxillary factor 1 (non-s	
7290	ATGCGGGAGAA	1,00	1,71	Hs.109748	Homo sapiens CAC-1 mRNA, partial cds	
7291	TTTGTGTCACG	1,00	1,74	Hs.15093	hypothetical protein	40
7292	TCCTCCCTCCC	1,00	1,74	Hs.1390	proteasome (prosome, macropain) subunit, beta type,	
7293	GGCACAGTAAA	1,00	1,74	Hs.11270	ESTs	
7294	CTAATAAATGC	1,00	1,75	Hs.43621	ESTs	
7295	TGTCGCTGGGG	2,00	3,49	Hs.227152	mannan-binding lectin serine protease 1 (C4/C2 activ	45
7296	GGCCATCTCTT	2,00	3,50	Hs.74405	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase	
7297	CACTTGAAAAG	1,00	1,76	Hs.7753	calumenin	50
7298	GACAGCTGAGC	1,00	1,77	Hs.76240	adenylate kinase 1	
7299	GCTGCTCCCTT	1,00	1,79	Hs.3804	DKFZP564C1940 protein	
7300	GCGGAGAGAGG	1,00	1,79	Hs.286	ribosomal protein L4	
7301	TCAGGCATTTT	2,00	3,58	Hs.5566	gap junction protein, beta 2, 26kD (connexin 26)	55
7302	CAATTAAAAGG	3,00	5,33	Hs.149923	X-box binding protein 1	
7303	CAACTAGTTT	3,00	5,36	Hs.180224	death-associated protein 6	60
7304	GCAGGTGGTTT	1,00	1,81	Hs.145696	splicing factor (CC1.3)	
7305	GCTGTCATCAG	1,00	1,82	Hs.4745	proteasome (prosome, macropain) 26S subunit, ATPase,	

7306	GAGCGGGATCA	1,00	1,85	Hs.73737	splicing factor, arginine/serine-rich 1 (splicing fa
7307	ATTAACAAAGC	5,00	9,03	Hs.113368	neuroendocrine secretory protein 55
7308	TGCCGTTTTGA	1,00	1,86	Hs.2006	glutathione S-transferase M3 (brain)
7309	CCGTGCTCATC	2,00	3,72	Hs.9857	carbonyl reductase
7310	AAGGCACAGAC	1,00	1,90	Hs.227107	CDP-diacylglycerol--inositol 3-phosphatidyltransfera
7311	ATTTGTCCCAG	3,00	5,62	Hs.139800	high-mobility group (nonhistone chromosomal) protein
7312	AAGGCCGAGTA	1,00	1,91	Hs.31387	DKFZP564J0123 protein
7313	ATAGTAGCTTC	1,00	1,92	Hs.118400	singed (Drosophila)-like (sea urchin fascin homolog
7314	GGACTGGCCCA	1,00	1,93	Hs.263812	nuclear distribution gene C (A.nidulans) homolog
7315	ACTCAGAAGAG	2,00	3,93	Hs.198272	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2
7316	CTGAGCTGTAC	1,00	1,97	Hs.8737	WD repeat domain 6
7317	ACTTAAGGAAC	1,00	1,98	Hs.76285	DKFZP564B167 protein
7318	GCTATTTGAAA	1,00	1,98	Hs.279009	seven in absentia (Drosophila) homolog 1
7319	TTCTCTCTGTT	1,00	1,99	Hs.77541	ADP-ribosylation factor 5
7320	GGGAGCCCGGG	1,00	1,99	Hs.183986	poliovirus receptor-related 2 (herpesvirus entry med
7321	AATATGTGGGC	5,00	9,71	Hs.74649	cytochrome c oxidase subunit VIc
7322	GCTCTCTATGC	2,00	4,01	Hs.102135	signal sequence receptor, delta (translocon-associat
7323	TGAGTGGTCAC	1,00	2,01	Hs.121849	ESTs, Weakly similar to GEF-2 protein [H.sapiens]
7324	ATTCAGCACCT	1,00	2,04	Hs.11125	HSPC033 protein
7325	CCTGTTCTCCT	1,00	2,08	Hs.109798	G8 protein
7326	TGGGAAGTGGG	2,00	4,16	Hs.112844	hypothetical protein PRO2160
7327	GATCCCAACTG	5,00	10,18	Hs.118786	metallothionein 2A
7328	TTAATAAAAGT	1,00	2,09	Hs.19077	CGI-113 protein
7329	CCTCGCTCAGT	1,00	2,11	Hs.75860	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coen
7330	ACTCCTGTCCT	1,00	2,11	Hs.7357	DKFZP586N1922 protein
7331	GAGCCGCCTCT	1,00	2,12	Hs.30026	HSPC182 protein
7332	CTTGATTCCCA	1,00	2,13	Hs.77266	quiescin Q6
7333	TGGCAACCTTT	1,00	2,13	Hs.279952	glutathione S-transferase subunit 13 homolog
7334	TTATGGGGAGG	1,00	2,14	Hs.75612	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organiz
7335	TCATAGAAACC	1,00	2,16	Hs.1600	chaperonin containing TCP1, subunit 5 (epsilon)
7336	GAGGAAGAAGA	2,00	4,31	Hs.82689	tumor rejection antigen (gp96) 1
7337	ACAAACCCCCA	1,00	2,17	Hs.78629	ATPase, Na+/K+ transporting, beta 1 polypeptide
7338	GCTTAGAAGTG	1,00	2,17	Hs.180532	heat shock 90kD protein 1, alpha
7339	ACTGGTACGTG	1,00	2,17	Hs.155751	ATP synthase, H+ transporting, mitochondrial F0 comp

7340	CCAGGAGGAAT	6,00	12,65	Hs.180414	heat shock 70kd protein 10 (HSC71)	
7341	GGGACGAGTGA	3,00	6,45	Hs.3337	transmembrane 4 superfamily member 1	
7342	GTACCCGGACA	1,00	2,19	Hs.74649	cytochrome c oxidase subunit VIc	5
7343	GGCTTTGATTT	1,00	2,20	Hs.75724	coatomer protein complex, subunit beta 2 (beta prime	
7344	TTGGGAGCAGG	1,00	2,22	Hs.172801	isoleucine-tRNA synthetase	
7345	TCTGCAAAAAA	1,00	2,23	Hs.81281	hypothetical protein	10
7346	GGGGATGGGGT	1,00	2,25	Hs.99093	Homo sapiens chromosome 19, cosmid R28379	
7347	CGTGGGTGGGG	1,00	2,27	Hs.202833	heme oxygenase (decycling) 1	
7348	TTCCGCGTGCC	1,00	2,29	Hs.153357	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3v	15
7349	GAGAACCGTAG	2,00	4,57	Hs.105547	neural proliferation, differentiation and control, 1	
7350	TTACGAGGAAG	1,00	2,32	Hs.227949	SEC13 (S. cerevisiae)-like 1	20
7351	TTGCTTTTGTT	1,00	2,33	Hs.75290	ADP-ribosylation factor 4	
7352	GAAGATGTGTG	3,00	7,05	Hs.112318	6.2 kd protein	
7353	GATTTTGTAGC	1,00	2,39	Hs.84264	acidic protein rich in leucines	
7354	TCGTGCGAGAA	1,00	2,39	Hs.19561	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex,	25
7355	GAGGCTCAATC	1,00	2,40	Hs.8123	chromobox homolog 3 (Drosophila HP1 gamma)	
7356	TAGAAAAATAA	1,00	2,42	Hs.944	glucose phosphate isomerase	30
7357	CCGGGTGATGG	2,00	4,84	Hs.279910	ATX1 (antioxidant protein 1, yeast) homolog 1	
7358	GAAGCTTTGCA	4,00	9,54	Hs.180532	heat shock 90kD protein 1, alpha	
7359	GGTTATTTTGG	1,00	2,47	Hs.82085	plasminogen activator inhibitor, type I	35
7360	TGTGCTCGGGG	2,00	4,97	Hs.76847	KIAA0088 protein	
7361	ATGGCGATCTA	1,00	2,53	Hs.180450	ribosomal protein S24	
7362	AAAATAAAGAG	1,00	2,56	Hs.73722	APEX nuclease (multifunctional DNA repair enzyme)	40
7363	GGTGCAGAGCC	1,00	2,56	Hs.539	ribosomal protein S29	
7364	CATTGAAGGGT	1,00	2,59	Hs.79026	myeloid leukemia factor 2	
7365	TGACTGAAGCC	1,00	2,62	Hs.3343	phosphoglycerate dehydrogenase	
7366	AACGCGGCCAA	7,00	18,26	Hs.73798	macrophage migration inhibitory factor (glycosylation	45
7367	GCCGTGTAGAC	1,00	2,69	Hs.83384	S100 calcium-binding protein, beta (neural)	
7368	AGGGTGAAACT	1,00	2,71	Hs.77608	splicing factor, arginine/serine-rich 9	50
7369	AAGGTAATGCT	1,00	2,73	Hs.23990	hypothetical protein FLJ20479	
7370	ACAGTGGGGAT	2,00	5,54	Hs.75839	zinc finger protein 6 (CMPX1)	
7371	GAACCCTGGGA	1,00	2,78	Hs.155637	protein kinase, DNA-activated, catalytic polypeptide	
7372	TAAATAATTTC	1,00	2,79	Hs.1197	heat shock 10kD protein 1 (chaperonin 10)	55
7373	GAAATAAAAGC	1,00	2,81	Hs.57783	eukaryotic translation initiation factor 3, subunit	
7374	GAATTAACATT	2,00	5,70	Hs.79474	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase	60
7375	GGTAGCAGGGA	1,00	2,88	Hs.179817	CGI-82 protein	

5	7376	GTTTAAATCGA	1,00	2,94	Hs.181309	proteasome (prosome, macropain) sub-unit, alpha type,
	7377	GACGTCTTAAT	1,00	3,01	Hs.251531	proteasome (prosome, macropain) sub-unit, alpha type,
	7378	TACTAGTCCTC	2,00	6,04	Hs.180532	heat shock 90kD protein 1, alpha
	7379	CGATTCTGGAG	1,00	3,03	Hs.177507	hypothetical protein
10	7380	ACTGGTAAAAA	1,00	3,03	Hs.155751	ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 comp
	7381	AAGGAGTTTGA	1,00	3,05	Hs.661	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7
15	7382	GTGACAACACT	1,00	3,06	Hs.149155	voltage-dependent anion channel 1
	7383	GGAGTCATTGT	1,00	3,11	Hs.82793	proteasome (prosome, macropain) sub-unit, beta type,
	7384	TGTATAAAAAT	1,00	3,12	Hs.82689	tumor rejection antigen (gp96) 1
20	7385	GCAGACATTGA	1,00	3,18	Hs.179662	nucleosome assembly protein 1-like 1
	7386	GAGGATGGTGT	1,00	3,19	Hs.19555	prostate tumor over expressed gene 1
	7387	TCAAATGCATC	1,00	3,31	Hs.182447	heterogeneous nuclear ribonucleoprotein C (C1/C2)
25	7388	TGCTTGTCCT	1,00	3,35	Hs.74571	ADP-ribosylation factor 1
	7389	AATGTGAGTCA	1,00	3,40	Hs.25001	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase
	7390	CGGCCCAACGC	1,00	3,41	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2
30	7391	GTTTCATCTCC	1,00	3,42	Hs.13451	dystrobrevin, beta
	7392	AAGGAATCGGG	1,00	3,43	Hs.89545	proteasome (prosome, macropain) sub-unit, beta type,
35	7393	AAAGTGAAGAT	1,00	3,44	Hs.284158	Homo sapiens mRNA; cDNA DKFZp762B195 (from clone DKF
	7394	TCAGAAGGTGC	1,00	3,49	Hs.74649	cytochrome c oxidase subunit VIc
	7395	GGGCCTGTGCC	1,00	3,51	Hs.85838	solute carrier family 16 (monocarboxylic acid transp
40	7396	AGAAATACCAA	1,00	3,56	Hs.74649	cytochrome c oxidase subunit VIc
	7397	GGAAGTTTCGA	1,00	3,56	Hs.55847	hypothetical protein
	7398	GGGGGTAAC TA	1,00	3,60	Hs.99969	fusion, derived from t(12;16) malignant liposarcoma
45	7399	CATTTCATAAC	1,00	3,68	Hs.73851	ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 comp
	7400	GGCTTTGGAGT	1,00	3,73	Hs.90918	chromosome 11 open reading frame 10
50	7401	GGCGTCCTGGC	1,00	4,03	Hs.44017	SIR2 (silent mating type information regulation 2, S
	7402	TAGACTAGCAA	1,00	4,12	Hs.100090	tetraspan 3
	7403	CCGATCACCGG	1,00	4,18	Hs.12163	eukaryotic translation initiation factor 2, subunit
55	7404	GAATCCAAC TG	1,00	4,35	Hs.111497	similar to mouse neuronal protein 15.6
	7405	CAGCGCGCCCT	1,00	4,49	Hs.152932	ESTs
	7406	GCATAGGCTGC	1,00	4,69	Hs.12084	Tu translation elongation factor, mitochondrial
60	7407	ATCCCTCAGTG	1,00	4,96	Hs.181243	activating transcription factor 4 (tax-responsive en
	7408	CTGTTGGCATT	1,00	5,14	Hs.184108	ribosomal protein L21 (gene or pseudo-gene)

7409	CAGGAACGGGG	1,00	5,52	Hs.72241	mitogen-activated protein kinase kinase 2
7410	GAAAAATTTAA	1,00	6,07	Hs.17775	p75NTR-associated cell death executor; ovarian granu
7411	GACTCTTCAGT	1,00	6,79	Hs.234726	alpha-1-antichymotrypsin
7412	CCTGGTCCCAA	1,00	6,89	Hs.23881	keratin 7
7413	GGGGACTGAAG	1,00	6,93	Hs.3709	low molecular mass ubiquinone-binding protein (9.5kD
7414	GGGCGCTGTGG	1,00	8,83	Hs.8372	ubiquinol-cytochrome c reductase (6.4kD) subunit
7415	TGAGGGAATAA	2,00	17,86	Hs.83848	triosephosphate isomerase 1
7416	GGAACAAACAG	1,00	9,05	Hs.278667	Homo sapiens cDNA FLJ20161 fis, clone COL09252, high
7417	AACGACCTCGT	1,00	11,88	Hs.179661	tubulin, beta polypeptide
7418	AAGGGAGCACC	1,00	12,05	Hs.181125	immunoglobulin lambda locus
7419	GCCGGGTGGGC	2,00	34,72	Hs.74631	basigin
7420	CCTCCAGCTAC	2,00	44,29	Hs.242463	keratin 8
7421	CAAACCATCCA	1,00	22,49	Hs.65114	keratin 18

Tabelle 5

Nr.	Tag_Sequence	CGAP	Rel. Expr. Haut	Quotient	signific.	UniGene Acc.-Nr.	Beschreibung
1	ATCCGCGAGGC	0,12	45,00	375,00	63,99	Hs.180142	CLSP Calmodulin-like skin protein
2	GAGATAAATGA	0,09	23,00	255,56	31,88	Hs.3185	lymphocyte antigen 6 complex, locus D
3	TAAACCTGCTG	0,47	110,00	234,04	150,08	Hs.99923	lectin, galactoside-binding, soluble, 7 (galectin 7)
4	GATGTGCACGA	1,08	216,00	200,00	289,47	Hs.117729	keratin 14 (epidermolysis bullosa simplex, Dowling-M
5	ACATTTCAAAG	0,00	161,00	161,00	248,57	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)
6	TTTGTAGAGGA	0,26	37,00	142,31	47,97	Hs.279671	katanin p60 (ATPase-containing) subunit A 1
7	ACCTCCACTGG	0,00	139,00	139,00	214,56	Hs.112457	ESTs
8	AATCTTGTTTC	0,88	93,00	105,68	115,24	Hs.32343	ESTs
9	GAAAACAAAGT	4,48	467,00	104,24	100,00	Hs.99936	keratin 10 (epidermolytic hyperkeratosis; keratosis
10	GCCCCTGCTGA	1,46	148,00	101,37	181,69	Hs.195850	keratin 5 (epidermolysis bullosa simplex, Dowling-Me
11	CACACGGGCGA	0,26	26,00	100,00	32,16	Hs.194679	WNT1 inducible signaling pathway protein 2

Tabelle 4

Nr.	Tag_Sequence	CGAP	Rel. Expr. Haut	Quo- tient	signific.	UniGene Acc.-Nr.	Beschreibung
12	GACAATAAATG	0,15	9	60,00	10,38	Hs.137556	Homo sapiens mRNA; cDNA DKFZp434A132 (from clone DKF
13	ACTACCATAAC	0,12	7	58,33	8,06	Hs.57929	slit (Drosophila) homo- log 3
14	CATTGTAAATA	0,12	7	58,33	8,06	Hs.55279	protease inhibitor 5 (maspin)
15	ACCGGCGCCCG	0,5	29	58,00	32,51	Hs.65424	tetranectin (plasmino- gen-binding protein)
16	CCACCACGCTT	0,29	16	55,17	17,84	Hs.285275	ESTs, Moderately simi- lar to ALU7_HUMAN ALU SUBFAMILY
17	CCCCGGCCACC	0,88	42	47,73	44,79	Hs.279604	(Manual assignment) desmin, muscle inter- mediate fila
18	TGAAATAAAAG	0,26	12	46,15	12,9	Hs.48516	ESTs
19	ACTGAGTAGGT	0,09	4	44,44	4,39	Hs.38095	ATP-binding cassette, sub-family A (ABC1), member 8
20	ATCCTTGCTGA	0,7	26	37,14	26,12	Hs.2621	cystatin A (stefin A)
21	CAGCCTGGGTG	0,15	5	33,33	5,1	Hs.171941	ESTs
22	GATATGTTATA	0,15	5	33,33	5,1	Hs.117938	collagen, type XVII, alpha 1
23	TGGCTTCATCA	0,12	4	33,33	4,1	Hs.646	carboxypeptidase A3 (mast cell)
24	CCTGTAACACC	0,09	3	33,33	3,09	Hs.74304	periplakin
25	CCCCGGAGGTC	0,09	3	33,33	3,09	Hs.47913	coagulation factor X
26	AGATCAGTTGA	0,09	3	33,33	3,09	Hs.191805	ESTs
27	CCCTCAGCACC	0,29	9	31,03	8,78	Hs.87268	annexin A8
28	CTTTATTCCAG	1,7	49	28,82	45,24	Hs.172928	collagen, type I, alpha 1
29	TCCACTGGCCT	0,82	23	28,05	21,32	Hs.57548	ESTs
30	CACGCAGTGGC	0,18	5	27,78	4,85	Hs.245545	EST
31	TACATTATATA	0,12	3	25,00	2,85	Hs.198862	fibulin 2
32	ATGGATACGGG	0,41	10	24,39	9,05	Hs.250722	(Manual assignment) unclear, probably re- verse tag o
33	CCGGGGGAGCC	1,93	43	22,28	36,36	Hs.172928	collagen, type I, alpha 1
34	CAGTTTTTTC	0,09	2	22,22	1,84	Hs.99597	ESTs
35	GTGGATTCAAG	0,09	2	22,22	1,84	Hs.93847	NADPH oxidase 4
36	TGTCTGTGTGT	0,09	2	22,22	1,84	Hs.93739	ESTs
37	TCTACACGTGC	0,09	2	22,22	1,84	Hs.53155	properdin P factor, complement
38	GAAATGGCAGT	0,09	2	22,22	1,84	Hs.30853	ESTs
39	ACGAAACCTCG	0,09	2	22,22	1,84	Hs.285785	Homo sapiens cDNA



							FLJ20115 fis, clone COL05594	
40	GGCAATGCAGT	0,09	2	22,22	1,84	Hs.275505	ESTs	5
41	CCTTTTCAGCA	0,09	2	22,22	1,84	Hs.25930	ESTs	
42	CCTCTTTAACA	0,09	2	22,22	1,84	Hs.25750	ESTs	
43	TATCTAGCTGC	0,09	2	22,22	1,84	Hs.241545	hypothetical protein	
44	GCTGTAATCCT	0,09	2	22,22	1,84	Hs.241382	tumor necrosis factor (ligand) superfamily, member 1	10
45	GGGCAGCCGCC	0,09	2	22,22	1,84	Hs.23598	CREB binding protein (Rubinstein-Taybi syndrome)	15
46	CGCTTGTTTAA	0,09	2	22,22	1,84	Hs.180398	LIM domain-containing preferred translocation partne	20
47	GCACACACCTG	0,09	2	22,22	1,84	Hs.171143	EST, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	25
48	CTGGAGTCGGC	0,09	2	22,22	1,84	Hs.166371	Interleukin-1 Superfamily z	
49	GAGGTCAGTTG	0,09	2	22,22	1,84	Hs.151696	DKFZP727G051 protein	
50	CCAGGCAAGAC	0,09	2	22,22	1,84	Hs.134194	distal-less homeo box 3	
51	GAAATCAAAAA	0,59	13	22,03	11,3	Hs.117005	sialic acid binding Ig-like lectin 5	30
52	AATCTAGTTCT	0	22	22,00	33,72	Hs.251440	Human profilaggrin gene exons 1-3, 5' end	35
53	AAGCTAATAAA	0,41	9	21,95	7,89	Hs.88474	prostaglandin-endoperoxide synthase 1 (prostaglandin	
54	TGTGCGGCTTC	0,23	5	21,74	4,43	Hs.162196	hypothetical protein FLJ20321	40
55	CAGGTTTCATA	3,08	66	21,43	54,72	Hs.24395	small inducible cytokine subfamily B (Cys-X-Cys), me	45
56	CTGTCGTCATC	0,35	7	20,00	5,98	Hs.183860	hypothetical protein FLJ20277	
57	ATAGCACGTGC	0,15	3	20,00	2,66	Hs.277329	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC	50
58	GTGAGAACTCG	0,15	3	20,00	2,66	Hs.250639	ESTs	

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(4)

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Tabelle 3

Nr.	Tag_Sequence	CGAP	Rel. Expr. Haut	Quo- tient	signific.	UniGene Acc.-Nr.	Beschreibung
59	ACTTATTATGC	1,49	29	19,46	23,46	Hs.76152	decorin
60	CTTGCAGTCCT	0,26	5	19,23	4,25	Hs.27018	Ris
61	CATCTGTACTC	0,73	14	19,18	11,49	Hs.180255	major histocompatibility complex, class II, DR beta
62	GTGGAGGGCAC	1,03	18	17,48	14,16	Hs.83393	cystatin E/M
63	AGGCAGGAAAA	0,29	5	17,24	4,09	Hs.133081	ESTs, Weakly similar to hypothetical protein [H.sapi]
64	AATTGAAAAGG	0,59	10	16,95	7,94	Hs.78344	myosin, heavy polypeptide 11, smooth muscle
65	CTTTAAAATGA	0,18	3	16,67	2,5	Hs.8217	stromal antigen 2
66	TGTGCCAGTTT	0,18	3	16,67	2,5	Hs.53358	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY
67	AGTAGCTGGGA	0,18	3	16,67	2,5	Hs.224534	EST, Weakly similar to alternatively spliced product
68	CCTCTGTCTCC	0,18	3	16,67	2,5	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (from clone
69	AACATTTAGGA	0,18	3	16,67	2,5	Hs.138380	KIAA0624 protein
70	CAATAAAATTT	0,18	3	16,67	2,5	Hs.137569	tumor protein 63 kDa with strong homology to p53
71	GCCGCTCAAGG	0,18	3	16,67	2,5	Hs.126064	ESTs
72	CCTGGTCAAGA	0,12	2	16,67	1,68	Hs.95972	silver (mouse homolog) like
73	CCACCGCAGGA	0,12	2	16,67	1,68	Hs.85112	insulin-like growth factor 1 (somatomedia C)
74	ACACTTCTCAA	0,12	2	16,67	1,68	Hs.75652	glutathione S-transferase M5
75	CCTCTCTGGTC	0,12	2	16,67	1,68	Hs.56874	heat shock 27kD protein family, member 7 (cardiovascular)
76	GCATATCTGTG	0,12	2	16,67	1,68	Hs.5459	KIAA1436 protein
77	AGCTGTGATGG	0,12	2	16,67	1,68	Hs.249983	ESTs
78	GCTAACTTAAA	0,12	2	16,67	1,68	Hs.20787	ESTs
79	CCTTGAAATCA	0,12	2	16,67	1,68	Hs.183161	ESTs
80	CTTTATCAATA	0,12	2	16,67	1,68	Hs.166017	microphthalmia-associated transcription factor
81	ACAGCCCTGAT	0,12	2	16,67	1,68	Hs.163593	ribosomal protein L18a
82	GATACTCAGAA	0,12	2	16,67	1,68	Hs.144726	ESTs
83	GCCTGGGAGAC	0,12	2	16,67	1,68	Hs.118346	ESTs

84	TGGGTGGTGGT	0,79	13	16,46	10,06	Hs.82712	fragile X mental retardation, autosomal homolog 1
85	AGCTACCACAG	0,59	9	15,25	6,87	Hs.169886	tenascin XB
86	ACAGCGGCAAT	4,63	69	14,90	49,04	Hs.74316	desmoplakin (DPI, DPII)
87	GTAAAATCCCA	0,21	3	14,29	2,36	Hs.278623	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY
88	CACTTGTAATC	0,21	3	14,29	2,36	Hs.268488	KIAA1185 protein
89	CTTGTAGTTCC	0,21	3	14,29	2,36	Hs.155983	KIAA0677 gene product
90	GGGTTTTCTGG	0,21	3	14,29	2,36	Hs.153703	ESTs, Moderately similar to DHSA_HUMAN SUCCINATE
91	CAGCAGAACTG	0,21	3	14,29	2,36	Hs.117582	CGI-43 protein
92	CCACAGGAGAA	5,68	81	14,26	56,23	Hs.169902	solute carrier family 2 (facilitated glucose transpo
93	ATAGCCAGGGA	0,29	4	13,79	3,02	Hs.95582	SRY (sex determining region Y)-box 20
94	GTACAAAAGTA	0,29	4	13,79	3,02	Hs.9552	binder of Arl Two
95	TCACAGGGTCC	0,29	4	13,79	3,02	Hs.77886	lamin A/C
96	TTCTGTGTGCC	0,29	4	13,79	3,02	Hs.58715	ESTs
97	TAGCCGGGACG	0,73	10	13,70	7,22	Hs.107740	Kruppel-like factor 2 (lung)
98	ATCACACAGCT	0,44	6	13,64	4,44	Hs.79386	leiomodulin 1 (smooth muscle)
99	ATCTCGAAAGG	0,59	8	13,56	5,84	Hs.10784	hypothetical protein FLJ20037
100	GACCCAACTGG	0,15	2	13,33	1,54	Hs.89575	CD79B antigen (immunoglobulin-associated beta)
101	CACAGGGAGGA	0,15	2	13,33	1,54	Hs.84753	KIAA0246 protein
102	CAGCTGGCCCA	0,15	2	13,33	1,54	Hs.79732	fibulin 1
103	GAGGGCTTTGC	0,15	2	13,33	1,54	Hs.78183	aldo-keto reductase family 1, member C3 (3-alpha hyd
104	GTGAGCCAAGA	0,15	2	13,33	1,54	Hs.75410	heat shock 70kD protein 5 (glucose-regulated protein
105	TACCCCAAAAA	0,15	2	13,33	1,54	Hs.6449	hypothetical protein FLJ20542
106	CAGGATGCTTG	0,15	2	13,33	1,54	Hs.56729	lymphocyte-specific protein 1
107	AGTGTGTTGCA	0,15	2	13,33	1,54	Hs.56105	ESTs, Weakly similar to WDNM_RAT WDNM1 PROTEIN
108	AGGACCTGAAG	0,15	2	13,33	1,54	Hs.32352	hypothetical protein DKFZp434K1210
109	ATTCTGGTCAT	0,15	2	13,33	1,54	Hs.18878	ESTs, Weakly similar to dJ876B10.4 [H.sapiens]
110	CCTTTTGGGAG	0,15	2	13,33	1,54	Hs.186600	ESTs

5	111	CGGTTCATACA	0,15	2	13,33	1,54	Hs.169487	Kreisler (mouse) maf-related leucine zipper homolog
	112	ATGGTGCCACC	0,15	2	13,33	1,54	Hs.161554	hypothetical protein FLJ20159
10	113	TAATGTTAATG	0,15	2	13,33	1,54	Hs.153924	death-associated protein kinase 1
	114	AGGGCCCTCTG	0,15	2	13,33	1,54	Hs.129014	hypothetical protein FLJ20207
15	115	GTGGCACGCGT	0,15	2	13,33	1,54	Hs.118243	deoxyribonuclease II, lysosomal
	116	AGCTTGAGTTC	0,15	2	13,33	1,54	Hs.117582	CGI-43 protein
	117	GTGGGGCCAAG	0,53	7	13,21	5,08	Hs.24194	folate receptor 2 (fetal)
	118	GTGAAGCCTCA	0,38	5	13,16	3,67	Hs.271823	ESTs
20	119	ACCAGACAGAC	0,23	3	13,04	2,23	Hs.7882	ESTs
	120	GTGAAACTCTT	0,23	3	13,04	2,23	Hs.29759	RNA POLYMERASE I AND TRANSCRIPT RELEASE
25	121	ATTTCCATTAA	0,23	3	13,04	2,23	Hs.284126	hairless (mouse) homolog
	122	GTGGTAAGCAC	0,23	3	13,04	2,23	Hs.271827	ESTs, Moderately similar to ALU7_HUMAN ALU
30	123	GTTTTGCCCAC	0,23	3	13,04	2,23	Hs.151407	cartilage intermediate layer protein, nucleotide pyr
	124	GCCCACACAGC	0,62	8	12,90	5,71	Hs.1690	heparin-binding growth factor binding protein
35	125	TTTCCTCTCAA	2,99	38	12,71	25,3	Hs.184510	stratifin
	126	CGGGAGCGCTA	1,05	13	12,38	8,84	Hs.148590	ESTs, Weakly similar to AF208846_1 BM-004 [H.sapiens]
40	127	TTGCATATCAG	0,82	10	12,20	6,84	Hs.82237	ataxia-telangiectasia group D-associated protein
45	128	AGGCCTCGGCA	0,41	5	12,20	3,55	Hs.286202	Homo sapiens cDNA FLJ11346 fis, clone PLACE1010900
	129	GTGGCGAATGA	0	12	12,00	18,26	Hs.69752	desmocollin 1
50	130	TGTGAAGCCTT	0	12	12,00	18,26	Hs.5476	serine protease inhibitor, Kazal type, 5
	131	TCAGACTTTTG	0,76	9	11,84	6,1	Hs.5889	ESTs, Weakly similar to AC004876_5 similar to predic
55	132	ATTTCTTCAAG	0,76	9	11,84	6,1	Hs.31386	ESTs, Highly similar to JE0174 frizzled protein-2
60	133	GAATTATACTT	0,85	10	11,76	6,73	Hs.104800	hypothetical protein FLJ10134
	134	TCTGGGGAACA	0,26	3	11,54	2,12	Hs.184390	similar to aspartate beta hydroxylase (ASPH)
65	135	GCAAAAACCCG	0,26	3	11,54	2,12	Hs.184109	ribosomal protein L37a

136	AATGTTGTGCA	0,35	4	11,43	2,78	Hs.91546	cytochrome P450 retinoid metabolizing protein
137	ACAATGTTGTA	0,18	2	11,11	1,43	Hs.7678	cellular retinoic acid-binding protein 1
138	CGAGAGTGTGA	0,18	2	11,11	1,43	Hs.58210	ESTs
139	GTATAAAAAA	0,18	2	11,11	1,43	Hs.27337	hypothetical protein FLJ20623
140	AGGTCGAGGCT	0,18	2	11,11	1,43	Hs.270125	ESTs
141	CCCGGCCAGT	0,18	2	11,11	1,43	Hs.243324	EST, Weakly similar to ALUA_HUMAN !!!! ALU CLASS A
142	TTGACCCAGCC	0,18	2	11,11	1,43	Hs.193745	ESTs
143	TATTTTATTG	0,18	2	11,11	1,43	Hs.189999	purinergic receptor (family A group 5)
144	GCATCATAGGT	0,18	2	11,11	1,43	Hs.184108	ribosomal protein L21 (gene or pseudogene)
145	TACCGCTCCCT	0,18	2	11,11	1,43	Hs.172803	Homo sapiens mRNA; cDNA DKFZp434G2416 (from clone)
146	CTCCTGTGGTC	0,18	2	11,11	1,43	Hs.169851	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAMILY
147	GGTGTCTCCTC	0,18	2	11,11	1,43	Hs.146038	ESTs
148	CAATCTTGTGA	0,18	2	11,11	1,43	Hs.104353	ESTs
149	CCTACAAAAA	0,09	1	11,11	0,69	Hs.98288	ESTs
150	TGTGCCCAGCC	0,09	1	11,11	0,69	Hs.97905	ovo (Drosophila) homolog-like 1
151	GATGGGGACAG	0,09	1	11,11	0,69	Hs.92195	ESTs
152	TAAAAATATTG	0,09	1	11,11	0,69	Hs.89695	insulin receptor
153	TTTAAGTTAGG	0,09	1	11,11	0,69	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatosis 1)
154	GTATATGTATT	0,09	1	11,11	0,69	Hs.7917	DKFZP564K247 protein
155	CTAAAGTGTC	0,09	1	11,11	0,69	Hs.7910	RING1 and YY1 binding protein
156	AATTTGGCTTT	0,09	1	11,11	0,69	Hs.7734	Homo sapiens cDNA FLJ20684 fis, clone KAIA3469
157	CCGTGGCACCA	0,09	1	11,11	0,69	Hs.77208	ESTs
158	AGCACCTTGT	0,09	1	11,11	0,69	Hs.75871	protein kinase C binding protein 1
159	CCTTTGAGAGC	0,09	1	11,11	0,69	Hs.71791	hypothetical protein
160	TAAATGTAAAT	0,09	1	11,11	0,69	Hs.64096	KIAA0427 gene product
161	TACAGACATAC	0,09	1	11,11	0,69	Hs.63984	cadherin 13, H-cadherin (heart)
162	GTAGCATTTGC	0,09	1	11,11	0,69	Hs.63302	myotubularin related protein 3
163	AAGTAGGTTTT	0,09	1	11,11	0,69	Hs.50216	zinc finger protein (ZFD25)
164	ATCACTCCCCA	0,09	1	11,11	0,69	Hs.37058	calcitonin/calcitonin-related polypeptide, alpha

5	165	TAGGCAGACCT	0,09	1	11,11	0,69	Hs.35488	ESTs, Moderately similar to ALU6_HUMAN ALU
	166	GCCTGGCCAGG	0,09	1	11,11	0,69	Hs.3343	phosphoglycerate dehydrogenase
10	167	GTCATCTTGTT	0,09	1	11,11	0,69	Hs.32366	ESTs, Moderately similar to TWST_HUMAN TWIST
	168	CTCAACAACCA	0,09	1	11,11	0,69	Hs.30036	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY
15	169	TTATATTAATA	0,09	1	11,11	0,69	Hs.29205	alpha integrin binding protein 63
	170	GATTAAACCTT	0,09	1	11,11	0,69	Hs.287357	ESTs, Moderately similar to meningioma-expressed ant
20	171	GATGGAGGTTA	0,09	1	11,11	0,69	Hs.285224	ESTs, Weakly similar to unnamed protein product [H.s
	172	TACAGGCGTGG	0,09	1	11,11	0,69	Hs.283329	ESTs
25	173	TGTGTGTGTAT	0,09	1	11,11	0,69	Hs.278676	Homo sapiens mRNA; cDNA DKFZp434J1630 (from clone
30	174	GGTGCCTGTAA	0,09	1	11,11	0,69	Hs.278425	ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C
	175	AAGTTGTGGCC	0,09	1	11,11	0,69	Hs.278242	tubulin, alpha, ubiquitous
35	176	ACAGGAGCGTT	0,09	1	11,11	0,69	Hs.275896	EST
	177	ATGCCTACTCT	0,09	1	11,11	0,69	Hs.274834	EST
	178	AGCACAATCTT	0,09	1	11,11	0,69	Hs.274128	Homo sapiens cDNA FLJ10131 fis, clone HEMBA1003041
40	179	GTTCTGTTTGG	0,09	1	11,11	0,69	Hs.271040	ESTs
	180	TTGTGATTATA	0,09	1	11,11	0,69	Hs.26320	TRABID protein
	181	TATGCAGATCA	0,09	1	11,11	0,69	Hs.254948	ESTs
	182	GTTGAGGACAT	0,09	1	11,11	0,69	Hs.250520	ESTs
45	183	GCCAGTGGCTG	0,09	1	11,11	0,69	Hs.249720	ESTs
	184	GCAGATCTTTC	0,09	1	11,11	0,69	Hs.248623	EST
	185	TTGAAACTTCT	0,09	1	11,11	0,69	Hs.242481	ESTs
50	186	CAAAAAGTTGA	0,09	1	11,11	0,69	Hs.241425	DKFZP586O1422 protein
	187	CTCCATTCTCA	0,09	1	11,11	0,69	Hs.23803	Homo sapiens mRNA; cDNA DKFZp434M2217 (from clone
55	188	GCCACAGCTGG	0,09	1	11,11	0,69	Hs.23565	ESTs
	189	GGGAAAGAAGG	0,09	1	11,11	0,69	Hs.233193	EST
	190	CAAAAGAATAA	0,09	1	11,11	0,69	Hs.233013	EST
	191	TAACAGTAATA	0,09	1	11,11	0,69	Hs.231913	ESTs
60	192	TGCCTAGGAAA	0,09	1	11,11	0,69	Hs.226356	Homo sapiens mRNA; cDNA DKFZp586F1922 (from clone
65	193	CCCTAGGAGAC	0,09	1	11,11	0,69	Hs.217484	ESTs

194	GGGTTGTTGTA	0,09	1	11,11	0,69	Hs.211258	ESTs
195	AACCCCCAAAC	0,09	1	11,11	0,69	Hs.207181	ESTs
196	CTTTTTTCTTT	0,09	1	11,11	0,69	Hs.204917	EST
197	TGGGAATTGTG	0,09	1	11,11	0,69	Hs.203750	EST
198	CATTCCAGCCT	0,09	1	11,11	0,69	Hs.201306	ESTs
199	GCTGGAGTGCA	0,09	1	11,11	0,69	Hs.195484	Homo sapiens mRNA full length insert cDNA clone EURO
200	GAAGGCCAGCT	0,09	1	11,11	0,69	Hs.194624	ESTs
201	ACGTATTTGAG	0,09	1	11,11	0,69	Hs.193488	Homo sapiens mRNA; cDNA DKFZp434O1521 (from clone
202	TAATTTAAACC	0,09	1	11,11	0,69	Hs.18800	hypothetical protein FLJ20281
203	CTAAATGTGAA	0,09	1	11,11	0,69	Hs.181163	high-mobility group (nonhistone chromosomal) protein
204	CCTGGCTCTAA	0,09	1	11,11	0,69	Hs.178705	Homo sapiens cDNA FLJ11333 fis, clone PLACE1010616
205	CTGTCCTTGTT	0,09	1	11,11	0,69	Hs.176333	ESTs
206	CAATATTTGAG	0,09	1	11,11	0,69	Hs.174030	a disintegrin and metalloproteinase domain 28
207	CAATGGATGGC	0,09	1	11,11	0,69	Hs.170673	ESTs, Weakly similar to AF126780_1 retinal short-cha
208	GTCCTTGACCA	0,09	1	11,11	0,69	Hs.170524	ESTs
209	GCAATGACCTG	0,09	1	11,11	0,69	Hs.1702	interleukin 9 receptor
210	TCCTAATTCAG	0,09	1	11,11	0,69	Hs.170162	KIAA1357 protein
211	TTAATGATCTT	0,09	1	11,11	0,69	Hs.165240	ESTs
212	TTAAGTGTTCT	0,09	1	11,11	0,69	Hs.159239	toll-like receptor 4
213	TGAAGCGTTTA	0,09	1	11,11	0,69	Hs.155693	protein tyrosine phosphatase, non-receptor type 21
214	GTGGAGCTTAA	0,09	1	11,11	0,69	Hs.152385	ESTs
215	GAGACTGGGGC	0,09	1	11,11	0,69	Hs.142854	ESTs
216	GTGGTACTCGC	0,09	1	11,11	0,69	Hs.141840	ESTs, Weakly similar to S59501 interferon receptor J
217	TGCAGTGCTTG	0,09	1	11,11	0,69	Hs.141660	chloride channel 2
218	AGCTTATTGGC	0,09	1	11,11	0,69	Hs.137732	KIAA1098 protein
219	ACTTCTGCTTA	0,09	1	11,11	0,69	Hs.13740	ESTs
220	GATAGAAATTT	0,09	1	11,11	0,69	Hs.131987	ESTs
221	TTTGACTAATT	0,09	1	11,11	0,69	Hs.131761	ESTs
222	TCAAAATGACA	0,09	1	11,11	0,69	Hs.131272	ESTs
223	CCAGCTAGTTT	0,09	1	11,11	0,69	Hs.128692	ESTs
224	TAGAGGAGTTG	0,09	1	11,11	0,69	Hs.125815	ESTs
225	GGGAAACACCA	0,09	1	11,11	0,69	Hs.123471	EST
226	GAAATGAGTGT	0,09	1	11,11	0,69	Hs.1200	arachidonate 12-lipoxygenase
227	ATCTTGGTACT	0,09	1	11,11	0,69	Hs.118162	fibronectin 1

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228	CATATCATCTC	0,09	1	11,11	0,69	Hs.118130	ESTs
229	ATGTGACTTTT	0,09	1	11,11	0,69	Hs.117582	CGI-43 protein
230	CCACTGTAAGC	0,09	1	11,11	0,69	Hs.117582	CGI-43 protein
231	TATAAGGCTGA	0,09	1	11,11	0,69	Hs.114547	ESTs, Weakly similar to ZN84_HUMAN ZINC FINGER
232	GCCACTGCCAC	0,09	1	11,11	0,69	Hs.112405	S100 calcium-binding protein A9 (calgranulin B)
233	TGAGGCCAGGG	0,09	1	11,11	0,69	Hs.110128	hypothetical protein FLJ10060
234	GTTTATTTGAA	0,09	1	11,11	0,69	Hs.109087	ESTs
235	AAAATTGTTAG	0,09	1	11,11	0,69	Hs.10760	hypothetical protein FLJ20129
236	GTGATGGGCTC	0,82	9	10,98	5,88	Hs.25482	envoplakin
237	AGGCTCCTGGC	4,81	52	10,81	31,57	Hs.24395	small inducible cytokine subfamily B (Cys-X-Cys), me
238	AACAGCAAGGA	0,47	5	10,64	3,33	Hs.20665	ESTs
239	CCACGGGATTC	1,32	14	10,61	8,79	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danlos syn- drome)
240	GATTTTCGTTTT	0,38	4	10,53	2,68	Hs.738	early growth response 1
241	TATAGCCCTCA	0,38	4	10,53	2,68	Hs.64311	a disintegrin and metal- loproteinase domain 17 (tumor)
242	GTGACACGTGC	0,38	4	10,53	2,68	Hs.282996	ESTs
243	AGCTGTCGTAG	0,29	3	10,34	2,02	Hs.86674	ESTs
244	ATTGTTTCAAG	0,29	3	10,34	2,02	Hs.32366	ESTs, Moderately similar to TWST_HUMAN TWIST
245	AGACCCTGTCT	0,29	3	10,34	2,02	Hs.239283	ESTs
246	TTGGCAAGGCT	0,29	3	10,34	2,02	Hs.184720	ESTs
247	ATCATAGCTCA	0,59	6	10,17	3,87	Hs.97876	ESTs, Moderately similar to ALU1_HUMAN ALU



Tabelle 2

Nr.	Tag_Sequence	CGAP	Rel. Expr. Haut	Quo- tient	signi- fic.	UniGene Acc.-Nr.	Beschreibung
248	CCTACCACCAT	1,11	11	9,91	6,73	Hs.8468	RelA-associated inhibitor
249	CCAGGGCAACA	4,1	40	9,76	23,03	Hs.120980	(Manual assignment) ORF-less transcript in MEN1 regi
250	TACAGTATTTT	0,21	2	9,52	1,33	Hs.82921	solute carrier family 35 (CMP-sialic acid trans- porte
251	TGCCAGGTGCA	0,21	2	9,52	1,33	Hs.75442	albumin
252	TTTTTTATTCC	0,21	2	9,52	1,33	Hs.327	interleukin 10 receptor, alpha
253	AATATTTTAT	0,21	2	9,52	1,33	Hs.31386	ESTs, Highly similar to JE0174 frizzled protein-2 -
254	GAGAACCACCT	0,21	2	9,52	1,33	Hs.30250	v-maf musculoaponeu- rotic fibrosarcoma (avian) oncogene
255	GACACACCGAA	0,21	2	9,52	1,33	Hs.274243	receptor tyrosine kinase- like orphan receptor 1
256	GGCTTGTCTAT	0,21	2	9,52	1,33	Hs.23294	ESTs, Weakly similar to weak similarity to HSP90 [C.
257	GGCAATATAGT	0,21	2	9,52	1,33	Hs.194429	ESTs, Weakly similar to unknown protein [H.sapiens]
258	AGGATAACTTC	0,21	2	9,52	1,33	Hs.184482	DKFZP586D0624 pro- tein
259	GATCAATCAGT	0,21	2	9,52	1,33	Hs.16530	small inducible cytokine subfamily A (Cys-Cys), memb
260	TTGAATATTAA	0,21	2	9,52	1,33	Hs.161554	hypothetical protein FLJ20159
261	TCCTCACTTCA	0,21	2	9,52	1,33	Hs.158455	ESTs
262	GTTGCAGCATT	0,21	2	9,52	1,33	Hs.147189	HYA22 protein
263	GTGTCTGTCTC	0,21	2	9,52	1,33	Hs.137432	ESTs
264	GGCCTCTCCGA	0,21	2	9,52	1,33	Hs.132834	hematopoietic protein 1
265	ACAGAATGCCT	1,79	17	9,50	9,96	Hs.79732	fibulin 1
266	GGGGCTGCCCA	1,58	15	9,49	8,82	Hs.195727	tumor endothelial marker 1 precursor
267	AAAATCGCTTG	0,53	5	9,43	3,14	Hs.226581	COX15 (yeast) homolog, cytochrome c oxidase assembly
268	GTATAAACGTC	0,32	3	9,38	1,93	Hs.237356	stromal cell-derived factor 1
269	CACTTTACCAG	0,32	3	9,38	1,93	Hs.170019	runt-related transcription factor 3

270	TTAATTACAGT	0,32	3	9,38	1,93	Hs.159640	serum/glucocorticoid regulated kinase
271	TCAGCGACCCT	0,44	4	9,09	2,49	Hs.169946	GATA-binding protein 3
272	ATGGCACATTC	0,44	4	9,09	2,49	Hs.14328	Homo sapiens mRNA; cDNA DKFZp762O124 (from clone
273	AGGCTCAGGTC	0	9	9,00	13,62	Hs.78344	myosin, heavy polypeptide 11, smooth muscle
274	AACAGGGGCCA	0,56	5	8,93	3,05	Hs.262958	ESTs, Weakly similar to alternatively spliced product
275	CTGAAATCTAT	0,56	5	8,93	3,05	Hs.253467	ESTs
276	GAGAAATCCCG	0,56	5	8,93	3,05	Hs.150298	ESTs
277	TCAAAGACCT	1,38	12	8,70	6,8	Hs.25647	v-fos FBJ murine osteosarcoma viral oncogene homolog
278	GAAAACAAACA	0,23	2	8,70	1,25	Hs.83004	interleukin 14
279	TGCATCTGTAC	0,23	2	8,70	1,25	Hs.58589	glycogenin 2
280	ATGAAACTCCA	0,23	2	8,70	1,25	Hs.277951	EST
281	TTTATTCCTCT	0,23	2	8,70	1,25	Hs.26290	ESTs
282	GGGAGACCTGT	0,23	2	8,70	1,25	Hs.256115	EST, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J
283	CACTATGTAAA	0,23	2	8,70	1,25	Hs.24143	Wiskott-Aldrich syndrome protein interacting protein
284	TACAGCGGCAG	0,23	2	8,70	1,25	Hs.205616	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY
285	AGTGCCTTGGG	0,23	2	8,70	1,25	Hs.178604	ESTs
286	CGATGCTGACG	0,23	2	8,70	1,25	Hs.161554	hypothetical protein FLJ20159
287	GTGGTGTAATC	0,35	3	8,57	1,84	Hs.261734	ESTs, Moderately similar to ALU7_HUMAN ALU
288	TATCCCAGAAT	0,35	3	8,57	1,84	Hs.175819	EST
289	TCTAAAAGGC	0,35	3	8,57	1,84	Hs.16622	zinc finger protein 185 (LIM domain)
290	TCGAAACGCTG	0,35	3	8,57	1,84	Hs.136528	ESTs, Moderately similar to ALU1_HUMAN ALU
291	ACATTCTTTT	2,58	22	8,53	11,94	Hs.82226	glycoprotein (transmembrane) nmb
292	CTGTTTGTTCA	0,94	8	8,51	4,59	Hs.211582	myosin, light polypeptide kinase
293	CAGTACTGTAT	0,47	4	8,51	2,41	Hs.9295	elastin (supravalvular aortic stenosis, Williams-Beu
294	GGTGAAACCCC	0,47	4	8,51	2,41	Hs.284878	EST
295	GCCAAACCCCA	0,47	4	8,51	2,41	Hs.194264	ESTs
296	GCCGACGCCAG	0,47	4	8,51	2,41	Hs.165565	ESTs
297	GAAGAGGACAA	0,59	5	8,47	2,97	Hs.120451	ESTs
298	TAAATAAGAAA	0,12	1	8,33	0,61	Hs.99875	zona pellucida binding

							protein
299	AAAGATCCCTC	0,12	1	8,33	0,61	Hs.94998	ESTs
300	ATCAAAGGTTA	0,12	1	8,33	0,61	Hs.94795	Homo sapiens mRNA; cDNA DKFZp564O222 (from clone
301	GCAAGGTTGGT	0,12	1	8,33	0,61	Hs.94761	ESTs, Weakly similar to KIAA0561 protein [H.sapiens]
302	GGGACAAAAAA	0,12	1	8,33	0,61	Hs.93788	ESTs
303	ACTACCTCTGA	0,12	1	8,33	0,61	Hs.92254	hypothetical protein FLJ20163
304	GCTGGGCCCAG	0,12	1	8,33	0,61	Hs.90964	Homo sapiens cDNA FLJ20812 fis, clone ADSE01316
305	CAAAGAAATAG	0,12	1	8,33	0,61	Hs.88653	ESTs
306	AATACAAGTAT	0,12	1	8,33	0,61	Hs.8707	KIAA1301 protein
307	CTCTGTGGCTC	0,12	1	8,33	0,61	Hs.85112	insulin-like growth factor 1 (somatomedia C)
308	TATTTGAAAGT	0,12	1	8,33	0,61	Hs.82664	ETAA16 protein
309	CCCGCCTCCGT	0,12	1	8,33	0,61	Hs.82071	Cbp/p300-interacting transactivator, with Glu/Asp-ri
310	TCACCGTAGCC	0,12	1	8,33	0,61	Hs.82042	solute carrier family 23 (nucleobase transport- ers),
311	CCAAAAATTAA	0,12	1	8,33	0,61	Hs.81424	ubiquitin-like 1 (sentrin)
312	ACTCGTATATG	0,12	1	8,33	0,61	Hs.81134	interleukin 1 receptor antagonist
313	TCAAGATGAAG	0,12	1	8,33	0,61	Hs.78948	Rab geranylgeranyltransferas
314	CGTCTATCCAT	0,12	1	8,33	0,61	Hs.76084	Arbit 2 subunit
315	AAAGTGAAATG	0,12	1	8,33	0,61	Hs.75912	KIAA0257 protein
316	TTCTGGTGCTG	0,12	1	8,33	0,61	Hs.75725	transgelin 2
317	CTGGCGTCGTC	0,12	1	8,33	0,61	Hs.75640	natriuretic peptide pre- cursor A
318	GGCTGGGGAGG	0,12	1	8,33	0,61	Hs.75061	MARCKS-like protein
319	TGCCCCCAAAA	0,12	1	8,33	0,61	Hs.74649	cytochrome c oxidase subunit VIc
320	TTTATTGAACA	0,12	1	8,33	0,61	Hs.74649	cytochrome c oxidase subunit VIc
321	CTTTCCTCATT	0,12	1	8,33	0,61	Hs.7381	voltage-dependent anion channel 3
322	TTGGACTGAGG	0,12	1	8,33	0,61	Hs.6518	ganglioside expression factor 2
323	AGCATTA AAAA	0,12	1	8,33	0,61	Hs.61638	myosin X
324	CTGCTTTAAAA	0,12	1	8,33	0,61	Hs.56023	brain-derived neurotro- phic factor
325	TGCTTAAAAAT	0,12	1	8,33	0,61	Hs.5534	ESTs
326	ATGAACCCCT	0,12	1	8,33	0,61	Hs.5011	RNA binding motif pro- tein 9
327	TGAAACTTCCC	0,12	1	8,33	0,61	Hs.4994	transducer of ERBB2, 2

328	CAAACAAAAA	0,12	1	8,33	0,61	Hs.43728	hypothetical protein
329	GAGGTAAC TAC	0,12	1	8,33	0,61	Hs.43712	ESTs
330	CATTAAAAAAT	0,12	1	8,33	0,61	Hs.36908	activating transcription factor 1
331	CAATGGTGAAA	0,12	1	8,33	0,61	Hs.35093	lymphoid blast crisis oncogene
332	CTAATGAATGT	0,12	1	8,33	0,61	Hs.29809	Homo sapiens mRNA; cDNA DKFZp434C185 (from clone
333	AGGGCTTTCAC	0,12	1	8,33	0,61	Hs.29797	ribosomal protein L10
334	TAACCGTGGA	0,12	1	8,33	0,61	Hs.29647	uncharacterized hematopoietic stem/progenitor cells
335	TCTCCACACC	0,12	1	8,33	0,61	Hs.2961	S100 calcium-binding protein A3
336	CCTGGATCTCC	0,12	1	8,33	0,61	Hs.28501	ESTs
337	GGCCTGGCACT	0,12	1	8,33	0,61	Hs.283388	ESTs
338	ACTTTGTTTT	0,12	1	8,33	0,61	Hs.28219	protein phosphatase 2 (formerly 2A), regulatory subu
339	GTGACGCCTGT	0,12	1	8,33	0,61	Hs.279361	EST
340	CCATAAGTCCT	0,12	1	8,33	0,61	Hs.279009	seven in absentia (Drosophila) homolog 1
341	AGCCCCCGCGC	0,12	1	8,33	0,61	Hs.272320	Homo sapiens mRNA; cDNA DKFZp434L1226 (from clone
342	TATCATCATTC	0,12	1	8,33	0,61	Hs.270877	ESTs
343	TTCCCTGAGCA	0,12	1	8,33	0,61	Hs.26198	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY
344	TAGTCTAAGGC	0,12	1	8,33	0,61	Hs.261782	ESTs
345	ATAGTAGTAAT	0,12	1	8,33	0,61	Hs.258863	EST
346	GATTTTAAATG	0,12	1	8,33	0,61	Hs.25333	interleukin 1 receptor, type II
347	CCTGGCTAACA	0,12	1	8,33	0,61	Hs.252124	ESTs
348	CTGTACAGACC	0,12	1	8,33	0,61	Hs.251653	tubulin, beta, 2
349	GGCACCAGAGC	0,12	1	8,33	0,61	Hs.249614	EST
350	GCGAACTCCGT	0,12	1	8,33	0,61	Hs.248844	ESTs
351	CGCGTCCGTGT	0,12	1	8,33	0,61	Hs.243929	ESTs
352	GTTTTGGTTTA	0,12	1	8,33	0,61	Hs.241336	Homo sapiens mRNA; cDNA DKFZp564G0422 (from clone
353	CTTTTTGCCAC	0,12	1	8,33	0,61	Hs.240165	ESTs
354	GTGGGGGGCGC	0,12	1	8,33	0,61	Hs.240031	EST, Weakly similar to ALU2_HUMAN ALU SUBFAMILY S
355	TCTTTCCA ACT	0,12	1	8,33	0,61	Hs.22394	hypothetical protein FLJ10893
356	TAGTAGGGCTC	0,12	1	8,33	0,61	Hs.21914	ESTs
357	AGGACATAACA	0,12	1	8,33	0,61	Hs.213793	ESTs
358	TTGTTTTAAGA	0,12	1	8,33	0,61	Hs.211519	hypothetical protein

							LOC56757	
359	GTGGCACATCT	0,12	1	8,33	0,61	Hs.208925	ESTs, Weakly similar to alternatively spliced produc	5
360	CACATTGAGGC	0,12	1	8,33	0,61	Hs.207122	EST	
361	AGGCTAGCACT	0,12	1	8,33	0,61	Hs.206259	Homo sapiens mRNA for KIAA1190 protein, partial cds	10
362	CCCCTGCCCTC	0,12	1	8,33	0,61	Hs.203317	EST	
363	TTGTCTCTTGA	0,12	1	8,33	0,61	Hs.20104	ESTs	
364	TGGGTACACTG	0,12	1	8,33	0,61	Hs.200030	ESTs, Weakly similar to ALUB_HUMAN !!!! ALU CLASS B	15
365	GGCAGTGGTAA	0,12	1	8,33	0,61	Hs.197075	ESTs	
366	CATAAATGTTA	0,12	1	8,33	0,61	Hs.19479	ESTs	20
367	AGATTACCCAC	0,12	1	8,33	0,61	Hs.192155	ESTs	
368	ACTGGCTCAGG	0,12	1	8,33	0,61	Hs.190719	ESTs	
369	CTTGTAAGTCTC	0,12	1	8,33	0,61	Hs.189073	ESTs	
370	AGCCCAGCTGG	0,12	1	8,33	0,61	Hs.18857	ESTs	25
371	GAGGGCAATCT	0,12	1	8,33	0,61	Hs.186753	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY	
372	CTGAAACAGGA	0,12	1	8,33	0,61	Hs.183601	regulator of G-protein signalling 16	30
373	GCCCTACCTGC	0,12	1	8,33	0,61	Hs.182740	ribosomal protein S11	
374	GCCAACGGCGT	0,12	1	8,33	0,61	Hs.181002	MLL septin-like fusion (NOTE: non-standard symbol an	35
375	GTAAAGATGAA	0,12	1	8,33	0,61	Hs.175941	B-cell receptor-associated protein BAP29	40
376	GGGGTAATTTT	0,12	1	8,33	0,61	Hs.173497	Sec23 (S. cerevisiae) homolog B	
377	AGGACAATGAA	0,12	1	8,33	0,61	Hs.173135	dual-specificity tyrosine-(Y)-phosphorylation regula	45
378	TTTGCACTTTT	0,12	1	8,33	0,61	Hs.167114	ESTs, Highly similar to AF070470_1 SPARC-related pro	50
379	CTGAAGTGCAG	0,12	1	8,33	0,61	Hs.166609	ESTs	
380	CCCATTCAAGTC	0,12	1	8,33	0,61	Hs.161554	hypothetical protein FLJ20159	
381	TAATGTTCTCA	0,12	1	8,33	0,61	Hs.160271	G protein-coupled receptor 48	55
382	GTTTCTGCAGA	0,12	1	8,33	0,61	Hs.159642	glucosaminyl (N-acetyl) transferase 1, core 2 (beta-	60
383	GCAGATTCTCA	0,12	1	8,33	0,61	Hs.157716	ESTs	
384	GGAATGAGGGG	0,12	1	8,33	0,61	Hs.156452	ESTs	
385	GAGAGGAAGTA	0,12	1	8,33	0,61	Hs.153523	ESTs	
386	TTCGACAGGCT	0,12	1	8,33	0,61	Hs.152925	KIAA1268 protein	65

387	CTCCAGCCTGG	0,12	1	8,33	0,61	Hs.145331	ESTs, Weakly similar to ALUF_HUMAN !!!! ALU CLASS F
388	AGTCTGTATTT	0,12	1	8,33	0,61	Hs.144906	ESTs
389	GAGTATTATTT	0,12	1	8,33	0,61	Hs.143738	ESTs, Weakly similar to EPS8_HUMAN EPI- DERMAL
390	TACTGTACTCC	0,12	1	8,33	0,61	Hs.143198	hypothetical protein similar to tumor suppres- sor p33
391	AAAATAAAATG	0,12	1	8,33	0,61	Hs.142908	E2F-like protein
392	CCCAGGAGTTT	0,12	1	8,33	0,61	Hs.13785	ESTs
393	AAAATACAGTG	0,12	1	8,33	0,61	Hs.136433	ESTs
394	CATTTGGCCGG	0,12	1	8,33	0,61	Hs.136031	ESTs
395	CAGGACCTGAA	0,12	1	8,33	0,61	Hs.135971	ESTs
396	TCATTAACAAA	0,12	1	8,33	0,61	Hs.135260	ESTs
397	CAGTAGGATAA	0,12	1	8,33	0,61	Hs.134541	ESTs
398	GCCTCACCTGG	0,12	1	8,33	0,61	Hs.128514	ESTs
399	TCTGTATCAA	0,12	1	8,33	0,61	Hs.128408	ESTs, Moderately similar to ALU1_HUMAN ALU
400	TGATTTGTGAA	0,12	1	8,33	0,61	Hs.12282	ESTs
401	AGGATATTGGA	0,12	1	8,33	0,61	Hs.117721	ESTs
402	GTGGTACACAG	0,12	1	8,33	0,61	Hs.117582	CGI-43 protein
403	TTGGCCAGATT	0,12	1	8,33	0,61	Hs.117582	CGI-43 protein
404	ATTCTTGTACA	0,12	1	8,33	0,61	Hs.117527	ESTs
405	CCTTCTTGGGG	0,12	1	8,33	0,61	Hs.117474	ESTs
406	TACTGGAAGGC	0,12	1	8,33	0,61	Hs.116874	ESTs, Weakly similar to putative p150 [H.sapiens]
407	GTGGTGGTTGG	0,12	1	8,33	0,61	Hs.114408	toll-like receptor 5
408	AGTAATGAAAA	0,12	1	8,33	0,61	Hs.11217	KIAA0877 protein
409	TTAGTTTTGCT	0,12	1	8,33	0,61	Hs.108885	collagen, type VI, alpha 1
410	GCTAATATATT	0,12	1	8,33	0,61	Hs.107883	ESTs
411	TCTTGACTCCC	0,12	1	8,33	0,61	Hs.107265	ESTs
412	TGTACTTAATT	0,12	1	8,33	0,61	Hs.107082	ESTs, Moderately similar to alternatively spliced pr
413	CTCAGCAGGAG	0,12	1	8,33	0,61	Hs.105489	ESTs, Weakly similar to AF109127_1 stromal cell-deri
414	GGTACAATCCG	0,12	1	8,33	0,61	Hs.104557	hypothetical protein FLJ10697
415	ACTCCAGACCT	0,12	1	8,33	0,61	Hs.104350	ESTs
416	GAGAACTCCG	1,08	9	8,33	5,04	Hs.184367	GTPase activating pro- tein-like
417	CCCAGAGACCC	2,31	19	8,23	10,13	Hs.21223	calponin 1, basic, smooth muscle
418	GCAAGAAAGTG	2,84	23	8,10	12,05	Hs.155376	hemoglobin, beta
419	AAACAATAAAA	0	8	8,00	12,08	Hs.229971	EST
420	CGTGGGACACT	0	8	8,00	12,08	Hs.110196	NICE-1 protein
421	CTGTTCTCTTG	0,5	4	8,00	2,33	Hs.46824	ESTs

422	TAGTTGAAAA	4,16	33	7,93	16,82	Hs.1119	nuclear receptor subfamily 4, group A, member 1	
423	GTGAAAGCCTG	0,76	6	7,89	3,35	Hs.258926	EST	5
424	TTGGTTTGCTG	0,38	3	7,89	1,76	Hs.284326	Human clone 23960 mRNA sequence	
425	CCTGTAATTCA	0,38	3	7,89	1,76	Hs.277331	EST, Weakly similar to ALU5_HUMAN ALU SUBFAMILY	10
426	AAACCCCGTCT	0,38	3	7,89	1,76	Hs.273464	ESTs, Weakly similar to ALU2_HUMAN ALU SUBFAMILY	
427	ATCGCACTACT	0,38	3	7,89	1,76	Hs.161721	ESTs	15
428	TTGAGGGGGTG	2,17	17	7,83	8,86	Hs.76549	(Manual assignment) MEMOREC unassignable (probably r	
429	TTTGGTTTTCC	14,74	115	7,80	56,2	Hs.179573	collagen, type I, alpha 2	20
430	ACAAAACCCCG	0,91	7	7,69	3,82	Hs.259505	EST	
431	GTGCTCAATAG	0,26	2	7,69	1,18	Hs.8687	ESTs	
432	CAACCAGTAAA	0,26	2	7,69	1,18	Hs.79914	lumican	25
433	AGTTTATGCCC	0,26	2	7,69	1,18	Hs.76591	KIAA0887 protein	
434	TTCACATTGTC	0,26	2	7,69	1,18	Hs.285804	ESTs	
435	CCTGGCCTAGA	0,26	2	7,69	1,18	Hs.285472	ESTs	
436	AAACTGGGAGG	0,26	2	7,69	1,18	Hs.231722	ESTs	30
437	GCCCGCCTTCT	0,26	2	7,69	1,18	Hs.201292	ESTs	
438	TGCAGGTTTGT	0,26	2	7,69	1,18	Hs.183800	Ran GTPase activating protein 1	
439	CTCAACTTGTA	0,26	2	7,69	1,18	Hs.117582	CGI-43 protein	35
440	TTTGCTTTTGT	1,32	10	7,58	5,27	Hs.234642	aquaporin 3	
441	TAAATGAAAAA	0,41	3	7,32	1,69	Hs.82120	nuclear receptor subfamily 4, group A, member 2	
442	GCCCCCTTCCT	0,41	3	7,32	1,69	Hs.212680	tumor necrosis factor receptor superfamily, member 1	40
443	CCTGTAATTGC	0,41	3	7,32	1,69	Hs.181464	ESTs	
444	TCACCCTCCAG	0,41	3	7,32	1,69	Hs.15251	hypothetical protein	45
445	AAGCTCTGTGT	0,7	5	7,14	2,67	Hs.19813	ESTs	
446	ATGGTGGGCGC	0,56	4	7,14	2,19	Hs.266417	EST	
447	CCTGTAGTTCT	0,56	4	7,14	2,19	Hs.231918	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY	50
448	CATCTGTAATC	0,56	4	7,14	2,19	Hs.153290	ESTs, Weakly similar to prostate-specific transgluta	
449	TCTATAATCCC	0,85	6	7,06	3,14	Hs.96866	ESTs	55
450	ATGGCACGTGC	1	7	7,00	3,61	Hs.179999	stromal cell protein	
451	CTGGTGCACTG	0,29	2	6,90	1,11	Hs.96752	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY	60
452	ATAAAAAGAAA	0,29	2	6,90	1,11	Hs.83942	cathepsin K (pseudosynthesis)	
453	CACTTGTAGTC	0,29	2	6,90	1,11	Hs.7845	Homo sapiens cDNA	

							FLJ20820 fis, clone ADSE00490
5	454	ATTTGGAGAGG	0,29	2	6,90	1,11	Hs.55777 Fukuyama type congeni- tal muscular dystrophy
	455	CAGCAGCTTGT	0,29	2	6,90	1,11	Hs.55405 ESTs, Weakly similar to Rab7 [H.sapiens]
10	456	GTATTTTCATA	0,29	2	6,90	1,11	Hs.42140 hypothetical protein FLJ10103
	457	CTTGTTGCAAT	0,29	2	6,90	1,11	Hs.29640 suppression of tumori- genicity 15 (reversion- inducing
15	458	CAGGGTGGGTG	0,29	2	6,90	1,11	Hs.278222 ESTs, Highly similar to endothelial nitric oxide syn
	459	AGCCACTACGC	0,29	2	6,90	1,11	Hs.249956 EST
20	460	TGGCATAATCA	0,29	2	6,90	1,11	Hs.237063 ESTs
	461	CCTTCCTCTCC	0,29	2	6,90	1,11	Hs.199752 ESTs
	462	CCCTGAATGAA	0,29	2	6,90	1,11	Hs.19545 frizzled (Drosophila) homolog 4
25	463	GATTAGCACCA	0,29	2	6,90	1,11	Hs.180946 ribosomal protein L5
	464	GCCGTGAAAAA	0,29	2	6,90	1,11	Hs.164257 ESTs
	465	AGAAAGAAGGA	0,29	2	6,90	1,11	Hs.1501 syndecan 2 (heparan sulfate proteoglycan 1, cell sur
30	466	GCTTCCTCCTC	0,73	5	6,85	2,6	Hs.85289 CD34 antigen
	467	TTTCTTCCCTT	0,73	5	6,85	2,6	Hs.283009 tuftelin 1
35	468	TGCCTGTAGTC	16,23	111	6,84	49,37	Hs.285275 ESTs, Moderately similar to ALU7 HUMAN ALU
	469	CCCTCAATCCC	0,88	6	6,82	3,07	Hs.83077 interleukin 18 (interferon- gamma-inducing factor)
40	470	ACAACTTTTAT	0,88	6	6,82	3,07	Hs.283213 EST
	471	GCAAACCTAAA	0,44	3	6,82	1,62	Hs.80686 prefoldin 5
	472	GAGTGCAACCC	0,44	3	6,82	1,62	Hs.54680 ESTs
	473	TTGAATAGTGA	0,59	4	6,78	2,12	Hs.38516 ESTs
45	474	AGCCGGATGCT	0,59	4	6,78	2,12	Hs.284232 KIAA0720 protein
	475	GCAAAACACTG	0,59	4	6,78	2,12	Hs.198552 Homo sapiens mRNA; cDNA DKFZp566B193 (from clone
50	476	CATTTGGGAAG	0,59	4	6,78	2,12	Hs.111334 ferritin, light polypeptide
	477	CAAGAGATGCT	0,15	1	6,67	0,54	Hs.99741 ESTs, Weakly similar to cell division control relate
55	478	AGTTTATTTCA	0,15	1	6,67	0,54	Hs.99016 Human DNA sequence from clone 310J6 on chromosome
	479	GAGGATCTGCG	0,15	1	6,67	0,54	Hs.90998 KIAA0128 protein; septin 2
60	480	ACTCTGGCTCA	0,15	1	6,67	0,54	Hs.88974 cytochrome b-245, beta polypeptide (chronic granulom
	481	GGGGTTAGGGG	0,15	1	6,67	0,54	Hs.85050 phospholamban
65	482	TAATATATCTG	0,15	1	6,67	0,54	Hs.8203 endomembrane protein



							emp70 precursor isolog
483	TAAGTCTATAT	0,15	1	6,67	0,54	Hs.78864	Fc fragment of IgG, low affinity IIa, receptor for (
484	CACAAAAGGAT	0,15	1	6,67	0,54	Hs.77603	ESTs
485	GAGAAACCCTT	0,15	1	6,67	0,54	Hs.7739	ESTs
486	GAAAACAGTAA	0,15	1	6,67	0,54	Hs.76111	dystroglycan 1 (dystrophin-associated glycoprotein 1
487	GGCAATTTACT	0,15	1	6,67	0,54	Hs.75813	polycystic kidney disease 1 (autosomal dominant)
488	TTTTGTGCTAG	0,15	1	6,67	0,54	Hs.74649	cytochrome c oxidase subunit VIc
489	TTCCCGTGGCT	0,15	1	6,67	0,54	Hs.70983	PTPL1-associated RhoGAP 1
490	GGCCCAGGCCT	0,15	1	6,67	0,54	Hs.575	aldehyde dehydrogenase 3
491	CGGCCACGTAT	0,15	1	6,67	0,54	Hs.55993	ESTs
492	TATAGCTGCAT	0,15	1	6,67	0,54	Hs.55964	ESTs, Weakly similar to C4HU complement C4A precursor
493	CTTGTGTTTAT	0,15	1	6,67	0,54	Hs.50748	chromosome 21 open reading frame 18
494	CACAAAAATGC	0,15	1	6,67	0,54	Hs.49944	ESTs
495	CTGTAATTTTA	0,15	1	6,67	0,54	Hs.48480	ESTs
496	CAATTCTTTCT	0,15	1	6,67	0,54	Hs.48403	hypothetical protein FLJ10847
497	ATTCTGCAGAG	0,15	1	6,67	0,54	Hs.47232	ESTs
498	TTTATATCATT	0,15	1	6,67	0,54	Hs.47099	ESTs
499	ACTCCATAAAA	0,15	1	6,67	0,54	Hs.4273	Human DNA sequence from clone RP1-104A17 on
500	TTTTCATTATA	0,15	1	6,67	0,54	Hs.42656	ESTs, Moderately similar to ALU1_HUMAN ALU
501	GACTCGACCAG	0,15	1	6,67	0,54	Hs.31922	ESTs
502	GGTGTGTTTTA	0,15	1	6,67	0,54	Hs.31566	ESTs
503	ATAAATTTATG	0,15	1	6,67	0,54	Hs.30715	ESTs
504	GGAGGCCGAGA	0,15	1	6,67	0,54	Hs.285565	ESTs
505	ATATTCAGCTG	0,15	1	6,67	0,54	Hs.285379	ESTs
506	GAACTTGTCTG	0,15	1	6,67	0,54	Hs.279934	Homo sapiens mRNA; cDNA DKFZp43410835 (from clone
507	CCCGTATATGT	0,15	1	6,67	0,54	Hs.279844	hypothetical protein FLJ10033
508	GTGGACCTGAG	0,15	1	6,67	0,54	Hs.279059	ESTs
509	AGCCTGGAAGG	0,15	1	6,67	0,54	Hs.278549	ESTs
510	TGGTTTTTGAG	0,15	1	6,67	0,54	Hs.275865	ribosomal protein S18
511	GCTTGTTCAAA	0,15	1	6,67	0,54	Hs.274969	ESTs
512	TCCACCAGCCA	0,15	1	6,67	0,54	Hs.27457	ESTs
513	GCACTCCAACC	0,15	1	6,67	0,54	Hs.273682	EST
514	CCCATAATCCT	0,15	1	6,67	0,54	Hs.270797	ESTs

515	AGTCACAGCTT	0,15	1	6,67	0,54	Hs.267448	hypothetical protein FLJ20039
516	TAGAAAAAACC	0,15	1	6,67	0,54	Hs.262476	S-adenosylmethionine decarboxylase 1
517	TAAAGATGGCA	0,15	1	6,67	0,54	Hs.25357	Homo sapiens clone 24488 mRNA sequence
518	GGCTATGCCCT	0,15	1	6,67	0,54	Hs.243855	ESTs
519	AGACATTGACA	0,15	1	6,67	0,54	Hs.239934	CGI-96 protein
520	TATGCTTTAAA	0,15	1	6,67	0,54	Hs.237225	ribosomal protein S5 pseudogene 1
521	TATTGCTAAAT	0,15	1	6,67	0,54	Hs.23590	solute carrier family 16 (monocarboxylic acid transp
522	CCAAGGCACTG	0,15	1	6,67	0,54	Hs.234863	ESTs
523	AACTTTCCAAA	0,15	1	6,67	0,54	Hs.23457	ESTs
524	TCTCACAAGGG	0,15	1	6,67	0,54	Hs.233476	ESTs
525	CCACTATGCCT	0,15	1	6,67	0,54	Hs.231229	ESTs
526	GGGCGCCTGGC	0,15	1	6,67	0,54	Hs.224242	EST
527	GGGGGGAAAAA	0,15	1	6,67	0,54	Hs.223590	EST, weakly similar to RL3_HUMAN 60S RI- BOSOMAL
528	TTGTTTATGTA	0,15	1	6,67	0,54	Hs.21958	Homo sapiens cDNA FLJ10532 fis, clone NT2RP2001044
529	TTGAGATAAGA	0,15	1	6,67	0,54	Hs.21887	ESTs
530	GCTATATCCAA	0,15	1	6,67	0,54	Hs.218008	ESTs
531	TTTGGTTTTCT	0,15	1	6,67	0,54	Hs.21431	suppressor of fused
532	GATTGTCCTTG	0,15	1	6,67	0,54	Hs.211517	ESTs
533	GGTTATCAAAG	0,15	1	6,67	0,54	Hs.208334	ESTs
534	GTCTCGCTGAC	0,15	1	6,67	0,54	Hs.207911	ESTs
535	AGCCATCGCGC	0,15	1	6,67	0,54	Hs.207749	EST
536	ACCACCCGTGT	0,15	1	6,67	0,54	Hs.202033	EST
537	ACACTCTTCCT	0,15	1	6,67	0,54	Hs.20103	ESTs
538	GGAGATGTTTG	0,15	1	6,67	0,54	Hs.199545	ESTs
539	CTCAACCTTAA	0,15	1	6,67	0,54	Hs.199243	KIAA0231 protein
540	GCAAGACTCCC	0,15	1	6,67	0,54	Hs.198011	ESTs
541	CAATACTATTC	0,15	1	6,67	0,54	Hs.197642	hypothetical protein FLJ10388
542	GTTGTGCTCAG	0,15	1	6,67	0,54	Hs.191228	hypothetical protein FLJ20284
543	GGGCTAGCACT	0,15	1	6,67	0,54	Hs.190722	ESTs
544	ACATTCACGCC	0,15	1	6,67	0,54	Hs.184141	glutaryl-Coenzyme A dehydrogenase
545	TATATTTAGTT	0,15	1	6,67	0,54	Hs.183037	protein kinase, cAMP- dependent, regulatory, type I,
546	CCAGCTAGCGA	0,15	1	6,67	0,54	Hs.179756	LW-1
547	TGAGGATACAG	0,15	1	6,67	0,54	Hs.177820	Homo sapiens mRNA; cDNA DKFZp564L102 (from clone
548	TGCCTACAGTC	0,15	1	6,67	0,54	Hs.176207	EST

549	CTCATATGCAA	0,15	1	6,67	0,54	Hs.173540	ATPase, Class V, type 10D
550	AAGGAGGTGGA	0,15	1	6,67	0,54	Hs.172730	ESTs
551	CAAGCCCTGCC	0,15	1	6,67	0,54	Hs.172035	hypothetical protein similar to mouse HN1 (Hematolo
552	GCGCTGGGAGG	0,15	1	6,67	0,54	Hs.171763	CD22 antigen
553	TCCTTGGCGTG	0,15	1	6,67	0,54	Hs.168640	Ank, mouse, homolog of
554	TTGCCATATGC	0,15	1	6,67	0,54	Hs.164024	ESTs, Weakly similar to unnamed protein product [H.s
555	GCTCCCTTCAC	0,15	1	6,67	0,54	Hs.162222	EST
556	CTGTGCAAGGA	0,15	1	6,67	0,54	Hs.161554	hypothetical protein FLJ20159
557	TGTGCTTGTGT	0,15	1	6,67	0,54	Hs.161554	hypothetical protein FLJ20159
558	CTTTTTCCCCC	0,15	1	6,67	0,54	Hs.156007	Down syndrome critical region gene 1-like 1
559	TCTTTTCTTT	0,15	1	6,67	0,54	Hs.155606	paired mesoderm homeo box 1
560	AAAAGCTGTTT	0,15	1	6,67	0,54	Hs.15550	ESTs
561	GTCCCCCCCCC	0,15	1	6,67	0,54	Hs.152454	ESTs
562	CCTGGCGGGAT	0,15	1	6,67	0,54	Hs.149347	ESTs, Highly similar to KIAA1043 protein [H.sapiens]
563	GATTGGTATGA	0,15	1	6,67	0,54	Hs.147049	cut (Drosophila)-like 1 (CCAAT displacement protein)
564	GTGAAGACTAC	0,15	1	6,67	0,54	Hs.14665	ESTs
565	TAAATGGGTTG	0,15	1	6,67	0,54	Hs.1395	early growth response 2 (Krox-20 (Drosophila) homolo
566	TGTAAACTTTG	0,15	1	6,67	0,54	Hs.13849	ESTs
567	GACACGTTGCC	0,15	1	6,67	0,54	Hs.136574	arachidonate 12-lipoxygenase, 12R type
568	TGTGAATTTTA	0,15	1	6,67	0,54	Hs.132834	hematopoietic protein 1
569	TAAACACTTG	0,15	1	6,67	0,54	Hs.130636	ESTs
570	TGGCAATTTTC	0,15	1	6,67	0,54	Hs.129636	ESTs
571	TCTGTAGCACA	0,15	1	6,67	0,54	Hs.128766	hypothetical protein FLJ10600
572	TCAGCAGTTAA	0,15	1	6,67	0,54	Hs.128571	ESTs
573	AATGAGGTGCT	0,15	1	6,67	0,54	Hs.128400	ESTs
574	TTCAGAATCTT	0,15	1	6,67	0,54	Hs.125914	ESTs
575	GAATAAGATAT	0,15	1	6,67	0,54	Hs.12479	associated molecule with the SH3 domain of STAM
576	TGTCCCAGCCA	0,15	1	6,67	0,54	Hs.1211	acid phosphatase 5, tartrate resistant
577	CCCATCTCAGA	0,15	1	6,67	0,54	Hs.120769	Homo sapiens cDNA FLJ20463 fis, clone KAT06143

578	AGAAGCTCCAG	0,15	1	6,67	0,54	Hs.120021	DKFZP434I092 protein
579	AGTCTTCAAAA	0,15	1	6,67	0,54	Hs.117582	CGI-43 protein
580	GAGTTTTTCATT	0,15	1	6,67	0,54	Hs.117582	CGI-43 protein
581	TTTTGCAATAA	0,15	1	6,67	0,54	Hs.11614	ESTs
582	AGCTCTATGAG	0,15	1	6,67	0,54	Hs.115831	ESTs
583	AATAGGTCCCA	0,15	1	6,67	0,54	Hs.113029	ribosomal protein S25
584	TAGTCTACTGT	0,15	1	6,67	0,54	Hs.112472	ESTs
585	ATCCTTACATC	0,15	1	6,67	0,54	Hs.111720	ESTs
586	AACTTTCATAT	0,15	1	6,67	0,54	Hs.108787	phosphatidylinositol glycan, class N
587	CCGTAAAAAAA	0,15	1	6,67	0,54	Hs.107187	divalent cation tolerant protein CUTA
588	TGAAGATGTAA	0,15	1	6,67	0,54	Hs.106217	ESTs
589	GAACCATTTGC	0,15	1	6,67	0,54	Hs.104305	KIAA0926 protein
590	CTGTGGAGCTG	0,15	1	6,67	0,54	Hs.103379	ESTs
591	AGAATTACAGA	0,15	1	6,67	0,54	Hs.101915	ESTs
592	TGTTGCTCCCA	0,76	5	6,58	2,54	Hs.82210	zinc finger protein 220
593	TAGTTTGAAGG	0,76	5	6,58	2,54	Hs.79033	glutamyl-peptide cyclo- transferase (glutamyl cycl
594	CCCAACGCGCT	7,18	47	6,55	20,67	Hs.272572	hemoglobin, alpha 2
595	CCTATAATCTC	1,99	13	6,53	6,08	Hs.117582	CGI-43 protein
596	TCTCCTGGACT	0,62	4	6,45	2,06	Hs.50915	kallikrein 5
597	ATCTTGCCACT	0,62	4	6,45	2,06	Hs.32945	glutamate receptor, metabotropic 1
598	AGGATAAAAAA	0,47	3	6,38	1,56	Hs.79404	neuron-specific protein
599	GACCACAAATA	0,47	3	6,38	1,56	Hs.76476	cathepsin H
600	AGCATATCTTC	0,47	3	6,38	1,56	Hs.275865	ribosomal protein S18
601	AACACAGGAGG	0,47	3	6,38	1,56	Hs.222874	ESTs, Moderately similar to zinc transporter 4 [H.sa
602	CGGGGACGAGG	0,47	3	6,38	1,56	Hs.124942	protein phosphatase 2A 48 kDa regulatory sub- unit
603	GCGAAGCCCCG	1,11	7	6,31	3,35	Hs.103804	heterogeneous nuclear ribonucleoprotein U (scaffold
604	GTGGCAGGTAC	1,44	9	6,25	4,21	Hs.190467	EST
605	TCTGTTGTTCA	1,44	9	6,25	4,21	Hs.117582	CGI-43 protein
606	CCTGTATCCCA	0,64	4	6,25	2	Hs.270072	ESTs
607	ATGGATGCTTG	0,32	2	6,25	1,05	Hs.89404	msh (Drosophila) homeo box homolog 2
608	GACTTCTGTCC	0,32	2	6,25	1,05	Hs.87539	aldehyde dehydro- genase 8
609	AAAAAGAACT	0,32	2	6,25	1,05	Hs.73287	KIAA1235 protein
610	TACTGAAAAAA	0,32	2	6,25	1,05	Hs.5111	hypothetical protein FLJ20729
611	CACCTGGAGGC	0,32	2	6,25	1,05	Hs.30864	ESTs
612	GCAAGAGCCCA	0,32	2	6,25	1,05	Hs.26670	Human PAC clone RP3- 515N1 from 22q11.2-q22

613	AACCCGGGGAG	0,32	2	6,25	1,05	Hs.228009	EST	
614	TTGCCCAGGGT	0,32	2	6,25	1,05	Hs.225093	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY	5
615	AAGCAGTTACA	0,32	2	6,25	1,05	Hs.22116	CDC14 (cell division cycle 14, <i>S. cerevisiae</i> ) homolo	10
616	GCAGTCATACA	0,32	2	6,25	1,05	Hs.182626	chromosome 22 open reading frame 5	
617	GGGGCACACAC	0,32	2	6,25	1,05	Hs.181900	ESTs	
618	AGGGAAGGTGA	0,32	2	6,25	1,05	Hs.126927	ESTs	
619	AGCCGCTGTGC	0,32	2	6,25	1,05	Hs.106771	ESTs	15
620	TCAAGCCATCA	5,68	35	6,16	14,85	Hs.738	early growth response 1	
621	GTGGCGGGCAT	0,82	5	6,10	2,42	Hs.230564	EST	
622	ACCTGGGTGCT	0,82	5	6,10	2,42	Hs.159643	ESTs, Weakly similar to MLD [ <i>H.sapiens</i> ]	20
623	TGTGGCGTATA	1,32	8	6,06	3,69	Hs.211582	myosin, light polypeptide kinase	
624	CGGGCACCTTC	0	6	6,00	8,99	Hs.198249	gap junction protein, beta 5 (connexin 31.1)	25
625	CCCTTGAGGAG	0	6	6,00	8,99	Hs.1076	(Manual assignment) SPRR1B, cornifin B	
626	AATGTTTTTAA	0,5	3	6,00	1,5	Hs.75335	glycine amidinotrans- ferase (L- arginine:glycine amidi	30
627	CCTCTCCCAT	0,5	3	6,00	1,5	Hs.177533	Homo sapiens mRNA; chromosome 1 specific transcript	35
628	TGTTCTGATTT	0,5	3	6,00	1,5	Hs.167835	acyl-Coenzyme A oxi- dase 1, palmitoyl	
629	CCTGTAGTGCC	0,85	5	5,88	2,36	Hs.269645	Homo sapiens cell-line E8CASS clone E24L estradiol-i	40
630	CCACTGTATTC	1,03	6	5,83	2,77	Hs.235041	EST	
631	AGAAATGTATG	1,03	6	5,83	2,77	Hs.232068	transcription factor 8 (represses interleukin 2 expr	45
632	AGGTCAGAAGA	1,73	10	5,78	4,38	Hs.23437	Homo sapiens mRNA; cDNA DKFZp586G0623 (from clone	50
633	ATTAAGAAAAT	2,43	14	5,76	5,95	Hs.76549	AHNAK nucleoprotein (desmoyokin)	
634	AACCCGGGGGG	1,05	6	5,71	2,72	Hs.6214	KIAA0731 protein	
635	CACCACAACAA	1,05	6	5,71	2,72	Hs.174139	chloride channel 3	55
636	TTCCCCAGGGT	0,35	2	5,71	0,99	Hs.59545	ring finger protein 15	
637	CACACTATAGG	0,35	2	5,71	0,99	Hs.58924	ESTs, Weakly similar to JC5594 jerky gene protein ho	60
638	GGGAAAGAGGG	0,35	2	5,71	0,99	Hs.35096	KIAA1538 protein	
639	GCTGGGCGCGG	0,35	2	5,71	0,99	Hs.278070	EST	
640	GGGGCAACAGC	0,35	2	5,71	0,99	Hs.276770	CDW52 antigen (CAM-	65

							PATH-1 antigen)
641	GTGGCAGGCC	0,35	2	5,71	0,99	Hs.266105	EST
642	CATATCCCCTC	0,35	2	5,71	0,99	Hs.250746	ESTs
643	CTTAGGAGTCA	0,35	2	5,71	0,99	Hs.23853	ESTs
644	CAGCACAGTGG	0,35	2	5,71	0,99	Hs.227806	ras GTPase activating protein-like
645	ATGCTCAAAGG	0,35	2	5,71	0,99	Hs.226018	Homo sapiens mRNA full length insert cDNA clone EURO
646	TTCTGTGCATA	0,35	2	5,71	0,99	Hs.16803	hypothetical protein FLJ10231
647	GCATAATGTTT	0,35	2	5,71	0,99	Hs.11050	F-box only protein 9
648	TGGCCAGCTCC	3,34	19	5,69	7,83	Hs.170121	protein tyrosine phosphatase, receptor type, C
649	TCTGGCCCCAGC	0,53	3	5,66	1,45	Hs.183	Duffy blood group
650	ATCCTGAGTTA	2,14	12	5,61	5,06	Hs.73931	major histocompatibility complex, class II, DQ beta
651	ACAAATGAAAA	0,18	1	5,56	0,49	Hs.96657	hypothetical protein
652	TACATTTCAAG	0,18	1	5,56	0,49	Hs.94376	proprotein convertase subtilisin/kexin type 5
653	GCAAAATGCTG	0,18	1	5,56	0,49	Hs.92254	hypothetical protein FLJ20163
654	TTTAAGAAATG	0,18	1	5,56	0,49	Hs.91139	ESTs
655	ACCCACCTGTG	0,18	1	5,56	0,49	Hs.8736	Homo sapiens mRNA; cDNA DKFZp564H203 (from clone
656	GCAGCAGTGTC	0,18	1	5,56	0,49	Hs.86538	ESTs
657	CCATTAATAAA	0,18	1	5,56	0,49	Hs.85885	ESTs
658	AAAGAGGGACG	0,18	1	5,56	0,49	Hs.84229	splicing factor, arginine/serine-rich 8 (suppressor-
659	ACACTTAATAAA	0,18	1	5,56	0,49	Hs.83381	guanine nucleotide binding protein 11
660	TCACAAAAAAA	0,18	1	5,56	0,49	Hs.7976	KIAA0332 protein
661	ATTTAATATAT	0,18	1	5,56	0,49	Hs.7972	KIAA0871 protein
662	AGTTCAAGGCT	0,18	1	5,56	0,49	Hs.79058	suppressor of Ty (S.cerevisiae) 4 homolog 1
663	GAGTTGCTATT	0,18	1	5,56	0,49	Hs.78575	prosaposin (variant Gaucher disease and variant meta
664	GACTGTCAAAA	0,18	1	5,56	0,49	Hs.69330	ESTs
665	GCGCAACAAC	0,18	1	5,56	0,49	Hs.61950	DKFZp434A0131 protein
666	TAAATCAGAGA	0,18	1	5,56	0,49	Hs.61929	Homo sapiens cDNA FLJ11010 fis, clone PLACE1003145
667	TAAATGAATGA	0,18	1	5,56	0,49	Hs.57967	ESTs
668	AATAGGAAGAT	0,18	1	5,56	0,49	Hs.50745	ESTs
669	CAATTAAAAAT	0,18	1	5,56	0,49	Hs.50123	zinc finger protein 189

670	GTGTATGTGGT	0,18	1	5,56	0,49	Hs.49881	fatty acid binding protein 3, muscle and heart (mamm
671	ACAAACCCACA	0,18	1	5,56	0,49	Hs.49282	hypothetical protein FLJ11088
672	CAAGTGAAAGG	0,18	1	5,56	0,49	Hs.47822	KIAA0380 gene product; RhoA-specific guanine nucleot
673	GAACAGAACGC	0,18	1	5,56	0,49	Hs.47566	ESTs
674	CTAATGGCCCT	0,18	1	5,56	0,49	Hs.3416	adipose differentiation-related protein
675	TAATGTTTTT	0,18	1	5,56	0,49	Hs.31930	ESTs
676	ATTTGGCCTGT	0,18	1	5,56	0,49	Hs.285519	Homo sapiens OVN6-2 mRNA, partial cds
677	TCTGGGAGGGG	0,18	1	5,56	0,49	Hs.285313	core promoter element binding protein
678	GACTAAATTGT	0,18	1	5,56	0,49	Hs.283643	ESTs
679	TATTTTCACAA	0,18	1	5,56	0,49	Hs.279896	hypothetical protein FLJ20546
680	GAGGTTTTCTG	0,18	1	5,56	0,49	Hs.279639	Homo sapiens mRNA; cDNA DKFZp586M2022 (from clone
681	CCTAGAATCCC	0,18	1	5,56	0,49	Hs.278982	PRO1779 protein
682	CAGCCCCTGTC	0,18	1	5,56	0,49	Hs.278234	Homo sapiens mRNA; cDNA DKFZp434H1323 (from clone
683	GTGTCGGGCTC	0,18	1	5,56	0,49	Hs.278010	EST
684	CACCTGTAAAC	0,18	1	5,56	0,49	Hs.277311	EST
685	GCGGCGACTGC	0,18	1	5,56	0,49	Hs.271980	mitogen-activated protein kinase 6
686	GGAATGAATGA	0,18	1	5,56	0,49	Hs.270824	ESTs
687	TGGGATATAGT	0,18	1	5,56	0,49	Hs.269888	ESTs
688	GTGGTTGATGC	0,18	1	5,56	0,49	Hs.267083	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY
689	GTGGTAGGTAC	0,18	1	5,56	0,49	Hs.264844	EST, Moderately similar to ALU1_HUMAN ALU
690	GCCTGCCTTTA	0,18	1	5,56	0,49	Hs.25371	ESTs, Weakly similar to A37232 mucin, tracheal [H.sa
691	GATCTCGCTTT	0,18	1	5,56	0,49	Hs.250773	signal sequence receptor, alpha (translocon-associat
692	CTCCTATTTTT	0,18	1	5,56	0,49	Hs.25010	hypothetical protein P15-2
693	GTGCGCACCTG	0,18	1	5,56	0,49	Hs.243957	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY
694	ATAAAATGTCT	0,18	1	5,56	0,49	Hs.24181	ESTs
695	TTTCACCCCGT	0,18	1	5,56	0,49	Hs.23492	ESTs
696	TATGTTTAAAA	0,18	1	5,56	0,49	Hs.234392	platelet-activating factor

							acetylhydrolase 2 (40kD)
5	697	GATCACTTGAG	0,18	1	5,56	0,49	Hs.231798 EST
	698	TTGAGAAAAA	0,18	1	5,56	0,49	Hs.22971 ESTs
	699	ACCCTGGGAGG	0,18	1	5,56	0,49	Hs.228529 ESTs
	700	TGTGGTGGTGC	0,18	1	5,56	0,49	Hs.223618 EST
10	701	GATTGGCCAGA	0,18	1	5,56	0,49	Hs.21739 Homo sapiens mRNA; cDNA DKFZp586l1518 (from clone)
	702	GCTGAGTTATT	0,18	1	5,56	0,49	Hs.216363 ESTs
15	703	AGTATTCCTAA	0,18	1	5,56	0,49	Hs.21621 hypothetical protein DKFZp762O076
	704	TGTCTGCCATT	0,18	1	5,56	0,49	Hs.21580 ESTs
	705	CCCCTGTACTC	0,18	1	5,56	0,49	Hs.213016 ESTs, Highly similar to cytokine receptor related pr
20	706	CTTTTAAAGA	0,18	1	5,56	0,49	Hs.212788 EST
	707	TACCCGAAAAC	0,18	1	5,56	0,49	Hs.210858 ESTs, Weakly similar to ALUD_HUMAN !!!! ALU CLASS D
25	708	TGCCTCTAGTC	0,18	1	5,56	0,49	Hs.209413 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY
	709	CCGCCGCACTC	0,18	1	5,56	0,49	Hs.204049 ESTs
30	710	CTAAGAGGGGT	0,18	1	5,56	0,49	Hs.196102 ESTs
	711	CTGCTGTAGTC	0,18	1	5,56	0,49	Hs.194319 ESTs
	712	GGACCCTCATT	0,18	1	5,56	0,49	Hs.191063 ESTs
35	713	AACTAATTCTC	0,18	1	5,56	0,49	Hs.189513 hypothetical protein FLJ10213
	714	GCAGTGCCAAG	0,18	1	5,56	0,49	Hs.183528 ESTs, Weakly similar to Bem46-like protein [D.melano]
40	715	ATTGGAGCGCA	0,18	1	5,56	0,49	Hs.180433 rTS beta protein
	716	TGAAAACCTCCC	0,18	1	5,56	0,49	Hs.180248 zinc finger protein 124 (HZF-16)
45	717	CTCCCAGCCAC	0,18	1	5,56	0,49	Hs.177582 surfactant, pulmonary- associated protein A1
	718	GTTTTAAAAA	0,18	1	5,56	0,49	Hs.174756 EST
	719	GAATCAAGCTG	0,18	1	5,56	0,49	Hs.17296 ESTs
50	720	CTGGGCATTTT	0,18	1	5,56	0,49	Hs.172207 non-POU-domain- containing, octamer- binding
	721	TTGTTTGTGTA	0,18	1	5,56	0,49	Hs.170162 KIAA1357 protein
	722	AGGACTGGCAT	0,18	1	5,56	0,49	Hs.170114 KIAA0061 protein
55	723	TCGCTTTTAAG	0,18	1	5,56	0,49	Hs.168640 Ank, mouse, homolog of
	724	AAGTGAAAAA	0,18	1	5,56	0,49	Hs.168159 apoptosis regulator
	725	CAAATTAGAAT	0,18	1	5,56	0,49	Hs.162271 ESTs, Moderately similar to CO3_HUMAN COM- PLEMENT
60	726	ATACCACTAAG	0,18	1	5,56	0,49	Hs.153792 5-methyltetrahydrofolate- homocysteine methyl- transfer



727	GGTGATGGAGG	0,18	1	5,56	0,49	Hs.149692	ESTs, Highly similar to G43284 zinc finger protein Z	
728	TTGGGTTTCTG	0,18	1	5,56	0,49	Hs.147975	ESTs	5
729	AATAAATGCCC	0,18	1	5,56	0,49	Hs.145522	ESTs	
730	CATACACACAT	0,18	1	5,56	0,49	Hs.143460	protein kinase C, nu	
731	GTTATACAACA	0,18	1	5,56	0,49	Hs.141183	ESTs	10
732	CTCACAGGCAC	0,18	1	5,56	0,49	Hs.139784	ESTs	
733	TACCCATTACC	0,18	1	5,56	0,49	Hs.136981	ESTs	
734	TTTCTTTCCCT	0,18	1	5,56	0,49	Hs.135055	ESTs	
735	CATCTGTA CTG	0,18	1	5,56	0,49	Hs.132892	Homo sapiens protocadherin 10 (PCDH10) mRNA, partial	15
736	GAGCTGTTTTG	0,18	1	5,56	0,49	Hs.127476	ESTs	
737	ACACGTACTAT	0,18	1	5,56	0,49	Hs.120828	Human DNA sequence from clone RP5-876B10 on	20
738	TTTATATTTCA	0,18	1	5,56	0,49	Hs.11958	oxidative 3 alpha hydroxysteroid dehydrogenase; reti	25
739	CACAGTTTTTAA	0,18	1	5,56	0,49	Hs.118918	ESTs	
740	TGGTTTTACCA	0,18	1	5,56	0,49	Hs.117582	CGI-43 protein	
741	GTGCCTGGTAT	0,18	1	5,56	0,49	Hs.116459	hypothetical protein PRO2198	30
742	TACCTTAGAAC	0,18	1	5,56	0,49	Hs.114963	Homo Sapiens (clone B3B3E13) chromosome 4p16.3 DNA	
743	GTGTAGGAGGT	0,18	1	5,56	0,49	Hs.113029	ribosomal protein S25	35
744	CCCTGGAGACA	0,18	1	5,56	0,49	Hs.111334	ferritin, light polypeptide	
745	CCTGTAGCCCA	0,18	1	5,56	0,49	Hs.109370	ESTs	
746	TATCCATATTA	0,18	1	5,56	0,49	Hs.107942	DKFZP564M112 protein	40
747	CTACTAATTGC	0,18	1	5,56	0,49	Hs.101916	Homo sapiens mRNA; cDNA DKFZp564K133 (from clone	
748	GGCCTCCAAGA	0,91	5	5,49	2,25	Hs.286220	ESTs	45
749	GTGGCTGACAC	0,73	4	5,48	1,83	Hs.202234	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAMILY	
750	CTGTACTTGTG	1,49	8	5,37	3,37	Hs.75678	FBJ murine osteosarcoma viral oncogene homolog B	50
751	ACAAAACCCCA	1,49	8	5,37	3,37	Hs.140208	ESTs	
752	AGCCACCACCC	0,56	3	5,36	1,4	Hs.232045	ESTs, Moderately similar to ALU1_HUMAN ALU	55
753	TGCCTGTAGTT	1,32	7	5,30	2,97	Hs.246646	EST	
754	GCTAACCCTG	2,84	15	5,28	5,92	Hs.279772	brain specific protein	
755	GCAAAACCTG	16,29	86	5,28	31,14	Hs.117582	CGI-43 protein	
756	AAACATTAAAA	3,98	21	5,28	8,08	Hs.77443	actin, gamma 2, smooth muscle, enteric	60
757	GTGGCACTTGC	0,76	4	5,26	1,78	Hs.272322	Homo sapiens mRNA; cDNA DKFZp434L092	65

							(from clone
5	758	GAAGCTACACC	0,76	4	5,26	1,78	Hs.107253 ESTs
	759	TAAGGTAGAGG	0,38	2	5,26	0,94	Hs.99908 nuclear receptor coactivator 4
	760	TGGGTCATTTG	0,38	2	5,26	0,94	Hs.98073 ESTs
	761	GCTCACTGAAG	0,38	2	5,26	0,94	Hs.9568 zinc finger protein 261
10	762	CACCTATCAAT	0,38	2	5,26	0,94	Hs.58617 Rho-associated, coiled-coil containing protein kinase
	763	CTTCAATCTTA	0,38	2	5,26	0,94	Hs.58419 DKFZP586L2024 protein
15	764	CAGTCCTCTTG	0,38	2	5,26	0,94	Hs.57553 tousel-like kinase 2
	765	TTACCAAAGCA	0,38	2	5,26	0,94	Hs.30246 solute carrier family 19 (thiamine transporter), mem
	766	ATGAAACCCTA	0,38	2	5,26	0,94	Hs.282671 EST
20	767	TCACTCCAGCC	0,38	2	5,26	0,94	Hs.270497 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY
	768	AAAGGCATCAG	0,38	2	5,26	0,94	Hs.256297 integrin, alpha 11
25	769	GACATCTGTCC	0,38	2	5,26	0,94	Hs.25566 ESTs
	770	TGTCCTTTCTG	0,38	2	5,26	0,94	Hs.250882 bradykinin receptor B2
	771	TGACTGTATTA	0,38	2	5,26	0,94	Hs.198241 amine oxidase, copper containing 3 (vascular adhesio
30							
	772	GCAAGACCTCA	0,38	2	5,26	0,94	Hs.181592 ESTs
	773	AGGAAGGAAAA	0,38	2	5,26	0,94	Hs.180532 heat shock 90kD protein 1, alpha
35							
	774	CTGCCGGAGCA	0,38	2	5,26	0,94	Hs.164779 ESTs
	775	TATTCCAGAAC	0,38	2	5,26	0,94	Hs.161554 hypothetical protein FLJ20159
	776	AGCGAAACTCC	0,38	2	5,26	0,94	Hs.106597 ESTs
40	777	CTGGGGGTCAG	0,38	2	5,26	0,94	Hs.102664 vesicle-associated membrane protein 4
	778	GCTGTAATCCC	2,9	15	5,17	5,82	Hs.184019 Homo sapiens clone 23551 mRNA sequence
45							
	779	CACCTGTGGTC	3,14	16	5,10	6,11	Hs.209585 EST
	780	CTCTAGAGAAA	0,59	3	5,08	1,35	Hs.97925 hypothetical protein
	781	GCAAATCCTGT	0,59	3	5,08	1,35	Hs.79059 transforming growth factor, beta receptor III (betag
50							
	782	TATATGCTGGG	0,59	3	5,08	1,35	Hs.2969 v-ski avian sarcoma viral oncogene homolog
	783	GGGAGACCCCA	0,59	3	5,08	1,35	Hs.24884 ESTs, Moderately similar to RNA polymerase I associa
55							
	784	TGGAAATGAAA	0,59	3	5,08	1,35	Hs.172928 collagen, type I, alpha 1
	785	CCTGTAATCTG	0,59	3	5,08	1,35	Hs.159975 ESTs
60	786	TGTATTGTACA	0,59	3	5,08	1,35	Hs.118562 Link guanine nucleotide exchange factor II
	787	ACATAGACCGA	1,38	7	5,07	2,87	Hs.173594 pigment epithelium-derived factor

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788	GTTCCACAGAA	2,37	12	5,06	4,66	Hs.179573	collagen, type I, alpha 2
789	GTGGCAGAGAC	0,79	4	5,06	1,74	Hs.75813	polycystic kidney disease 1 (autosomal dominant)
790	AGCCGAGATCG	0,79	4	5,06	1,74	Hs.278053	EST
791	CCTGTAGTTCC	4,75	24	5,05	8,84	Hs.189242	Homo sapiens mRNA; cDNA DKFZp434A202 (from clone
792	GTAAAACCCCTG	5,77	29	5,03	10,5	Hs.281680	peroxisomal trans 2-enoyl CoA reductase; putative sh
793	AGTCTGCTGGG	0	5	5,00	7,44	Hs.259508	ESTs
794	CTGGGCAGAGA	0	5	5,00	7,44	Hs.200735	ESTs, Moderately similar to AF105377_1 heparan sulfa
795	TCACACAAAGG	1	5	5,00	2,11	Hs.46783	ESTs
796	CGCCTGTAATT	1	5	5,00	2,11	Hs.14333	ESTs

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Tabelle 1

Nr.	Tag_Sequence	CGAP	Rel. Expr. Haut	Quotient	signific.	UniGene Acc.-Nr.	Beschreibung
798	ATTGCTCTCTG	1,61	8	4,97	3,18	Hs.245188	tissue inhibitor of metalloproteinase 3 (Sorsby fund
799	CCTGTGGTTCC	2,02	10	4,95	3,88	Hs.286061	ESTs
800	TGTCCACACAT	0,82	4	4,88	1,69	Hs.5897	Homo sapiens mRNA; cDNA DKFZp586P1622 (from clo
801	GACGGAGCCTT	0,82	4	4,88	1,69	Hs.37482	COPZ2 for nonclathrin coat protein zeta-COP
802	ACTGGGCAGTG	0,82	4	4,88	1,69	Hs.241257	latent transforming growth factor beta binding prote
803	CGGCACCTTAA	0,82	4	4,88	1,69	Hs.209100	DKFZP434C171 protein
804	CTGAAACAGCT	0,82	4	4,88	1,69	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like 1
805	TGTTACCTGGT	0,41	2	4,88	0,9	Hs.79227	myomesin (M-protein) 2 (165kD)
806	TCTTTGCTCTT	0,41	2	4,88	0,9	Hs.44077	hypothetical protein FLJ10793
807	AAATCACCAAT	0,41	2	4,88	0,9	Hs.4082	lectin, galactoside-binding, soluble, 8 (galectin 8)
808	TGTATTGACTG	0,41	2	4,88	0,9	Hs.29280	ESTs
809	TTCACCTCAAC	0,41	2	4,88	0,9	Hs.250911	Homo sapiens clone 23967 unknown mRNA, partial cds
810	CGTGGGGCTGC	0,41	2	4,88	0,9	Hs.221986	aquaporin 5
811	TCACAGAGTCT	0,41	2	4,88	0,9	Hs.194149	Homo sapiens mRNA; cDNA DKFZp434M011 (from
812	TGCCACTGTGC	0,41	2	4,88	0,9	Hs.183165	ESTs, Highly similar to protein kinase [H.sapiens]
813	CTATAAAAGTG	0,41	2	4,88	0,9	Hs.154145	guanine nucleotide binding protein (G protein), alph
814	TTGGCTAGGCT	2,67	13	4,87	4,86	Hs.252259	ribosomal protein S3
815	AGGGAGCAGAG	2,26	11	4,87	4,17	Hs.118223	microfibrillar-associated protein 4
816	TTGGTGTGCTG	1,44	7	4,86	2,78	Hs.240399	EST
817	TGGAAAGTGAA	10,31	50	4,85	17,06	Hs.25647	v-fos FBJ murine osteosarcoma viral oncogene homolog
818	TTGATTGAGTG	0,62	3	4,84	1,31	Hs.9879	ESTs
819	CAGGGATCTGC	0,62	3	4,84	1,31	Hs.7634	ESTs, Moderately similar to semaphorin B (M.musculus
820	ATTGCACCACC	0,62	3	4,84	1,31	Hs.44259	ESTs, Weakly similar to ALU1_HUMAN ALU
821	CTGGTGGCCAC	0,62	3	4,84	1,31	Hs.286028	Human alpha-2 collagen

							type VI mRNA, 3' end	
822	AATCATTGAGG	0,62	3	4,84	1,31	Hs.19150	Homo sapiens mRNA; cDNA DKFZp564A2164 (from	5
823	ACCCCCTTCCT	0,62	3	4,84	1,31	Hs.181392	major histocompatibility complex, class I, E	
824	CCTGGCCAAAA	0,62	3	4,84	1,31	Hs.126824	EST	
825	TTAACCCTCC	6,21	30	4,83	10,46	Hs.78224	ribonuclease, RNase A family, 1 (pancreatic)	10
826	ACAGGCTACGG	24,47	118	4,82	39	Hs.75777	transgelin	
827	AGATGAGATGA	3,57	17	4,76	6,08	Hs.285313	core promoter element binding protein	15
828	AAAAAAAAGGC	0,21	1	4,76	0,44	Hs.90077	TG-interacting factor (TALE family homeobox)	
829	TACGCTAAAC	0,21	1	4,76	0,44	Hs.87354	ESTs	
830	GTAGAAGTGTA	0,21	1	4,76	0,44	Hs.8705	ESTs	20
831	TGCCAGCAAT	0,21	1	4,76	0,44	Hs.76297	G protein-coupled receptor kinase 6	
832	AGCAGGTTTGC	0,21	1	4,76	0,44	Hs.7434	ESTs	
833	AGAGAGAGCCC	0,21	1	4,76	0,44	Hs.724	thyroid hormone receptor, alpha (avian erythroblasti	25
834	GCACTGATTAA	0,21	1	4,76	0,44	Hs.71741	ESTs, Highly similar to I38945 melanoma ubiqui- tous m	30
835	CAGAGACAAGC	0,21	1	4,76	0,44	Hs.71721	ESTs	
836	CAGTTGTCTAG	0,21	1	4,76	0,44	Hs.58882	Microfibril-associated glycoprotein-2	
837	TGTGTGTGCTA	0,21	1	4,76	0,44	Hs.55533	ESTs	35
838	GCCTGGACCAG	0,21	1	4,76	0,44	Hs.55407	Homo sapiens mRNA; cDNA DKFZp434K0621 (from	
839	TGTTTAATAAA	0,21	1	4,76	0,44	Hs.50841	ESTs	40
840	CATTTTCTAAT	0,21	1	4,76	0,44	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	
841	AGCTTTCCCAA	0,21	1	4,76	0,44	Hs.45109	ESTs	
842	ACTCAGTAGCC	0,21	1	4,76	0,44	Hs.44197	hypothetical protein DKFZp564D0462	45
843	TCAAATTGAAA	0,21	1	4,76	0,44	Hs.44038	pellino (Drosophila) ho- molog 2	
844	GGCCAGCCCTG	0,21	1	4,76	0,44	Hs.4243	ESTs	50
845	ACATTTTGTTT	0,21	1	4,76	0,44	Hs.42116	ESTs	
846	GGCAAGCAGGC	0,21	1	4,76	0,44	Hs.41688	dual specificity phos- phatase 8	
847	TGCTTGGTACA	0,21	1	4,76	0,44	Hs.393	prostaglandin I2 (prosta- cyclin) receptor (IP)	55
848	TAAGTCTAATT	0,21	1	4,76	0,44	Hs.35804	hect domain and RLD 3	
849	TATTTTACTTG	0,21	1	4,76	0,44	Hs.30340	hypothetical protein KIAA1165	
850	CTCTCTCCAG	0,21	1	4,76	0,44	Hs.30172	ESTs	60
851	AGCAAATTTTC	0,21	1	4,76	0,44	Hs.29423	ESTs, Weakly similar to macrophage lectin 2	

							[H.sapie
852	CCAAGACCTCT	0,21	1	4,76	0,44	Hs.283619	zinc finger protein 236
853	GACAGGTTCTG	0,21	1	4,76	0,44	Hs.272023	transforming, acidic coiled-coil containing protein
854	CTTCTGGAGAA	0,21	1	4,76	0,44	Hs.267263	hypothetical protein
855	TGGGTTTTGTT	0,21	1	4,76	0,44	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PLACE1007402
856	CACCGCTGCAG	0,21	1	4,76	0,44	Hs.261373	adenosine A2b receptor pseudogene
857	GAAACAGGAAA	0,21	1	4,76	0,44	Hs.257387	EST
858	CCTTCTTGCTA	0,21	1	4,76	0,44	Hs.24743	hypothetical protein FLJ20171
859	ATAATCTGAAG	0,21	1	4,76	0,44	Hs.2441	KIAA0022 gene product
860	CTAAATATAGG	0,21	1	4,76	0,44	Hs.23581	leptin receptor gene-related protein
861	AATGCTATGGT	0,21	1	4,76	0,44	Hs.23450	ESTs
862	GTGAATGAAAC	0,21	1	4,76	0,44	Hs.223437	EST
863	TCCACAAAAAA	0,21	1	4,76	0,44	Hs.21035	KIAA1130 protein
864	AGAATTGCTTA	0,21	1	4,76	0,44	Hs.203188	EST
865	CCTCTAATTCC	0,21	1	4,76	0,44	Hs.192949	ESTs, Moderately similar to ALU1_HUMAN ALU
866	TTGGACAAGAA	0,21	1	4,76	0,44	Hs.189902	ESTs
867	GGCTGGGCGCG	0,21	1	4,76	0,44	Hs.188339	ESTs
868	CAACACAAAGC	0,21	1	4,76	0,44	Hs.185013	ESTs, Moderately similar to ALU7_HUMAN ALU
869	GGCCCGGCCTC	0,21	1	4,76	0,44	Hs.183994	protein phosphatase 1, catalytic subunit, alpha isoform
870	GCTAAAAAATT	0,21	1	4,76	0,44	Hs.183760	glucose regulated protein, 58kD
871	TTTTCTTGTT	0,21	1	4,76	0,44	Hs.182937	peptidylprolyl isomerase A (cyclophilin A)
872	GCCGCCTCTGT	0,21	1	4,76	0,44	Hs.180799	ESTs, Moderately similar to ALU5_HUMAN ALU
873	GGCTGGTTCCA	0,21	1	4,76	0,44	Hs.179943	ribosomal protein L11
874	AAGGAAATGAA	0,21	1	4,76	0,44	Hs.174131	ribosomal protein L6
875	AATAGATGATA	0,21	1	4,76	0,44	Hs.174104	ESTs
876	TATAAGTGGAC	0,21	1	4,76	0,44	Hs.17301	ESTs
877	GAAAACATAAT	0,21	1	4,76	0,44	Hs.169329	DKFZP564A043 protein
878	CTTTGTAAAAA	0,21	1	4,76	0,44	Hs.16578	ESTs
879	AGCTGTTTAAA	0,21	1	4,76	0,44	Hs.164480	ESTs
880	GGGGACAGAGC	0,21	1	4,76	0,44	Hs.161554	hypothetical protein FLJ20159
881	ATAAAGCCAAA	0,21	1	4,76	0,44	Hs.159471	ZAP3 protein
882	CCCCTGCATTC	0,21	1	4,76	0,44	Hs.158302	chromosome 1 open reading frame 1
883	GCTGAGAAGCA	0,21	1	4,76	0,44	Hs.155975	protein tyrosine phosphatase, receptor type, C-assoc
884	GAATACGTTGG	0,21	1	4,76	0,44	Hs.155596	BCL2/adenovirus E1B 19kD-interacting protein 2

885	ATTTCTAACAA	0,21	1	4,76	0,44	Hs.155049	hypothetical protein FLJ11282
886	AGATCTTCTTG	0,21	1	4,76	0,44	Hs.14894	trans-Golgi network protein (46, 48, 51kD isoforms)
887	AAAACTCTAC	0,21	1	4,76	0,44	Hs.146226	ESTs
888	AGGATAAACTC	0,21	1	4,76	0,44	Hs.14427	ESTs
889	CTTGTGAGGCC	0,21	1	4,76	0,44	Hs.142428	KIAA1161 protein
890	GTAACAGTAAT	0,21	1	4,76	0,44	Hs.137396	ESTs
891	TAAACGAAAAT	0,21	1	4,76	0,44	Hs.135465	ESTs
892	AGGGGAATGGG	0,21	1	4,76	0,44	Hs.134933	ESTs
893	GGCCGTGCTGC	0,21	1	4,76	0,44	Hs.131034	ESTs
894	GGAACCTATCC	0,21	1	4,76	0,44	Hs.128807	ESTs
895	CCAGTGCCCTC	0,21	1	4,76	0,44	Hs.128630	ESTs
896	ATTTTGCTTAA	0,21	1	4,76	0,44	Hs.126558	ESTs
897	AGCCAAGAGCC	0,21	1	4,76	0,44	Hs.125877	ESTs
898	GTAGACTGAAA	0,21	1	4,76	0,44	Hs.124165	ESTs
899	TGGTATGCACC	0,21	1	4,76	0,44	Hs.1191	KIAA0073 protein
900	TCTGTTTTGTG	0,21	1	4,76	0,44	Hs.118923	ESTs
901	CCAATCAATGG	0,21	1	4,76	0,44	Hs.116674	pre-mRNA splicing factor
902	TTCCCCAGGCT	0,21	1	4,76	0,44	Hs.116296	ESTs
903	CAACAGCCCCA	0,21	1	4,76	0,44	Hs.11455	ESTs
904	CTCCTGGAATA	0,21	1	4,76	0,44	Hs.11367	hypothetical protein RP1-317E23
905	TGGTGAAGAAC	0,21	1	4,76	0,44	Hs.113052	RNA cyclase homolog
906	CACACCGCCCG	0,21	1	4,76	0,44	Hs.112015	ESTs, Moderately similar to alpha tubulin [H.sapiens]
907	CCCCCCCCCCA	0,21	1	4,76	0,44	Hs.110953	Homo sapiens mRNA; cDNA DKFZp434A139 (from clone)
908	TTTTGTTGCTC	0,21	1	4,76	0,44	Hs.109641	ESTs
909	GTAAAACCCCG	5,48	26	4,74	9	Hs.258881	EST, Weakly similar to ALU8_HUMAN ALU SUB-FAMILY
910	TAATAAAGAAT	0,85	4	4,71	1,65	Hs.80342	keratin 15
911	AAAATAAACCT	0,85	4	4,71	1,65	Hs.74304	periplakin
912	GTGGTAGGTGC	0,85	4	4,71	1,65	Hs.254237	EST
913	GTGAAATTCCA	0,85	4	4,71	1,65	Hs.228168	ESTs, Weakly similar to ALU1_HUMAN ALU
914	CCTCTAGTCCC	0,85	4	4,71	1,65	Hs.145501	ESTs, Weakly similar to ALU1_HUMAN ALU
915	TGGAAATGACC	22,53	106	4,70	34,28	Hs.172928	collagen, type I, alpha 1
916	AACCCTGGAGG	1,49	7	4,70	2,69	Hs.283927	Homo sapiens cytomegalovirus partial fusion receptor
917	AGGATCACTTG	0,64	3	4,69	1,26	Hs.287355	ESTs
918	CCACTGCATTG	0,64	3	4,69	1,26	Hs.278551	ESTs, Weakly similar to ALU2_HUMAN ALU
919	AACTGGCTGCT	0,64	3	4,69	1,26	Hs.173381	dihydropyrimidinase-like 2
920	CCTGTAACCCC	5,98	28	4,68	9,54	Hs.176541	ESTs

5	921	GCACTCCAGCC	6,91	32	4,63	10,69	Hs.274580	Homo sapiens mRNA; cDNA DKFZp434P1019 (from
	922	GTGGTGAGCAC	1,08	5	4,63	1,97	Hs.27311	single-minded (Drosophila) homolog 2
10	923	ATGGCAGGTGC	3,46	16	4,62	5,61	Hs.236479	EST, Weakly similar to ALU7_HUMAN ALU SUB- FAMILY
	924	CCATTACACTC	1,73	8	4,62	3	Hs.8594	KIAA1191 protein
	925	GGTGACAGAGT	2,61	12	4,60	4,3	Hs.278314	hypothetical protein
15	926	GTGGTTTGCTG	1,96	9	4,59	3,31	Hs.157773	ESTs, Moderately similar to OPSB_HUMAN BLUE-
	927	TCTGCCTATGC	0,88	4	4,55	1,6	Hs.90291	laminin, beta 2 (laminin S)
	928	GCGAAAACCCC	0,88	4	4,55	1,6	Hs.272837	ESTs
20	929	TACCCCTTGAA	0,44	2	4,55	0,86	Hs.95834	ESTs
	930	TAAATGGAAGT	0,44	2	4,55	0,86	Hs.6942	ESTs
	931	TGTGTCTGGA	0,44	2	4,55	0,86	Hs.60548	hypothetical protein PRO1635
25	932	GCTTCAGTGGG	0,44	2	4,55	0,86	Hs.54828	ESTs
	933	CTTTACTGTGT	0,44	2	4,55	0,86	Hs.279853	HSPC018 protein
	934	CACTTTGTGTG	0,44	2	4,55	0,86	Hs.24752	spectrin SH3 domain binding protein 1
30	935	GGTGACAGAAC	0,44	2	4,55	0,86	Hs.234890	EST
	936	ACTAAGATTGA	0,44	2	4,55	0,86	Hs.227716	KIAA0934 protein
	937	CCAATGTTGTT	0,44	2	4,55	0,86	Hs.22209	ESTs
35	938	GTGGTGTGAGC	0,44	2	4,55	0,86	Hs.194637	Homo sapiens mRNA; cDNA DKFZp564D113 (from clone
	939	TGAAGAATGTG	0,44	2	4,55	0,86	Hs.112557	ESTs, Moderately similar to ZN85_HUMAN ZINC
40	940	GCCAGTGCCTG	0,44	2	4,55	0,86	Hs.106061	RD RNA-binding protein
	941	CCACTGCTCTC	2,64	12	4,55	4,26	Hs.23510	Kruppel-like factor 12
	942	CTATTGCACTC	1,32	6	4,55	2,29	Hs.160483	erythrocyte membrane protein band 7.2 (stomatin)
45	943	ATGTACCTGAT	1,55	7	4,52	2,61	Hs.29191	epithelial membrane pro- tein 2
	944	GTGGGGGGGAG	1,55	7	4,52	2,61	Hs.10700	hypothetical protein
	945	CACCTGTAGTC	8,23	37	4,50	11,92	Hs.267812	sorting nexin 4
50	946	TCTGCACACAC	0,67	3	4,48	1,22	Hs.78518	natriuretic peptide receptor B/guanylate cyclase B (
	947	GACAATTCTGT	0,67	3	4,48	1,22	Hs.186571	hypothetical protein FLJ10700
55	948	AGGGGAAGGTG	1,79	8	4,47	2,92	Hs.112540	EST
	949	CAAGACGGGGG	4,31	19	4,41	6,29	Hs.106185	ral guanine nucleotide dissociation stimulator
	950	TAATTTGCGTT	0,91	4	4,40	1,56	Hs.79368	epithelial membrane pro- tein 1
60	951	AGAATCGTTTG	0,91	4	4,40	1,56	Hs.136299	ESTs
	952	AACAGTCAAAA	3,87	17	4,39	5,66	Hs.26557	plakophilin 3
	953	GCAAACTCTG	2,29	10	4,37	3,49	Hs.278746	ESTs, Moderately similar to ALU8_HUMAN ALU



954	GCCAGCCAGTG	2,29	10	4,37	3,49	Hs.149098	smoothelin	
955	GCGAAATCCCA	1,38	6	4,35	2,21	Hs.268728	ESTs	
956	TCTGTGGTCCC	1,38	6	4,35	2,21	Hs.227894	ESTs, Weakly similar to ALU1_HUMAN ALU	5
957	CCTATAATTCC	1,38	6	4,35	2,21	Hs.135491	ESTs	
958	GCAATAAAATA	0,23	1	4,35	0,4	Hs.99621	ESTs	
959	TGGAATCCAGG	0,23	1	4,35	0,4	Hs.98135	ESTs	10
960	CTTTTGTGTCAGC	0,23	1	4,35	0,4	Hs.90858	Homo sapiens clone 25023 mRNA sequence	
961	TTATTGTATTG	0,23	1	4,35	0,4	Hs.89474	ADP-ribosylation factor 6	
962	ATGGAGGTATG	0,23	1	4,35	0,4	Hs.8944	procollagen C- endopeptidase enhancer 2	15
963	TCGTGTTTTCG	0,23	1	4,35	0,4	Hs.87595	translocase of inner mito- chondrial membrane 22 (yeas	
964	TTGTGGCCCCA	0,23	1	4,35	0,4	Hs.84630	ESTs	20
965	TTTGTTTGTIT	0,23	1	4,35	0,4	Hs.8355	ESTs	
966	GTCACGAACAT	0,23	1	4,35	0,4	Hs.82933	protein x 013	
967	GTTAAGGTAAA	0,23	1	4,35	0,4	Hs.79241	B-cell CLL/lymphoma 2	
968	AAGAAGAAAAG	0,23	1	4,35	0,4	Hs.78293	ESTs	25
969	TAGCCAGTTAA	0,23	1	4,35	0,4	Hs.74101	spleen tyrosine kinase	
970	CTGCCCGGGGC	0,23	1	4,35	0,4	Hs.74097	mercaptopyruvate sulfur- transferase	
971	AACGGTGTTTG	0,23	1	4,35	0,4	Hs.71371	ESTs	30
972	CATAAACGGGC	0,23	1	4,35	0,4	Hs.69954	laminin, gamma 3	
973	TCCTTAGATTA	0,23	1	4,35	0,4	Hs.69743	GM2 ganglioside activator protein	
974	CTGGCATAGAA	0,23	1	4,35	0,4	Hs.61272	ESTs	35
975	ACTGCCCTGA	0,23	1	4,35	0,4	Hs.59729	semaphorin sem2	
976	TCTGCTGCCTG	0,23	1	4,35	0,4	Hs.58006	ESTs	
977	GAAGATGAATA	0,23	1	4,35	0,4	Hs.54982	ESTs, Weakly similar to ALU4_HUMAN ALU	40
978	GACCAAAGAAG	0,23	1	4,35	0,4	Hs.48948	ESTs	
979	GAATGAATGCA	0,23	1	4,35	0,4	Hs.48604	DKFZP434B168 protein	
980	GCACAACTAAA	0,23	1	4,35	0,4	Hs.47587	ESTs	
981	GAATTTTACAC	0,23	1	4,35	0,4	Hs.47522	ESTs	45
982	AAGGGGCGGCG	0,23	1	4,35	0,4	Hs.456	leukotriene C4 synthase	
983	AGGGACTTTAT	0,23	1	4,35	0,4	Hs.43148	ESTs	
984	TATTCAGAACC	0,23	1	4,35	0,4	Hs.40289	ESTs	
985	ACAACCTGGAAT	0,23	1	4,35	0,4	Hs.37372	Homo sapiens DNA bind- ing peptide mRNA, partial cds	50
986	TAATAAAATGC	0,23	1	4,35	0,4	Hs.29008	ESTs	
987	TTATGCTTGTA	0,23	1	4,35	0,4	Hs.284153	Fanconi anemia, comple- mentation group A	55
988	TTTTGAAGATA	0,23	1	4,35	0,4	Hs.283322	hypothetical protein	
989	GCAATCAGAT	0,23	1	4,35	0,4	Hs.279477	ESTs	
990	GTAAAACCCCT	0,23	1	4,35	0,4	Hs.277896	EST	
991	GGCCAGGCGTG	0,23	1	4,35	0,4	Hs.276994	EST	60
992	AATGTTAGAGC	0,23	1	4,35	0,4	Hs.270331	ESTs	

993	TACCTATAGTC	0,23	1	4,35	0,4	Hs.269838	ESTs
994	TGTGAGAAAGT	0,23	1	4,35	0,4	Hs.241493	natural killer-tumor recognition sequence
995	AATTGTGCATT	0,23	1	4,35	0,4	Hs.240443	chondroitin 4-sulfotransferase
996	GTGGTGCGCAT	0,23	1	4,35	0,4	Hs.236505	EST, Weakly similar to ALU6_HUMAN ALU SUB-FAMILY
997	GTTTATAATTA	0,23	1	4,35	0,4	Hs.231966	ESTs
998	CTGGCACCCCTG	0,23	1	4,35	0,4	Hs.212716	EST
999	AAAAATGGTGG	0,23	1	4,35	0,4	Hs.204930	EST
1000	GAGCAGGCAAA	0,23	1	4,35	0,4	Hs.200333	apolipoprotein B48 receptor
1001	CCAAAAAAGTG	0,23	1	4,35	0,4	Hs.184242	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase)
1002	CCAGAGGAATG	0,23	1	4,35	0,4	Hs.180414	heat shock 70kd protein 10 (HSC71)
1003	CCACAAAAAAA	0,23	1	4,35	0,4	Hs.179091	EST
1004	GCTTACCTGCT	0,23	1	4,35	0,4	Hs.174031	cytochrome c oxidase subunit VIb
1005	TATTAGACACC	0,23	1	4,35	0,4	Hs.17258	ESTs
1006	GAATGTTGACA	0,23	1	4,35	0,4	Hs.16959	ESTs
1007	TGAGGGGTGGG	0,23	1	4,35	0,4	Hs.166293	EST
1008	TATATAAGTAC	0,23	1	4,35	0,4	Hs.166011	catenin (cadherin-associated protein), delta 1
1009	TAATAATACAA	0,23	1	4,35	0,4	Hs.16349	KIAA0431 protein
1010	TGGGAGGCTGA	0,23	1	4,35	0,4	Hs.161554	hypothetical protein FLJ20159
1011	AGCTCCTTAAG	0,23	1	4,35	0,4	Hs.159509	alpha-2-plasmin inhibitor
1012	CTTTTGTGGT	0,23	1	4,35	0,4	Hs.153106	Homo sapiens clone 23728 mRNA sequence
1013	CTGTTTTTGAA	0,23	1	4,35	0,4	Hs.152720	M-phase phosphoprotein 6
1014	GCAGACTATCC	0,23	1	4,35	0,4	Hs.151696	DKFZP727G051 protein
1015	GTTCCCTGGTG	0,23	1	4,35	0,4	Hs.146090	ESTs
1016	CCTACAGTCCC	0,23	1	4,35	0,4	Hs.144874	Homo sapiens mRNA; cDNA DKFZp761C0524 (from
1017	CAATCCTCCTG	0,23	1	4,35	0,4	Hs.138407	ESTs
1018	AACAAGTAATA	0,23	1	4,35	0,4	Hs.134350	ESTs
1019	TCCAGTACAGA	0,23	1	4,35	0,4	Hs.12969	hypothetical protein
1020	GGAGGCTGGGG	0,23	1	4,35	0,4	Hs.127452	ESTs
1021	ACTCTGCTCGG	0,23	1	4,35	0,4	Hs.126900	ESTs
1022	TTCTGTGAGTG	0,23	1	4,35	0,4	Hs.122559	ESTs
1023	TCCTGTGATTT	0,23	1	4,35	0,4	Hs.12253	ESTs
1024	AAAGCACAAGT	0,23	1	4,35	0,4	Hs.111758	keratin 6B
1025	TTTTTGAAAAA	0,23	1	4,35	0,4	Hs.109646	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6
1026	AAGTCCTGGCC	0,23	1	4,35	0,4	Hs.109314	ESTs, Weakly similar to

						2202255A AT motif-binding fa
1027	TGTTACTGGAT	0,23	1	4,35	0,4	Hs.100861 ESTs, Weakly similar to spastin protein [H.sapiens]
1028	CCTGTAATCTT	1,85	8	4,32	2,84	Hs.120882 ESTs, Moderately similar to ALU1_HUMAN ALU
1029	GTGGCGGGCAC	19,81	85	4,29	25,22	Hs.283044 hypothetical protein PRO2859
1030	CCACTTGCACT	0,7	3	4,29	1,18	Hs.220962 EST, Weakly similar to ALU1_HUMAN ALU SUB-FAMILY
1031	TTCCATACCCC	0,7	3	4,29	1,18	Hs.180398 LIM domain-containing preferred translocation partne
1032	ATTGCATCACT	1,17	5	4,27	1,85	Hs.209111 EST
1033	GAGTTAAAAAA	1,17	5	4,27	1,85	Hs.180255 major histocompatibility complex, class II, DR beta
1034	GGGCCCTGGCC	0,94	4	4,26	1,53	Hs.25895 ESTs, Weakly similar to PI-3 kinase [H.sapiens]
1035	CAGATGGAGGC	0,94	4	4,26	1,53	Hs.127273 hypothetical protein FLJ10044
1036	CCTCTCCCACA	0,47	2	4,26	0,82	Hs.99197 ESTs
1037	GCCAGGGGGTA	0,47	2	4,26	0,82	Hs.96875 ESTs
1038	CTCAGTCTTTT	0,47	2	4,26	0,82	Hs.76722 CCAAT/enhancer binding protein (C/EBP), delta
1039	GATGTATTCTA	0,47	2	4,26	0,82	Hs.75844 ESTs, Highly similar to AF151903_1 CGI-145 protein [
1040	CCCTTCTGTAA	0,47	2	4,26	0,82	Hs.75716 plasminogen activator inhibitor, type II (arginine-s
1041	TGGAAGTGTCA	0,47	2	4,26	0,82	Hs.285802 ESTs
1042	GGCCTGTAATC	0,47	2	4,26	0,82	Hs.267400 ESTs, Moderately similar to ALU7_HUMAN ALU
1043	AGGTATATATC	0,47	2	4,26	0,82	Hs.24715 Homo sapiens mRNA; cDNA DKFZp434D0215 (from
1044	TTCTGAAAGGA	0,47	2	4,26	0,82	Hs.227209 DKFZP586F1019 protein
1045	AGCCTGTGGTC	0,47	2	4,26	0,82	Hs.154919 KIAA0625 protein
1046	TTGCGTGTGTC	0,47	2	4,26	0,82	Hs.1183 dual specificity phosphatase 2
1047	CATAATTCTC	0,47	2	4,26	0,82	Hs.104660 eIF-5A2 protein
1048	TGGGACGTGAG	1,67	7	4,19	2,45	Hs.3796 EphB6
1049	GCGAAATCCCG	2,4	10	4,17	3,34	Hs.194251 ESTs, Weakly similar to ALU2_HUMAN ALU
1050	ACCAAAAACCA	28,92	120	4,15	34,01	Hs.172928 collagen, type I, alpha 1
1051	AACCCAGGAGG	30,47	126	4,14	35,53	Hs.161554 hypothetical protein FLJ20159
1052	TCTCTGTGTAG	0,97	4	4,12	1,49	Hs.79187 coxsackie virus and adenovirus receptor
1053	CGCAGTAGGGG	0,97	4	4,12	1,49	Hs.17411 KIAA0699 protein
1054	CGAGAGGGAGA	0,97	4	4,12	1,49	Hs.158159 FAT tumor suppressor

							(Drosophila) homolog 2	
	1055	GTGGCATCTGC	0,97	4	4,12	1,49	Hs.1244	CD9 antigen (p24)
5	1056	CTAACGGGGCG	1,7	7	4,12	2,42	Hs.102171	immunoglobulin super-family containing leucine-rich r
	1057	GCAAAACCCCT	1,46	6	4,11	2,1	Hs.75238	chromatin assembly factor 1, subunit B (p60)
10	1058	ACTGCTTTACT	1,46	6	4,11	2,1	Hs.72157	DKFZP564I1922 protein
	1059	CCCCAGGCTGC	0,73	3	4,11	1,15	Hs.9645	ESTs
	1060	TAAAATGTTTA	0,73	3	4,11	1,15	Hs.94109	ESTs
15	1061	CCTACTGCACT	0,73	3	4,11	1,15	Hs.225641	ESTs, Moderately similar to KIAA0680 protein [H.sapi
	1062	GTGGCTCATTC	0,73	3	4,11	1,15	Hs.116577	prostate differentiation factor
20	1063	AAGCACAAAAA	2,93	12	4,10	3,87	Hs.9963	TYRO protein tyrosine kinase binding protein
	1064	GTGGCGGGCGC	22,97	94	4,09	26,43	Hs.129710	malignancy-associated protein
25	1065	AGAACCTTAAA	3,43	14	4,08	4,43	Hs.181244	major histocompatibility complex, class I, A
	1066	CCTGAAATCCC	1,96	8	4,08	2,69	Hs.182124	ESTs
	1067	GCGAAACCCAG	3,22	13	4,04	4,1	Hs.142442	HP1-BP74
30	1068	ATGTAGGTGCC	2,23	9	4,04	2,96	Hs.173717	phosphatidic acid phosphatase type 2B
	1069	TTAAATAGCAC	2,49	10	4,02	3,23	Hs.172928	collagen, type I, alpha 1
35	1070	TTTTATTCCA	0	4	4,00	5,89	Hs.93780	ESTs, Weakly similar to ALUB_HUMAN !!!! ALU CLASS
	1071	AATTACAGCCA	0	4	4,00	5,89	Hs.74471	gap junction protein, alpha 1, 43kD (connexin 43)
40	1072	CCTTACCTAAG	0	4	4,00	5,89	Hs.240217	dopachrome tautomerase (dopachrome delta-isomerase,
	1073	CTCCCTGAACG	0	4	4,00	5,89	Hs.11006	ESTs
45	1074	AACACGAATGA	1	4	4,00	1,45	Hs.259855	ESTs
	1075	GTGGCAAGCAC	1	4	4,00	1,45	Hs.138860	Rho GTPase activating protein 1
	1076	TTCACCATCCT	1	4	4,00	1,45	Hs.101395	ESTs, Weakly similar to tetraspan NET-4 [H.sapiens]
50	1077	AGAGGGAGTGA	0,5	2	4,00	0,78	Hs.85201	C-type (calcium dependent, carbohydrate-recognition
55	1078	AGTCCTTGAAA	0,5	2	4,00	0,78	Hs.81665	v-kit Hardy-Zuckerman 4 feline sarcoma viral onco-gen
	1079	CCCAGCCTAAA	0,5	2	4,00	0,78	Hs.47986	Homo sapiens mRNA; cDNA DKFZp586H051 (from clone
60	1080	TTTAACTGACA	0,5	2	4,00	0,78	Hs.24880	ESTs

1081	CCTTGTAATCC	0,5	2	4,00	0,78	Hs.197054	EST	
1082	GAAGGCTTATC	0,5	2	4,00	0,78	Hs.172674	nuclear factor of activated T-cells, cytoplasmic 3	
1083	TAGCAAAGATT	0,5	2	4,00	0,78	Hs.166172	aryl hydrocarbon receptor nuclear translocator	5
1084	CACATCTGTAA	0,5	2	4,00	0,78	Hs.16533	myosin phosphatase, target subunit 1	
1085	TTCAGTAATAA	0,5	2	4,00	0,78	Hs.13479	hypothetical protein FLJ20847	10
1086	GGTGAAACCCT	0,5	2	4,00	0,78	Hs.117582	CGI-43 protein	
1087	CTTCTGCCTCA	0,5	2	4,00	0,78	Hs.115896	ESTs	
1088	GAGAGGTGATT	0,5	2	4,00	0,78	Hs.114062	protein tyrosine phosphatase-like (proline instead o	15
1089	ATGTATTTTFA	0,5	2	4,00	0,78	Hs.108396	ALR-like protein	
1090	CTATAGGAGAC	1,26	5	3,97	1,75	Hs.8966	integral membrane protein 1	20
1091	TCCGTGTATAA	1,26	5	3,97	1,75	Hs.3321	ESTs, Highly similar to IRX3_MOUSE IRO-QUOIS-	25
1092	GCAAAACCCCA	24,76	98	3,96	26,53	Hs.129708	tumor necrosis factor (ligand) superfamily, member 1	
1093	TTCCATAGCCT	1,52	6	3,95	2,03	Hs.8546	Notch (Drosophila) homolog 3	30
1094	CTGTGAAATGC	0,76	3	3,95	1,11	Hs.23618	hypothetical protein FLJ10704	
1095	AAAGAACATAG	0,76	3	3,95	1,11	Hs.104558	ESTs	35
1096	CACCTGTAATC	9,41	37	3,93	10,41	Hs.275819	EST	
1097	GGCAACAAGAG	2,29	9	3,93	2,89	Hs.205739	ESTs, Weakly similar to ALU7_HUMAN ALU	
1098	GTGGCGGGTGC	18,52	72	3,89	19,32	Hs.277015	EST	40
1099	ACCTTCAAAAA	1,03	4	3,88	1,42	Hs.28444	hypothetical protein FLJ10567	
1100	ACATCTGGCTT	1,03	4	3,88	1,42	Hs.194035	KIAA0737 gene product	
1101	GTACGTATTCT	1,55	6	3,87	2	Hs.76325	immunoglobulin J polypeptide, linker protein for imm	45
1102	ATCCGCCTGCC	1,55	6	3,87	2	Hs.167956	ESTs, Weakly similar to KIAA0309 [H.sapiens]	
1103	ACCCACGTCAG	6,21	24	3,86	6,84	Hs.198951	jun B proto-oncogene	50
1104	TAATCCCAGCT	3,63	14	3,86	4,18	Hs.238384	EST	
1105	ATTGCACCACT	11,93	46	3,86	12,5	Hs.117582	CGI-43 protein	
1106	AGGACCAAGGA	0,26	1	3,85	0,37	Hs.99539	ESTs, Weakly similar to ALU7_HUMAN ALU	55
1107	TAAGCTACTAA	0,26	1	3,85	0,37	Hs.97469	ESTs, Weakly similar to I49698 alpha-1,3-galactosylt	
1108	CTCCATTGTCT	0,26	1	3,85	0,37	Hs.93005	slug (chicken homolog), zinc finger protein	60
1109	TGACATTAAAC	0,26	1	3,85	0,37	Hs.87432	ESTs	
1110	GGATTCAAGAG	0,26	1	3,85	0,37	Hs.86947	a disintegrin and metallo-	

							proteinase domain 8
5	1111	ATGTTATCATA	0,26	1	3,85	0,37	Hs.8325 mitogen-activated protein kinase 9
	1112	TACTCTGTTGA	0,26	1	3,85	0,37	Hs.82587 phospholipase D1, phosphatidylcholine-specific
10	1113	GGAAAAGAAAA	0,26	1	3,85	0,37	Hs.82141 Human clone 23612 mRNA sequence
	1114	TATACGTTATG	0,26	1	3,85	0,37	Hs.78894 KIAA0161 gene product
	1115	CACTTGGTGAT	0,26	1	3,85	0,37	Hs.77348 hydroxyprostaglandin dehydrogenase 15-(NAD)
15	1116	ATGAATGTAAA	0,26	1	3,85	0,37	Hs.76853 Homo sapiens mRNA full length insert cDNA clone EURO
	1117	TGTTTTCATAA	0,26	1	3,85	0,37	Hs.75703 small inducible cytokine A4 (homologous to mouse Mip)
20	1118	AGTTTACGATT	0,26	1	3,85	0,37	Hs.74649 cytochrome c oxidase subunit VIc
	1119	GTGGTTCATTC	0,26	1	3,85	0,37	Hs.6853 carbohydrate (N-acetylglucosamine 6-O) sulfotransfer
25	1120	CAACAAAAGCA	0,26	1	3,85	0,37	Hs.66450 ESTs
	1121	CATTTTTTGCG	0,26	1	3,85	0,37	Hs.59525 ESTs
30	1122	CTGCTAAACTA	0,26	1	3,85	0,37	Hs.46826 ESTs
	1123	ACCCTGAATGG	0,26	1	3,85	0,37	Hs.43086 ESTs
	1124	TTGTAACAAAA	0,26	1	3,85	0,37	Hs.40154 jumonji (mouse) homolog
	1125	TGCTGTTTATA	0,26	1	3,85	0,37	Hs.37958 ESTs
35	1126	TATGTGGGTTA	0,26	1	3,85	0,37	Hs.34359 ESTs
	1127	CAGCAATTATA	0,26	1	3,85	0,37	Hs.32309 inositol polyphosphate-1-phosphatase
	1128	CTCCATTGCCA	0,26	1	3,85	0,37	Hs.31869 ESTs
40	1129	GGGTGGGTCAC	0,26	1	3,85	0,37	Hs.31500 ESTs
	1130	ATTCCACCACT	0,26	1	3,85	0,37	Hs.2934 ribonucleotide reductase M1 polypeptide
	1131	TCTTACTCAGA	0,26	1	3,85	0,37	Hs.285081 ESTs
45	1132	AATAAAAAATA	0,26	1	3,85	0,37	Hs.284275 Homo sapiens PAK2 mRNA, complete cds
	1133	GAGACAGTGAC	0,26	1	3,85	0,37	Hs.284146 hypothetical protein DKFZp762N0610
50	1134	CCTGGGCAACA	0,26	1	3,85	0,37	Hs.273683 EST
	1135	CCTTTGCACTC	0,26	1	3,85	0,37	Hs.265124 ESTs
	1136	TGCAGACAGGG	0,26	1	3,85	0,37	Hs.264363 hypothetical protein FLJ10110
55	1137	TTGGCCCAGTC	0,26	1	3,85	0,37	Hs.25951 Rho guanine nucleotide exchange factor (GEF) 3
	1138	TCTTTAAAGTA	0,26	1	3,85	0,37	Hs.25155 guanine nucleotide regulatory protein (oncogene)
60	1139	ATATTGGTGGT	0,26	1	3,85	0,37	Hs.250692 hepatic leukemia factor
	1140	GTGGCGAATGC	0,26	1	3,85	0,37	Hs.230479 EST
	1141	TATTAACATTC	0,26	1	3,85	0,37	Hs.226573 inhibitor of kappa light polypeptide gene enhan-

							cer i	
1142	TCTCCATTCT	0,26	1	3,85	0,37	Hs.226573	inhibitor of kappa light polypeptide gene enhancer i	5
1143	TATATAGAATG	0,26	1	3,85	0,37	Hs.22581	ESTs	
1144	GCGAGATCCTG	0,26	1	3,85	0,37	Hs.22529	ESTs, Weakly similar to ALU1_HUMAN ALU	10
1145	CACTCCAACCT	0,26	1	3,85	0,37	Hs.205899	ESTs, Weakly similar to ALU5_HUMAN ALU	
1146	CGATGTTAAAA	0,26	1	3,85	0,37	Hs.20072	myosin regulatory light chain interacting protein	15
1147	CCTTCTGAATA	0,26	1	3,85	0,37	Hs.194660	ceroid-lipofuscinosis, neuronal 3, juvenile (Batten,	
1148	TGAGGATCCAG	0,26	1	3,85	0,37	Hs.191621	ESTs	20
1149	ATTGTACAACA	0,26	1	3,85	0,37	Hs.184326	CDC10 (cell division cycle 10, S. cerevisiae, homolo	
1150	AGCCTATTAAA	0,26	1	3,85	0,37	Hs.183593	zinc finger protein 24 (KOX 17)	25
1151	GCCCCTGCGCC	0,26	1	3,85	0,37	Hs.183202	ESTs	
1152	GTGAATGCACT	0,26	1	3,85	0,37	Hs.176065	ESTs	30
1153	TTCATTAAGAA	0,26	1	3,85	0,37	Hs.17411	KIAA0699 protein	
1154	ACCGAGGTGCA	0,26	1	3,85	0,37	Hs.171882	ESTs	35
1155	TTGGTATTGCA	0,26	1	3,85	0,37	Hs.163541	ESTs	
1156	ATGTATTTTCA	0,26	1	3,85	0,37	Hs.161554	hypothetical protein FLJ20159	40
1157	GTTGAATTGCA	0,26	1	3,85	0,37	Hs.156828	Homo sapiens cDNA FLJ10522 fis, clone	
1158	TCTGTCATCCC	0,26	1	3,85	0,37	Hs.150158	ESTs	45
1159	GTGGTGCAAAC	0,26	1	3,85	0,37	Hs.149852	EST, Weakly similar to ALU1_HUMAN ALU SUB-FAMILY	
1160	GGCTTTGGAAT	0,26	1	3,85	0,37	Hs.146481	ESTs	50
1161	TTTGCTTTTGA	0,26	1	3,85	0,37	Hs.144504	hypothetical protein FLJ10624	
1162	AAAGCATTAGA	0,26	1	3,85	0,37	Hs.14155	KIAA0653 protein	55
1163	AAACAACCCCA	0,26	1	3,85	0,37	Hs.1369	decay accelerating factor for complement (CD55, Crom	
1164	CTCCTTGTCCT	0,26	1	3,85	0,37	Hs.135530	EST	60
1165	GTGCTGCACAC	0,26	1	3,85	0,37	Hs.133272	ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS	
1166	TTTAAACTTGG	0,26	1	3,85	0,37	Hs.12431	ESTs	65
1167	CGGCCAGGTT	0,26	1	3,85	0,37	Hs.122823	thousand and one amino acid protein kinase	
1168	CTGACTGATGG	0,26	1	3,85	0,37	Hs.121509	collagen, type XI, alpha 2	
1169	ATAGATACACA	0,26	1	3,85	0,37	Hs.120850	ESTs	
1170	TGGCAGTAGTG	0,26	1	3,85	0,37	Hs.120644	ESTs	
1171	AAATCCTTCTA	0,26	1	3,85	0,37	Hs.119301	S100 calcium-binding protein A10 (annexin II	

							ligand,
5	1172	TCAAAC TTTGT	0,26	1	3,85	0,37	Hs.117582 CGI-43 protein
	1173	TACACCTGGAA	0,26	1	3,85	0,37	Hs.114624 ESTs
	1174	CAAGGATTTT	0,26	1	3,85	0,37	Hs.111323 Protein inhibitor of activated STAT X
	1175	CTAGTATAAAA	0,26	1	3,85	0,37	Hs.106650 hypothetical protein FLJ20533
10	1176	AATATAAAAAA	0,26	1	3,85	0,37	Hs.103548 ESTs, Weakly similar to ALU1_HUMAN ALU
	1177	CAATATGGTT	0,26	1	3,85	0,37	Hs.10351 KIAA0308 protein
15	1178	CAAGAACAGGG	0,26	1	3,85	0,37	Hs.102135 signal sequence receptor, delta (translocon-associated)
	1179	TCACCGGTCAG	15,94	61	3,83	16,2	Hs.80562 gelsolin (amyloidosis, Finnish type)
20	1180	GTGAAAACCCC	1,05	4	3,81	1,38	Hs.277213 EST, Weakly similar to ALU7_HUMAN ALU SUB-FAMILY
	1181	GTGGTGGGCAC	15,76	60	3,81	15,85	Hs.77510 isovaleryl Coenzyme A dehydrogenase
25	1182	GTGGTGGGTGC	15,79	60	3,80	15,81	Hs.136509 EST
	1183	CCGTTGCACTC	1,58	6	3,80	1,96	Hs.278329 ESTs
	1184	CATCACGGATC	0,79	3	3,80	1,08	Hs.82112 interleukin 1 receptor, type I
30	1185	GTATGTACAGG	0,79	3	3,80	1,08	Hs.164255 ESTs, Moderately similar to ALU2_HUMAN ALU
	1186	CCCTTTATATC	0,79	3	3,80	1,08	Hs.13766 ESTs
	1187	GCTCGTGGTCA	0,79	3	3,80	1,08	Hs.119475 cold inducible RNA-binding protein
35	1188	CCCATCTAGCT	0,79	3	3,80	1,08	Hs.106070 cyclin-dependent kinase inhibitor 1C (p57, Kip2)
	1189	TCTCAAAAAA	2,11	8	3,79	2,52	Hs.194841 ESTs, Moderately similar to ALU8_HUMAN ALU
40	1190	CCCCTGGCTGG	1,32	5	3,79	1,68	Hs.920 modulator recognition factor I
	1191	GGTTATTTAGT	1,32	5	3,79	1,68	Hs.8110 adducin 3 (gamma)
45	1192	GCAAAACCTCA	1,85	7	3,78	2,24	Hs.156596 ESTs, Weakly similar to ALU7_HUMAN ALU
	1193	AGTTGTTTGGT	0,53	2	3,77	0,75	Hs.96418 ESTs
	1194	TCATAGCCTTG	0,53	2	3,77	0,75	Hs.78846 heat shock 27kD protein 2
50	1195	AGGACTGGACT	0,53	2	3,77	0,75	Hs.75258 H2A histone family, member Y
	1196	TAAACCTAGGA	0,53	2	3,77	0,75	Hs.56186 EGF-like-domain, multiple 3
	1197	GTGGCTCACTT	0,53	2	3,77	0,75	Hs.285616 ESTs
55	1198	TCATTGGTGT	0,53	2	3,77	0,75	Hs.285439 ESTs
	1199	GCCTTGGCAGT	0,53	2	3,77	0,75	Hs.25351 iroquois-class homeodomain protein
60	1200	CCCTTGTTCTT	0,53	2	3,77	0,75	Hs.250723 FK506 binding protein 12-rapamycin associated protein
	1201	GAACAGTATGA	0,53	2	3,77	0,75	Hs.189762 ESTs



1202	ATGGCAGGCGG	0,53	2	3,77	0,75	Hs.161554	hypothetical protein FLJ20159	
1203	ACACAGCAAGA	36,07	136	3,77	34,48	Hs.80562	gelsolin (amyloidosis, Finnish type)	5
1204	GATCAGGCCAG	7,97	30	3,76	8,16	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danlos syndrome	
1205	GTGAAACTCTG	8,58	32	3,73	8,57	Hs.188853	Homo sapiens cDNA FLJ10150 fis, clone	10
1206	GGCCTGCAGGA	1,61	6	3,73	1,93	Hs.71869	apoptosis-associated speck-like protein contain- ing a	
1207	AAATCAATACA	1,88	7	3,72	2,21	Hs.94953	ESTs, Highly similar to C1QC_HUMAN COM- PLEMENT	15
1208	ATTGTACCACT	1,88	7	3,72	2,21	Hs.7099	hypothetical protein FLJ20265	20
1209	CGCCTGTAGTC	7,79	29	3,72	7,81	Hs.60088	ESTs	
1210	GCAAAACCCAG	1,08	4	3,70	1,35	Hs.210610	ESTs, Moderately similar to ALU6_HUMAN ALU	
1211	CTTTGATGCGG	1,08	4	3,70	1,35	Hs.183601	regulator of G-protein signalling 16	25
1212	GGCCCTAGGCA	8,94	33	3,69	8,73	Hs.78909	butyrate response factor 2 (EGF-response factor 2)	
1213	CCTGGCTAATT	7,88	29	3,68	7,72	Hs.25661	ESTs, Weakly similar to ALUF_HUMAN !!!! ALU CLASS	30
1214	CTTCCTGGCCT	2,72	10	3,68	2,96	Hs.83623	nuclear receptor subfamily 1, group I, member 3	35
1215	GCGGGGTGGAG	10,08	37	3,67	9,65	Hs.85155	butyrate response factor 1 (EGF-response factor 1)	
1216	GTGGCAGGCGC	23,18	85	3,67	21,18	Hs.48604	DKFZP434B168 protein	
1217	AGCCCAGGAGG	2,46	9	3,66	2,69	Hs.136340	ESTs, Weakly similar to unnamed protein product [H.s	40
1218	ATAGTGCCACT	1,64	6	3,66	1,9	Hs.246717	ESTs, Weakly similar to ALU7_HUMAN ALU	
1219	CATTTGTAAAA	0,82	3	3,66	1,05	Hs.84429	KIAA0971 protein	45
1220	CGTACAGCCCC	0,82	3	3,66	1,05	Hs.32580	KIAA1448 protein	
1221	GGGCTACGTCC	0,82	3	3,66	1,05	Hs.123107	kallikrein 1, re- nal/pancreas/salivary	
1222	ATCACACCACT	7,41	27	3,64	7,14	Hs.234786	KIAA0707 protein	50
1223	CACTCCAGCCT	3,57	13	3,64	3,69	Hs.193451	ESTs, Weakly similar to ALU7_HUMAN ALU	
1224	CTTGTAATCCC	12,66	46	3,63	11,69	Hs.183253	ESTs, Weakly similar to ALU1_HUMAN ALU	55
1225	GTGAAACCTCA	12,95	47	3,63	11,91	Hs.153029	ESTs	
1226	ATCTCAGCTCA	3,31	12	3,63	3,43	Hs.246192	ESTs, Weakly similar to RMS1_HUMAN REGU- LATOR	60
1227	TATGTGCTGTA	1,38	5	3,62	1,61	Hs.20084	retinoid X receptor, alpha	
1228	ACTCGAATATC	1,11	4	3,60	1,32	Hs.95655	secreted and transmem-	

								brane 1
5	1229	GAGTCCCTGGT	1,11	4	3,60	1,32	Hs.68398	period (Drosophila) homolog 1
	1230	TGCAATATGCC	1,67	6	3,59	1,87	Hs.750	fibrillin 1 (Marfan syndrome)
10	1231	GAAGCAATAAA	1,67	6	3,59	1,87	Hs.198253	major histocompatibility complex, class II, DQ alpha
	1232	GTGAAACTCCG	10,34	37	3,58	9,36	Hs.261734	ESTs, Moderately similar to ALU7_HUMAN ALU
15	1233	GGCTGCCGAGT	0,56	2	3,57	0,72	Hs.99829	hypothetical protein FLJ20565
	1234	CTTAGCCCCAG	0,56	2	3,57	0,72	Hs.96908	ESTs
	1235	TTATTCCACAA	0,56	2	3,57	0,72	Hs.93765	lipoma HMGIC fusion partner
20	1236	TCACAGCCCCC	0,56	2	3,57	0,72	Hs.8619	SRY (sex determining region Y)-box 18
	1237	TTTTCTTTTG	0,56	2	3,57	0,72	Hs.78546	ATPase, Ca++ transporting, plasma membrane 1
25	1238	CTTGCATAAGA	0,56	2	3,57	0,72	Hs.72912	cytochrome P450, subfamily I (aromatic compound-indu
	1239	TATGTGTTCTC	0,56	2	3,57	0,72	Hs.3353	beta-1,3-glucuronyltransferase 1 (glucuronosyltransf
30	1240	ACTATCATCTT	0,56	2	3,57	0,72	Hs.29117	H.sapiens mRNA for pur alpha extended 3'untranslated
35	1241	CGCCTATAGTC	0,56	2	3,57	0,72	Hs.271166	ESTs, Moderately similar to ALU7_HUMAN ALU
	1242	CCCGCCAGTGC	0,56	2	3,57	0,72	Hs.256297	integrin, alpha 11
40	1243	TTCTAATTTTT	0,56	2	3,57	0,72	Hs.170414	paired basic amino acid cleaving system 4
	1244	CGGGAAGACAT	0,56	2	3,57	0,72	Hs.154525	KIAA1076 protein
	1245	CCAGTAGTCCC	0,56	2	3,57	0,72	Hs.147959	EST
45	1246	CAGTTTGTGTT	0,56	2	3,57	0,72	Hs.144477	hypothetical protein PRO2975
	1247	TCCTTTAAAAT	0,56	2	3,57	0,72	Hs.10587	KIAA0353 protein
	1248	GTGCTAAGCGG	12,92	46	3,56	11,41	Hs.4217	collagen, type VI, alpha 2
	1249	AGAATCACTTG	11,6	41	3,53	10,16	Hs.117582	CGI-43 protein
50	1250	GTGGTGTACGC	2,55	9	3,53	2,6	Hs.182225	RNA binding motif protein 3
	1251	GCCCCAGAATC	0,85	3	3,53	1,02	Hs.8682	ESTs, Moderately similar to ALU1_HUMAN ALU
55	1252	TTGGGAGGCTG	0,85	3	3,53	1,02	Hs.118269	ESTs, Weakly similar to A46010 X-linked retinopathy
	1253	GTGGCACGCGC	5,39	19	3,53	5,01	Hs.187346	ESTs
60	1254	CAAGCGCTCTA	1,14	4	3,51	1,29	Hs.23598	CREB binding protein (Rubinstein-Taybi syndrome)

1255	AGTTCGAGACC	1,14	4	3,51	1,29	Hs.232540	ESTs	
1256	AGAACCAAAAA	1,14	4	3,51	1,29	Hs.181244	major histocompatibility complex, class I, A	
1257	CTGGCTATCCG	1,14	4	3,51	1,29	Hs.10784	hypothetical protein FLJ20037	5
1258	TAGTCCCAGCT	3,14	11	3,50	3,08	Hs.274579	ancient conserved domain protein 1	
1259	GTGAAATCCTG	8	28	3,50	7,06	Hs.53531	lipoic acid synthetase	10
1260	CCTGTAATTCC	13,48	47	3,49	11,36	Hs.23582	tumor-associated calcium signal transducer 2	
1261	CTTCTTGCCCC	5,74	20	3,48	5,17	Hs.251577	hemoglobin, alpha 1	
1262	TGGTTGGTGGT	3,16	11	3,48	3,05	Hs.12701	plasmolipin	15
1263	CCCGTAATCCC	4,89	17	3,48	4,46	Hs.274168	Homo sapiens mRNA; cDNA DKFZp761P0212 (from	
1264	CCTGGCCAGAA	1,44	5	3,47	1,55	Hs.261734	ESTs, Moderately similar to ALU7 HUMAN ALU	20
1265	CGTGTAAATCCC	3,46	12	3,47	3,28	Hs.187761	ESTs	
1266	GCGAAACCTCA	1,73	6	3,47	1,81	Hs.42644	thioredoxin-like	
1267	TGGTTACAAAA	1,73	6	3,47	1,81	Hs.3850	Homo sapiens clone 23596 mRNA sequence	25
1268	CCACAGCACTC	2,02	7	3,47	2,06	Hs.273828	ESTs	
1269	GTGGCACGTGC	29,86	103	3,45	23,64	Hs.278588	ESTs, Weakly similar to ALU2 HUMAN ALU	30
1270	ATGTCTTTTCT	5,22	18	3,45	4,66	Hs.1516	insulin-like growth factor-binding protein 4	
1271	CTTGTAGTCCC	3,19	11	3,45	3,02	Hs.272202	hypothetical protein FLJ20825	
1272	CTCATCTGCTG	2,9	10	3,45	2,78	Hs.82109	syndecan 1	35
1273	AGGACATAATT	0,29	1	3,45	0,34	Hs.93454	ESTs	
1274	GAGCTACACCA	0,29	1	3,45	0,34	Hs.82171	Human clone 191B7 placenta expressed mRNA from	40
1275	TTGCTACTAAA	0,29	1	3,45	0,34	Hs.7790	ESTs	
1276	CTTAGTGTTTT	0,29	1	3,45	0,34	Hs.7720	dynein, cytoplasmic, heavy polypeptide 1	
1277	CTGGTCCTGGA	0,29	1	3,45	0,34	Hs.76476	cathepsin H	45
1278	GGTGGCAGTTG	0,29	1	3,45	0,34	Hs.75794	endothelial differentiation, lysophosphatidic acid G	
1279	CTGATATAGAC	0,29	1	3,45	0,34	Hs.74002	nuclear receptor coactivator 1	50
1280	TGGAAATCATT	0,29	1	3,45	0,34	Hs.5028	DKFZP564O0423 protein	
1281	ACTTTGAAAGG	0,29	1	3,45	0,34	Hs.44077	hypothetical protein FLJ10793	
1282	AAAGGCACTGA	0,29	1	3,45	0,34	Hs.3994	ESTs	55
1283	GTTCTCTTTTT	0,29	1	3,45	0,34	Hs.3843	dual specificity phosphatase 7	
1284	AGCGCAGCTGT	0,29	1	3,45	0,34	Hs.34771	ESTs	
1285	ATTGTGAAGAG	0,29	1	3,45	0,34	Hs.34578	alpha2,3-sialyltransferase	(a)
1286	GCCTTCGGAAA	0,29	1	3,45	0,34	Hs.33104	Homo sapiens mRNA; cDNA DKFZp434H2121	

							(from
5	1287	GCTATTTTGAT	0,29	1	3,45	0,34	Hs.32250 ESTs
	1288	TATCTCTTAAA	0,29	1	3,45	0,34	Hs.286228 ESTs
	1289	TGTGATTTTAA	0,29	1	3,45	0,34	Hs.286163 ESTs
	1290	TATTTTCAGATT	0,29	1	3,45	0,34	Hs.285585 ESTs
	1291	ATGATTTTGAG	0,29	1	3,45	0,34	Hs.285306 putative selenocysteine lyase
10	1292	AATATTCATAT	0,29	1	3,45	0,34	Hs.284311 Homo sapiens clone 25038 mRNA sequence
	1293	AGACCCCATTT	0,29	1	3,45	0,34	Hs.279297 EST
	1294	CACCCATAGTC	0,29	1	3,45	0,34	Hs.278018 EST
15	1295	GTCTTGCTGCA	0,29	1	3,45	0,34	Hs.26966 KIAA1171 protein
	1296	CGGCCCATCTG	0,29	1	3,45	0,34	Hs.26290 ESTs
	1297	CAATCTGATGC	0,29	1	3,45	0,34	Hs.26176 hypothetical protein FLJ10261
20	1298	ATGTTGGGTGT	0,29	1	3,45	0,34	Hs.260855 Homo sapiens mRNA; cDNA DKFZp761G2311 (from
	1299	ACTCTGTCTCC	0,29	1	3,45	0,34	Hs.259339 EST
25	1300	GGAATACAGAA	0,29	1	3,45	0,34	Hs.250825 ESTs, Highly similar to vacuolar protein sorting hom
	1301	ACTGGGCAAGC	0,29	1	3,45	0,34	Hs.240062 hypothetical protein
30	1302	GGTCAGAAATT	0,29	1	3,45	0,34	Hs.211581 metal-regulatory transcription factor 1
	1303	AACCGAAGGGA	0,29	1	3,45	0,34	Hs.20596 ESTs
	1304	GGGATAGAGAC	0,29	1	3,45	0,34	Hs.202955 hypothetical protein FLJ20507
35	1305	TTTCAGTTAGT	0,29	1	3,45	0,34	Hs.196284 ESTs
	1306	GCTATTGATGT	0,29	1	3,45	0,34	Hs.193398 ESTs
	1307	AAGAGGAGGCC	0,29	1	3,45	0,34	Hs.183639 hypothetical protein FLJ10210
40	1308	TAATACACTAA	0,29	1	3,45	0,34	Hs.183475 Homo sapiens clone 25061 mRNA sequence
	1309	GCAGATGCTTT	0,29	1	3,45	0,34	Hs.180799 ESTs, Moderately similar to ALU5_HUMAN ALU
45	1310	TCACAAGGCTG	0,29	1	3,45	0,34	Hs.17998 ESTs
	1311	TGCGAGCTGGG	0,29	1	3,45	0,34	Hs.179573 collagen, type I, alpha 2
	1312	GGATTTGCTGC	0,29	1	3,45	0,34	Hs.177956 Homo sapiens mRNA; cDNA DKFZp434C0926 (from
50	1313	CACGCACACAC	0,29	1	3,45	0,34	Hs.177664 KIAA0914 gene product
	1314	ATGTGGACTGA	0,29	1	3,45	0,34	Hs.174905 KIAA0033 protein
55	1315	GGAGGCAGAGC	0,29	1	3,45	0,34	Hs.172838 Human clone Z'3-1 placenta expressed mRNA from
	1316	GCTTTCTGTAA	0,29	1	3,45	0,34	Hs.172674 nuclear factor of activated T-cells, cytoplasmic 3
60	1317	TGATTATTTAC	0,29	1	3,45	0,34	Hs.16930 ESTs
	1318	ACATCTGCCTG	0,29	1	3,45	0,34	Hs.161554 hypothetical protein FLJ20159

1319	CTTAGTTTTAA	0,29	1	3,45	0,34	Hs.161554	hypothetical protein FLJ20159	
1320	AGGAAGAGTCA	0,29	1	3,45	0,34	Hs.154655	imogen 38	5
1321	CAATGCAGAGG	0,29	1	3,45	0,34	Hs.150748	malonyl-CoA decarboxy- lase	
1322	TAATTCTTGTA	0,29	1	3,45	0,34	Hs.146123	ESTs	
1323	CAAGGGCCCAC	0,29	1	3,45	0,34	Hs.14587	ESTs, Weakly similar to AF151859_1 CGI-101 protein [	10
1324	TTTTGAAGAAA	0,29	1	3,45	0,34	Hs.144465	ESTs	
1325	TGTCTCCGTCT	0,29	1	3,45	0,34	Hs.135150	lung type-I cell membrane- associated glycoprotein	15
1326	TTTTCTTCAGG	0,29	1	3,45	0,34	Hs.125753	chromosome 2 open read- ing frame 2	
1327	TCCTCCCTCT	0,29	1	3,45	0,34	Hs.125384	ESTs	
1328	TCTGCCTTTCT	0,29	1	3,45	0,34	Hs.125019	ESTs, Highly similar to KIAA0886 protein [H.sapiens]	20
1329	ATAACTGTCAG	0,29	1	3,45	0,34	Hs.12040	STE20-like kinase	
1330	TTGCAGTTTTT	0,29	1	3,45	0,34	Hs.117582	CGI-43 protein	25
1331	TATTTAAAAAA	0,29	1	3,45	0,34	Hs.117304	ESTs	
1332	GGCTCAGGGGC	0,29	1	3,45	0,34	Hs.116489	ESTs, Weakly similar to GCP170 [H.sapiens]	
1333	TTTATTGAAAC	0,29	1	3,45	0,34	Hs.112193	mutS (E. coli) homolog 5	30
1334	CTGGCTTAAAT	0,29	1	3,45	0,34	Hs.11171	APG5 (autophagy 5, S. cerevisiae)-like	
1335	GCTTTATGTGG	0,29	1	3,45	0,34	Hs.111460	ESTs, Weakly similar to Con1 [H.sapiens]	35
1336	GCATACTTTAT	0,29	1	3,45	0,34	Hs.109370	ESTs	
1337	AGAATACTGAG	0,29	1	3,45	0,34	Hs.106705	neuronal PAS domain protein 2	
1338	ACCCAAAAAAA	0,29	1	3,45	0,34	Hs.101840	major histocompatibility complex, class I-like seque	40
1339	GGACATTAGGG	0,29	1	3,45	0,34	Hs.101265	MEMOREC NSM2 (CCA1) sphingomyeli	
1340	AAAAATAAATT	0,29	1	3,45	0,34	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (from clone	45
1341	AGATACATAGC	1,46	5	3,42	1,53	Hs.84045	Homo sapiens cDNA FLJ20288 fis, clone HEP04414	50
1342	TGGATATCAGT	1,46	5	3,42	1,53	Hs.7327	claudin 1	
1343	TTTTCCACTTT	1,46	5	3,42	1,53	Hs.6900	ring finger protein 13	
1344	GTGGCTCAGGC	1,17	4	3,42	1,26	Hs.259047	ESTs	
1345	CCTGTGATTCC	1,17	4	3,42	1,26	Hs.227961	EST	55
1346	GGCGACAGAGC	3,22	11	3,42	2,99	Hs.92254	hypothetical protein FLJ20163	
1347	CCTGTGGTCCT	3,22	11	3,42	2,99	Hs.120769	Homo sapiens cDNA FLJ20463 fis, clone KAT06143	60
1348	TGCCTGTGGTC	4,69	16	3,41	4,15	Hs.277100	ESTs, Weakly similar to	

							ALU2_HUMAN ALU
5	1349	GTAAAAAAGCC	0,88	3	3,41	0,99	Hs.98988 ESTs
	1350	TGTGAACACAT	0,88	3	3,41	0,99	Hs.80645 interferon regulatory factor 1
	1351	AAACGAAGTTG	0,88	3	3,41	0,99	Hs.78353 SFRS protein kinase 2
	1352	TACATCAGTAA	0,88	3	3,41	0,99	Hs.65029 growth arrest-specific 1
10	1353	CCTGTAGGCC	0,88	3	3,41	0,99	Hs.207938 EST
	1354	GTGAGACCTCG	0,88	3	3,41	0,99	Hs.203206 ESTs, Moderately similar to ALU1_HUMAN ALU
	1355	TGCCACCACAC	2,64	9	3,41	2,51	Hs.239993 ESTs
15	1356	GCTGGATTTTG	0,59	2	3,39	0,69	Hs.82124 laminin, beta 1
	1357	TCACTTTTTTA	0,59	2	3,39	0,69	Hs.8045 ESTs
	1358	ATTATCCTCAG	0,59	2	3,39	0,69	Hs.7987 DKFZP434F162 protein
20	1359	GGATCCAATTT	0,59	2	3,39	0,69	Hs.61796 transcription factor AP-2 gamma (activating enhancer
	1360	CCAATTGAAGA	0,59	2	3,39	0,69	Hs.40328 ESTs
	1361	TTACTTTTGGT	0,59	2	3,39	0,69	Hs.285861 hypothetical protein FLJ10359
25	1362	GAGAGCTTTGC	0,59	2	3,39	0,69	Hs.275374 aldo-keto reductase family 1, member C1 (dihydrodiol
	1363	TACCCCCAAAC	0,59	2	3,39	0,69	Hs.241926 ESTs
30	1364	GGGCAGACACT	0,59	2	3,39	0,69	Hs.18878 ESTs, Weakly similar to dJ876B10.4 [H.sapiens]
	1365	ATGGCGCACGC	0,59	2	3,39	0,69	Hs.124984 ESTs, Moderately similar to unnamed protein product
35	1366	AGGTTGCCGAG	0,59	2	3,39	0,69	Hs.105399 KIAA0809 protein
	1367	CCACTGCACCC	5,92	20	3,38	5	Hs.6853 carbohydrate (N-acetylglucosamine 6-O) sulfotransfer
40	1368	ATGGTGGGGGA	5,33	18	3,38	4,55	Hs.1665 zinc finger protein homologous to Zfp-36 in mouse
	1369	CCCTCTCCCTT	2,37	8	3,38	2,24	Hs.85087 latent transforming growth factor beta binding prote
45	1370	TCACCAAAAAA	1,79	6	3,35	1,75	Hs.84753 KIAA0246 protein
	1371	GTGAAACCCCC	17,64	59	3,34	13,37	Hs.265865 EST
	1372	CCTGCAATCCC	10,2	34	3,33	7,97	Hs.3280 caspase 6, apoptosis-related cysteine protease
50	1373	GTGAAGCCCCG	6,62	22	3,32	5,34	Hs.285592 Homo sapiens mRNA; cDNA DKFZp564M113 (from
55	1374	CCACTGTACTC	16	53	3,31	11,94	Hs.220261 ESTs, Moderately similar to ALU4_HUMAN ALU
	1375	GTGGTGGGCGC	15,12	50	3,31	11,28	Hs.136810 ESTs, Weakly similar to ALU1_HUMAN ALU
60	1376	AGTATGACCTA	0,91	3	3,30	0,96	Hs.74649 cytochrome c oxidase subunit VIc
	1377	GTGACAGCCAC	0,91	3	3,30	0,96	Hs.74441 chromodomain helicase DNA binding protein 4

1378	GGGCTTTTGAG	0,91	3	3,30	0,96	Hs.29893	Homo sapiens mRNA full length insert cDNA clone EURO	
1379	GTGAGACCCCT	0,91	3	3,30	0,96	Hs.269952	ESTs, Weakly similar to ALU1_HUMAN ALU	5
1380	GTGGTGACAT	0,91	3	3,30	0,96	Hs.269030	ESTs	
1381	CCTGTAGTCAC	0,91	3	3,30	0,96	Hs.268900	ESTs	
1382	TGGTAACTGGC	0,91	3	3,30	0,96	Hs.108741	ESTs	10
1383	GTGGTATGTGC	1,52	5	3,29	1,47	Hs.277102	ESTs, Weakly similar to ALU1_HUMAN ALU	
1384	GTAAGATTAGC	1,52	5	3,29	1,47	Hs.250705	ESTs	
1385	GCGAAACCCCA	21,97	72	3,28	15,71	Hs.210682	ESTs, Weakly similar to ALU6_HUMAN ALU	15
1386	ATCGTGCCACT	6,12	20	3,27	4,81	Hs.7615	Homo sapiens mRNA; cDNA DKFZp434N2030 (from	20
1387	TCTGTAATCCC	13,48	44	3,26	9,85	Hs.142	sulfotransferase family, cytosolic, 1A, phenol-prefe	
1388	TTAGCCAGGCT	3,37	11	3,26	2,85	Hs.71367	ESTs, Moderately similar to ALU7_HUMAN ALU	25
1389	ACAAAACCCCTG	1,23	4	3,25	1,21	Hs.268591	ESTs	
1390	ATCTCGGCTCA	4,31	14	3,25	3,49	Hs.29809	Homo sapiens mRNA; cDNA DKFZp434C185 (from clone	30
1391	CCTGTAATGCC	4,01	13	3,24	3,26	Hs.7179	RAD1 (S. pombe) homolog	
1392	CCACCGCACTC	6,8	22	3,24	5,18	Hs.222669	ESTs, Moderately similar to ALU4_HUMAN ALU	35
1393	GTGGTGTGTGC	11,75	38	3,23	8,5	Hs.27038	Homo sapiens mRNA; cDNA DKFZp434G2127 (from	
1394	ATGAAACCCCA	8,35	27	3,23	6,22	Hs.285341	ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS	40
1395	CCTGTAGCCCC	2,17	7	3,23	1,92	Hs.277320	EST, Weakly similar to ALU6_HUMAN ALU SUB-FAMILY	45
1396	TTTTTAAAAA	0,62	2	3,23	0,66	Hs.77840	annexin A4	
1397	AAGGAGCAAGT	0,62	2	3,23	0,66	Hs.76688	carboxylesterase 1 (monocyte/macrophage serine ester	50
1398	ACTTTTTTATG	0,62	2	3,23	0,66	Hs.697	cytochrome c-1	
1399	ATTGAGCCACA	0,62	2	3,23	0,66	Hs.63290	2-hydroxyphytanoyl-CoA lyase	
1400	ACCACAAAAA	0,62	2	3,23	0,66	Hs.469	succinate dehydrogenase complex, subunit A, flavo-pro	55
1401	ATCACAGCTCA	0,62	2	3,23	0,66	Hs.29590	ESTs	
1402	TGGTTCCAGCT	0,62	2	3,23	0,66	Hs.278541	ESTs, Weakly similar to alternatively spliced product	60

5	1403	TGACTGGCTTT	0,62	2	3,23	0,66	Hs.274439	Homo sapiens cDNA FLJ11265 fis, clone PLACE1009158
	1404	GTGGTGGACCC	0,62	2	3,23	0,66	Hs.270901	ESTs
	1405	CTGCTGTACTC	0,62	2	3,23	0,66	Hs.22826	tropomodulin 3 (ubiqui- tous)
10	1406	ATGATAATTAA	0,62	2	3,23	0,66	Hs.170142	ESTs
	1407	TAAAATAAGGG	0,62	2	3,23	0,66	Hs.169487	Kreisler (mouse) maf- related leucine zipper homolog
	1408	GAGAGAGAGAA	0,62	2	3,23	0,66	Hs.169391	ESTs
15	1409	TACCCTGAAAC	0,62	2	3,23	0,66	Hs.144018	ESTs
	1410	ACTGCCCCGCTG	3,72	12	3,23	3,03	Hs.81071	extracellular matrix protein 1
	1411	GGTGAGCGTGT	1,55	5	3,23	1,44	Hs.2913	EphB3
20	1412	GTGGTGGATGC	1,55	5	3,23	1,44	Hs.277904	EST
	1413	ACTGTGCCACT	1,55	5	3,23	1,44	Hs.161554	hypothetical protein FLJ20159
25	1414	GTGGCAGGCAC	21,15	68	3,22	14,52	Hs.246935	ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS
	1415	CCCCTTGTA	3,75	12	3,20	3	Hs.75922	brain protein I3
30	1416	GCCCTTTCTCT	4,07	13	3,19	3,21	Hs.7835	endocytic receptor (macrophage mannose receptor fami
	1417	AGACCTCCTTC	1,88	6	3,19	1,67	Hs.281706	sortilin 1
	1418	AGTGGTGGCTA	1,88	6	3,19	1,67	Hs.230	fibromodulin
35	1419	GGACAGATGTA	0,94	3	3,19	0,93	Hs.75356	transcription factor 4
	1420	GTGGCGAGCAC	0,94	3	3,19	0,93	Hs.261831	EST
	1421	ATGGTGTGTGC	0,94	3	3,19	0,93	Hs.193347	ESTs
40	1422	GGA CTGAGTCA	0,94	3	3,19	0,93	Hs.18387	transcription factor AP-2 alpha (activating enhancer
	1423	GTGAGTGCCCT	0,94	3	3,19	0,93	Hs.171872	DEAD/H (Asp-Glu-Ala- Asp/His) box polypeptide 8 (RNA
45	1424	GCGGAACCTCA	0,94	3	3,19	0,93	Hs.10700	hypothetical protein
	1425	GTGTGGGGGGC	12,86	41	3,19	8,95	Hs.2340	junction plakoglobin
	1426	GTGAAACTCCA	10,05	32	3,18	7,12	Hs.140002	ESTs, Moderately similar to ALU7_HUMAN ALU
50	1427	CCACTACACTC	9,11	29	3,18	6,5	Hs.83429	tumor necrosis factor (ligand) superfamily, member 1
55	1428	ACGGAAGTTTT	1,26	4	3,17	1,18	Hs.144974	ESTs, Highly similar to unnamed protein product [H.s
	1429	GTGAAACCCGT	4,1	13	3,17	3,18	Hs.278577	Homo sapiens mRNA; cDNA DKFZp564P073 (from clone
60	1430	TCAA ACTGTGA	1,58	5	3,16	1,42	Hs.94881	ESTs
	1431	CATCGAAAGTT	0,64	2	3,13	0,64	Hs.80618	hypothetical protein
	1432	AGTAATCATCA	0,64	2	3,13	0,64	Hs.75925	proteasome (prosome,



						macropain) inhibitor sub-unit 1	
1433	AATAATCCTGG	0,64	2	3,13	0,64	Hs.62908	ESTs
1434	GTATTCCTAAA	0,64	2	3,13	0,64	Hs.5724	ESTs, Weakly similar to multi PDZ domain protein MUP
1435	CTGGGAAGCAT	0,64	2	3,13	0,64	Hs.42311	ESTs
1436	GATCAAACTG	0,64	2	3,13	0,64	Hs.41267	c21orf7 form A-D
1437	GTGACAGGCGC	0,64	2	3,13	0,64	Hs.278879	ESTs, Moderately similar to ALUA HUMAN !!!! ALU
1438	GCACCGTGGAA	0,64	2	3,13	0,64	Hs.27299	transcriptional regulator protein
1439	TTAACTGTATT	0,64	2	3,13	0,64	Hs.180952	actin, beta
1440	ATGTTAGAGAC	0,64	2	3,13	0,64	Hs.1592	CDC16 (cell division cycle 16, S. cerevisiae, homolo
1441	ATCGCATCACT	0,64	2	3,13	0,64	Hs.158126	ESTs
1442	GACTCTGGAGA	0,64	2	3,13	0,64	Hs.154567	supervillin
1443	AAACTGTTCAA	0,64	2	3,13	0,64	Hs.118978	KIAA0256 gene product
1444	ACCAACACGGG	0,64	2	3,13	0,64	Hs.109005	ESTs
1445	AAAGATGTATC	0,32	1	3,13	0,32	Hs.979	pyruvate dehydrogenase (lipoamide) beta
1446	AAAACAGCAAG	0,32	1	3,13	0,32	Hs.92909	SON DNA binding protein
1447	TTTTCAGGTAA	0,32	1	3,13	0,32	Hs.91773	protein phosphatase 2 (formerly 2A), catalytic subun
1448	TGCCTCCCAGC	0,32	1	3,13	0,32	Hs.90527	HSPC128 protein
1449	TAAGTGAACAT	0,32	1	3,13	0,32	Hs.83164	collagen, type XV, alpha 1
1450	TTTTGCTCAGA	0,32	1	3,13	0,32	Hs.8102	ribosomal protein S20
1451	CATTCTCCCAG	0,32	1	3,13	0,32	Hs.79110	nucleolin
1452	GTTTCAGCACT	0,32	1	3,13	0,32	Hs.77502	methionine adenosyltransferase II, alpha
1453	GTA ACTCTATG	0,32	1	3,13	0,32	Hs.7277	peroxisomal biogenesis factor 3
1454	GTTCTATTGTA	0,32	1	3,13	0,32	Hs.6909	DKFZP564G202 protein
1455	CTATATTGTAA	0,32	1	3,13	0,32	Hs.65919	ESTs
1456	GTGAAACATTG	0,32	1	3,13	0,32	Hs.6567	Homo sapiens mRNA; cDNA DKFZp434C136 (from clone
1457	GTATTGAAGTT	0,32	1	3,13	0,32	Hs.6079	B cell RAG associated protein
1458	CTTTAGAAGCA	0,32	1	3,13	0,32	Hs.5669	ESTs
1459	TGACTCCTCAA	0,32	1	3,13	0,32	Hs.47007	mitogen-activated protein kinase kinase kinase 14
1460	CTTTTATGGAC	0,32	1	3,13	0,32	Hs.44833	ESTs
1461	TAAATCTACAA	0,32	1	3,13	0,32	Hs.44701	ESTs
1462	TTCCCAAATGA	0,32	1	3,13	0,32	Hs.44257	Homo sapiens mRNA; cDNA DKFZp762O2215 (from
1463	GTAAGAGTTCT	0,32	1	3,13	0,32	Hs.4084	KIAA1025 protein
1464	ATGCCATTGGA	0,32	1	3,13	0,32	Hs.30213	ceroid-lipofuscinosis, neuronal 5

1465	AGGAAATGGAT	0,32	1	3,13	0,32	Hs.30194	ESTs
1466	AACAAGCTGGG	0,32	1	3,13	0,32	Hs.29759	RNA POLYMERASE I AND TRANSCRIPT RE- LEASE
1467	TGCACTTGAGA	0,32	1	3,13	0,32	Hs.29055	ESTs
1468	GCATTCTGGTT	0,32	1	3,13	0,32	Hs.286261	ESTs
1469	GTGGCCACCCT	0,32	1	3,13	0,32	Hs.286217	KIAA0685 gene product
1470	AAGGTGGTTGT	0,32	1	3,13	0,32	Hs.285999	trinucleotide repeat con- taining 15
1471	AGAACTACGTG	0,32	1	3,13	0,32	Hs.284176	hypothetical protein PRO2221
1472	AATTTGGGAGA	0,32	1	3,13	0,32	Hs.279882	PC326 protein
1473	GGGAAACCCCT	0,32	1	3,13	0,32	Hs.279408	EST
1474	CTTACTCTTGA	0,32	1	3,13	0,32	Hs.27342	ESTs
1475	ACCGTGCCACT	0,32	1	3,13	0,32	Hs.270667	ESTs
1476	AGGCTGGTTTA	0,32	1	3,13	0,32	Hs.26322	cell cycle related kinase
1477	TCTTTTGGGAG	0,32	1	3,13	0,32	Hs.257312	EST
1478	ACTGATCTTGT	0,32	1	3,13	0,32	Hs.251871	CTP synthase
1479	AAGTCTGTAGA	0,32	1	3,13	0,32	Hs.250863	ESTs
1480	ATGGGGGAAAGA	0,32	1	3,13	0,32	Hs.24989	ESTs
1481	ACAGTGCCACT	0,32	1	3,13	0,32	Hs.246374	ESTs
1482	TGTGGGGGACAA	0,32	1	3,13	0,32	Hs.245017	EST
1483	CAAGTCTCCAG	0,32	1	3,13	0,32	Hs.241515	COX11 (yeast) homolog, cytochrome c oxidase assembly
1484	TTCCCTCCAAA	0,32	1	3,13	0,32	Hs.239727	desmocollin 2
1485	ATGTATAGGGC	0,32	1	3,13	0,32	Hs.238809	ESTs
1486	GGTTGTTGCGG	0,32	1	3,13	0,32	Hs.23823	ESTs
1487	TCTTCTTAATA	0,32	1	3,13	0,32	Hs.23047	ESTs, Weakly similar to predicted using Gene- finder [
1488	GCTCATTTTCAG	0,32	1	3,13	0,32	Hs.22870	Homo sapiens mRNA full length insert cDNA clone EURO
1489	AGTTCCAGACC	0,32	1	3,13	0,32	Hs.223935	EST
1490	AGTCAGTGGGA	0,32	1	3,13	0,32	Hs.21943	ESTs, Weakly similar to ORF YGL221c [S.cerevisiae]
1491	TTTCCAATGGA	0,32	1	3,13	0,32	Hs.21756	translation factor sui1 homolog
1492	TACATTTGAAT	0,32	1	3,13	0,32	Hs.21537	protein phosphatase 1, catalytic subunit, beta isofo
1493	TTTTCTGTATT	0,32	1	3,13	0,32	Hs.21356	hypothetical protein DKFZp762K2015
1494	AGAAAGATGGA	0,32	1	3,13	0,32	Hs.211577	kinectin 1 (kinesin recep- tor)
1495	TTTACCTTTGG	0,32	1	3,13	0,32	Hs.21108	ESTs
1496	TACGATATTCA	0,32	1	3,13	0,32	Hs.207776	aspartylglucosaminidase
1497	GCACTGGGGCA	0,32	1	3,13	0,32	Hs.206259	Homo sapiens mRNA for KIAA1190 protein, partial

							cds
1498	GCTGCTAGAAA	0,32	1	3,13	0,32	Hs.197751	KIAA0666 protein
1499	GGGTAGAGAGT	0,32	1	3,13	0,32	Hs.196437	hypothetical protein FLJ10788
1500	ATCGGCTCCCA	0,32	1	3,13	0,32	Hs.194478	Homo sapiens mRNA; cDNA DKFZp434O1572 (from
1501	ATAATGGAGTG	0,32	1	3,13	0,32	Hs.17850	ESTs
1502	GAAGAAAGACT	0,32	1	3,13	0,32	Hs.172506	myosin VB
1503	TGCCTGACAAG	0,32	1	3,13	0,32	Hs.169160	ESTs
1504	TTCCTGTAATC	0,32	1	3,13	0,32	Hs.167106	proteasome (prosome, macropain) subunit, alpha type,
1505	AAATATTAAAC	0,32	1	3,13	0,32	Hs.16364	hypothetical protein FLJ10955
1506	ATAAAGCCGAA	0,32	1	3,13	0,32	Hs.159471	ZAP3 protein
1507	AGGCTGAGGCG	0,32	1	3,13	0,32	Hs.156292	ESTs
1508	TAGTGCTCTCA	0,32	1	3,13	0,32	Hs.154424	deiodinase, iodothyronine, type II
1509	TTCATAAAAAA	0,32	1	3,13	0,32	Hs.154057	matrix metalloproteinase 19
1510	GTGGCTACAGT	0,32	1	3,13	0,32	Hs.151251	ESTs
1511	TAATCTTTCTT	0,32	1	3,13	0,32	Hs.151236	highly charged protein
1512	GATGGGGAAAT	0,32	1	3,13	0,32	Hs.14520	eukaryotic translation initiation factor 2C, 1
1513	ACTAAGTGCTA	0,32	1	3,13	0,32	Hs.132739	I-mfa domain-containing protein
1514	CGGTTATTTAA	0,32	1	3,13	0,32	Hs.119488	cystein-rich hydrophobic domain 2
1515	AGTGTGGGACT	0,32	1	3,13	0,32	Hs.118821	CGI-62 protein
1516	ATAGTTTAGCA	0,32	1	3,13	0,32	Hs.112157	ESTs
1517	CACCGAGACCA	0,32	1	3,13	0,32	Hs.107169	insulin-like growth factor, binding protein 5
1518	AAATGACAATA	0,32	1	3,13	0,32	Hs.104904	ESTs
1519	TGACCAGGCGC	0,32	1	3,13	0,32	Hs.1019	parathyroid hormone receptor 1
1520	GGGCATCTCTT	12,19	38	3,12	8,11	Hs.76807	major histocompatibility complex, class II, DR alpha
1521	GTGGCGGGAGC	1,93	6	3,11	1,62	Hs.68257	general transcription factor IIF, polypeptide 1 (74k
1522	GAGAAACCCCG	12,89	40	3,10	8,44	Hs.5486	clone FLB5214
1523	AAATGCGAACA	1,29	4	3,10	1,16	Hs.5672	ESTs, Weakly similar to Similarity to Yeast D-lactat
1524	ATCCACCTGCC	0,97	3	3,09	0,91	Hs.231656	EST
1525	GCCAGCTGACA	0,97	3	3,09	0,91	Hs.118913	ESTs
1526	AGAAAGAATCT	0,97	3	3,09	0,91	Hs.107979	small membrane protein 1
1527	TGCCCCTTGCC	0,97	3	3,09	0,91	Hs.105700	secreted frizzled-related protein 4
1528	GAGAAACCCTG	11,34	35	3,09	7,42	Hs.194359	ESTs, Weakly similar to ALUC_HUMAN !!!! ALU

							CLASS
5	1529	TTGCTGACTTT	11,75	36	3,06	7,54	Hs.108885 collagen, type VI, alpha 1
	1530	AGGCTGAGGCA	3,6	11	3,06	2,64	Hs.17834 downstream neighbor of SON
	1531	TCAGTGCATTC	1,64	5	3,05	1,37	Hs.235587 EST
	1532	CTTAAAAAAA	1,64	5	3,05	1,37	Hs.176626 hypothetical protein EDAG-1
10	1533	GTGAAAACCTG	2,96	9	3,04	2,22	Hs.283606 ESTs, Moderately similar to ALU5_HUMAN ALU
	1534	AGCCACCGTGC	10,2	31	3,04	6,52	Hs.240845 DKFZP434D146 protein
15	1535	GTGGCACATAC	1,99	6	3,02	1,57	Hs.205353 ectonucleoside triphosphate diphosphohydrolase 1
	1536	CCATTGTAATC	4,98	15	3,01	3,39	Hs.108740 DKFZP586A0522 protein
20	1537	TGCCTGTAATC	16,99	51	3,00	10,11	Hs.167135 Homo sapiens cDNA FLJ10728 fis, clone
	1538	TTAGCCAGGAT	6,33	19	3,00	4,15	Hs.211457 EST
	1539	TAGGGAATGAA	0	3	3,00	4,35	Hs.59545 ring finger protein 15
25	1540	AAAGCATTTCT	0	3	3,00	4,35	Hs.36688 ESTs, Moderately similar to WAP four-disulfide core
	1541	ATGACCCGCAG	0	3	3,00	4,35	Hs.286254 ESTs, Weakly similar to AF170723_1 protein kinase ST
30	1542	ATTTTTTTCAG	0	3	3,00	4,35	Hs.278004 EST
	1543	GCAAGCCATTT	0	3	3,00	4,35	Hs.272813 dual oxidase 1
	1544	GATTTTTTTTT	0	3	3,00	4,35	Hs.227913 API5-like 1
35	1545	TCTCTTGGGGT	0	3	3,00	4,35	Hs.16740 hypothetical protein FLJ11036
	1546	TGTGTGTAACA	0	3	3,00	4,35	Hs.156457 ESTs
	1547	CCTTTGTCTTT	1	3	3,00	0,88	Hs.99654 protein-O-mannosyltransferase 1
40	1548	AATTGTAGTTA	1	3	3,00	0,88	Hs.6809 RAP2A, member of RAS oncogene family
	1549	AGCCACTGTAC	1	3	3,00	0,88	Hs.55346 ESTs, Weakly similar to Z141_HUMAN ZINC FINGER
45	1550	CAAACCTCAAAA	1	3	3,00	0,88	Hs.279809 hypothetical protein PRO1741
	1551	GAGCACTTGGG	1	3	3,00	0,88	Hs.182937 peptidylprolyl isomerase A (cyclophilin A)
50	1552	AAGTTTTTAGT	1	3	3,00	0,88	Hs.149917 ESTs
	1553	TTTGAGGATTG	1	3	3,00	0,88	Hs.147916 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3
55	1554	TAGTTGGAAC	1	3	3,00	0,88	Hs.1119 nuclear receptor subfamily 4, group A, member 1
	1555	TTGACCAGGCT	4,34	13	3,00	2,98	Hs.285080 ESTs
	1556	CTTATTTGTTT	1,67	5	2,99	1,34	Hs.4114 plastin 3 (T isoform)
60	1557	AGCTTCCAGCC	1,67	5	2,99	1,34	Hs.144974 ESTs, Highly similar to unnamed protein product [H.s
	1558	CACCCCTCGC	0,67	2	2,99	0,61	Hs.91246 hypothetical protein

							DKFZp547O146
1559	TCTCCAGGACA	0,67	2	2,99	0,61	Hs.8025	Homo sapiens clone 23767 and 23782 mRNA sequences
1560	TATTTCAATTG	0,67	2	2,99	0,61	Hs.79507	KIAA0582 protein
1561	CAGGTTGAAGT	0,67	2	2,99	0,61	Hs.79219	RalGDS-like gene; KIAA0959 protein
1562	TATGTTAATGT	0,67	2	2,99	0,61	Hs.7341	ESTs, Weakly similar to DUS8_HUMAN DUAL
1563	GACTGCTCTGG	0,67	2	2,99	0,61	Hs.36475	ESTs
1564	GAAGAGTGCTC	0,67	2	2,99	0,61	Hs.32204	ESTs
1565	GAGCCAAAGAA	0,67	2	2,99	0,61	Hs.29423	ESTs, Weakly similar to macrophage lectin 2 [H.sapie
1566	CTTGTAATCTC	0,67	2	2,99	0,61	Hs.278002	EST
1567	TTACAATCACA	0,67	2	2,99	0,61	Hs.21276	ESTs
1568	GTGAAATCCAG	0,67	2	2,99	0,61	Hs.183275	ESTs
1569	CCTGTAATACC	3,02	9	2,98	2,17	Hs.92254	hypothetical protein FLJ20163
1570	AAAAGCAGAAA	1,35	4	2,96	1,11	Hs.84728	Kruppel-like factor 5 (intestinal)
1571	TTTGGGCCTAA	6,09	18	2,96	3,88	Hs.230320	EST
1572	CCTGTGGTCCC	17,64	52	2,95	10,04	Hs.249373	Homo sapiens clone FLB2543
1573	TAGCTCCCTTG	1,7	5	2,94	1,32	Hs.199160	myeloid/lymphoid or mixed-lineage leukemia (trithora
1574	GTGAGACCCTG	7,5	22	2,93	4,58	Hs.135756	polymerase (DNA-directed) kappa
1575	GCGAAACCCCG	22,18	65	2,93	12,25	Hs.30376	hypothetical protein
1576	CCACTGCATTC	12,98	38	2,93	7,45	Hs.270403	ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS
1577	GGGATCGCCCC	2,05	6	2,93	1,52	Hs.12865	p47
1578	TTCCAAGGCAG	3,08	9	2,92	2,13	Hs.317	topoisomerase (DNA) I
1579	ATGGTGGGTGC	3,08	9	2,92	2,13	Hs.209602	ESTs, Weakly similar to ubiquitous TPR motif, Y isof
1580	ATCTTGGCTCA	2,4	7	2,92	1,72	Hs.86958	interferon (alpha, beta and omega) receptor 2
1581	GTGAAACACCG	3,43	10	2,92	2,32	Hs.207766	EST
1582	CGTTCATTCAT	1,03	3	2,91	0,86	Hs.6139	synaptogyrin 1
1583	CCATAATGTTG	1,03	3	2,91	0,86	Hs.39957	pleckstrin 2 (mouse) homolog
1584	CTCTACGCATT	1,03	3	2,91	0,86	Hs.278573	H-2K binding factor-2
1585	ATGCAGAGGTG	1,03	3	2,91	0,86	Hs.210706	ESTs, Weakly similar to AF211175_1 unknown [H.sapien
1586	GCCAAACAGCAT	1,03	3	2,91	0,86	Hs.155606	paired mesoderm homeo box 1
1587	CCTGTAATCAC	2,75	8	2,91	1,92	Hs.266136	ESTs

1588	GGATATGTGGT	7,24	21	2,90	4,34	Hs.738	early growth response 1
1589	GCTCACACCTG	1,38	4	2,90	1,09	Hs.60617	sialyltransferase 4A (beta-galactosidase alpha-2,3-s
1590	CATACAGAAAA	1,38	4	2,90	1,09	Hs.3107	CD97 antigen
1591	TATCCCAGAAC	9,32	27	2,90	5,4	Hs.169286	crystallin, beta B2
1592	CGCCTGTAATC	11,4	33	2,89	6,46	Hs.235083	EST
1593	GTGGCACACAC	16,96	49	2,89	9,23	Hs.71475	hypothetical protein
1594	ATCATACCACT	2,08	6	2,88	1,5	Hs.224071	EST, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C
1595	GTGGCGTGCAC	6,59	19	2,88	3,94	Hs.228163	EST
1596	TTGCCCAGGCT	17,35	50	2,88	9,38	Hs.56027	Homo sapiens mRNA; cDNA DKFZp586J1717 (from
1597	CCGGTAATCCC	2,43	7	2,88	1,7	Hs.272813	dual oxidase 1
1598	AGCCACTGTGC	8,35	24	2,87	4,81	Hs.180606	EST
1599	GTGGTGCACAC	16,79	48	2,86	8,93	Hs.272173	ESTs, Weakly similar to ALU1_HUMAN ALU
1600	CCCACTCTTTG	1,05	3	2,86	0,84	Hs.9414	KIAA1488 protein
1601	CAAAATCTTGA	1,05	3	2,86	0,84	Hs.75431	fibrinogen, gamma polypeptide
1602	CCTGTAGACCC	1,05	3	2,86	0,84	Hs.5123	inorganic pyrophosphatase
1603	TCCTGGTTATT	1,05	3	2,86	0,84	Hs.4084	KIAA1025 protein
1604	TGCTAGATTGG	1,05	3	2,86	0,84	Hs.239663	myeloid/lymphoid or mixed-lineage leukemia (trithora
1605	AACCCGGGAGA	1,05	3	2,86	0,84	Hs.236241	EST
1606	TACTCGGTTGT	1,05	3	2,86	0,84	Hs.119394	ESTs
1607	GACGGGGTGGA	1,05	3	2,86	0,84	Hs.111279	hypothetical protein
1608	ATTTGTGTGTA	0,7	2	2,86	0,59	Hs.94499	ESTs
1609	GTTCCAAGCAA	0,7	2	2,86	0,59	Hs.94011	ESTs, Weakly similar to MAGE-B4 [H.sapiens]
1610	CTATCTGTGGA	0,7	2	2,86	0,59	Hs.9176	ESTs
1611	GGCCCAGAGCC	0,7	2	2,86	0,59	Hs.91246	hypothetical protein DKFZp547O146
1612	TTGATGCCCAG	0,7	2	2,86	0,59	Hs.8503	ESTs
1613	TATTGTTAAAA	0,7	2	2,86	0,59	Hs.7984	ESTs
1614	CAATCTTCAA	0,7	2	2,86	0,59	Hs.78909	butyrate response factor 2 (EGF-response factor 2)
1615	CTTCCTTGTGT	0,7	2	2,86	0,59	Hs.6298	KIAA1151 protein
1616	GACAGTGATAG	0,7	2	2,86	0,59	Hs.53913	hypothetical protein FLJ10252
1617	GGCCTCTGATG	0,7	2	2,86	0,59	Hs.46670	PRO1575 protein
1618	GCCTCCCCCAC	0,7	2	2,86	0,59	Hs.40109	KIAA0872 protein
1619	GGAGCAGACGC	0,7	2	2,86	0,59	Hs.31718	Homo sapiens cDNA FLJ11034 fis, clone PLA-CE1004258
1620	CTGCCCTCTGC	0,7	2	2,86	0,59	Hs.27801	zinc finger protein 278
1621	GGCTCTTCTGG	0,7	2	2,86	0,59	Hs.27721	hypothetical protein FLJ20353

1622	TTGCAATAGGT	0,7	2	2,86	0,59	Hs.25625	hypothetical protein FLJ11323
1623	TGATGATCATT	0,7	2	2,86	0,59	Hs.22394	hypothetical protein FLJ10893
1624	CCCAAACGGTA	0,7	2	2,86	0,59	Hs.195453	ribosomal protein S27 (metallopanstimulin 1)
1625	TTGGCCAAGAT	0,7	2	2,86	0,59	Hs.19522	hypothetical protein PRO2849
1626	TTTACCTGTTG	0,7	2	2,86	0,59	Hs.173381	dihydropyrimidinase-like 2
1627	TGTCAATGGGG	0,7	2	2,86	0,59	Hs.169055	golgi autoantigen, golgin subfamily a, 2
1628	CTTCCGGGTAA	0,7	2	2,86	0,59	Hs.108924	DKFZP586P1422 protein
1629	AAGGTTCTTCT	0,35	1	2,86	0,29	Hs.89695	insulin receptor
1630	TAATTTTAAAC	0,35	1	2,86	0,29	Hs.8861	ESTs
1631	TTAAATGCTCT	0,35	1	2,86	0,29	Hs.82501	similar to mouse Xrn1 / Dhms2 protein
1632	AGCTCCCAAGA	0,35	1	2,86	0,29	Hs.80475	polymerase (RNA) II (DNA directed) polypeptide J (13
1633	TGCTGCGGAAG	0,35	1	2,86	0,29	Hs.80306	Homo sapiens mRNA, clone:RES4-4
1634	GAGCAGTGCTG	0,35	1	2,86	0,29	Hs.7636	feline sarcoma (Snyder-Theilen) viral (v-fes)/Fujina
1635	CAAGGAAATGT	0,35	1	2,86	0,29	Hs.64840	ESTs
1636	GCAACACCGGA	0,35	1	2,86	0,29	Hs.63525	poly(rC)-binding protein 2
1637	GCCAAAGATGT	0,35	1	2,86	0,29	Hs.58636	squamous cell carcinoma antigen recognized by T cell
1638	GTTGCAGGCGC	0,35	1	2,86	0,29	Hs.5811	hypothetical protein FLJ20467
1639	TCTTTAAAAAA	0,35	1	2,86	0,29	Hs.55999	ESTs
1640	TGTGCTTCTAG	0,35	1	2,86	0,29	Hs.38613	ESTs
1641	TATCAAAAAAA	0,35	1	2,86	0,29	Hs.32491	ESTs
1642	TAATCCTAGT	0,35	1	2,86	0,29	Hs.31845	ESTs
1643	TGATATTAAAG	0,35	1	2,86	0,29	Hs.30661	electron-transferring-flavoprotein dehydrogenase
1644	AAACCAATTTT	0,35	1	2,86	0,29	Hs.30483	Homo sapiens mRNA; cDNA DKFZp434O1311 (from
1645	AAGAACTCAGG	0,35	1	2,86	0,29	Hs.30250	v-maf musculoaponeurotic fibrosarcoma (avian) oncogene
1646	CAGTCCCAAAA	0,35	1	2,86	0,29	Hs.29846	Human DNA sequence from clone 717M23 on
1647	AAACCGGTCCC	0,35	1	2,86	0,29	Hs.285490	ESTs, Weakly similar to unnamed protein product [H.s
1648	AACATTCCTAA	0,35	1	2,86	0,29	Hs.285429	ESTs
1649	TTAACATTTAT	0,35	1	2,86	0,29	Hs.279763	hypothetical protein FLJ10504
1650	ATGGCGTGTGC	0,35	1	2,86	0,29	Hs.278880	ESTs

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1651	GAGCTCTTCCT	0,35	1	2,86	0,29	Hs.274598	cytochrome P450, subfamily IID (debrisoquine, sparte
1652	GCAAGACCTTG	0,35	1	2,86	0,29	Hs.273603	ESTs
1653	AGGTTAAGAGA	0,35	1	2,86	0,29	Hs.272046	ESTs
1654	CCCGTAATCTC	0,35	1	2,86	0,29	Hs.270062	Homo sapiens mRNA; cDNA DKFZp586D0924 (from
1655	GCGGCACGCAC	0,35	1	2,86	0,29	Hs.269867	ESTs
1656	GACTTCAGCA	0,35	1	2,86	0,29	Hs.265168	ESTs, Moderately similar to T10_MOUSE SER/THR-
1657	GCTGTTCTAAG	0,35	1	2,86	0,29	Hs.24422	regulatory factor X-associated protein
1658	GCACTGAGAAG	0,35	1	2,86	0,29	Hs.239499	KIAA0185 protein
1659	GCGAGACCTTG	0,35	1	2,86	0,29	Hs.232157	ESTs
1660	TTGCATTCTCC	0,35	1	2,86	0,29	Hs.21379	ESTs
1661	TGCTTGTAGTC	0,35	1	2,86	0,29	Hs.209680	ESTs, Weakly similar to ALU1_HUMAN ALU
1662	AACGCAGCCTT	0,35	1	2,86	0,29	Hs.20060	KIAA0229 protein
1663	TAGGAAACCTG	0,35	1	2,86	0,29	Hs.200596	KIAA0547 gene product
1664	GGCTTTATTCT	0,35	1	2,86	0,29	Hs.200412	Homo sapiens mRNA; cDNA DKFZp434G0719 (from
1665	AATACTTCTCT	0,35	1	2,86	0,29	Hs.2003	T cell receptor beta locus
1666	GGTGACAGAGG	0,35	1	2,86	0,29	Hs.200235	ESTs
1667	AGAAAAAAAT	0,35	1	2,86	0,29	Hs.200057	ESTs, Weakly similar to ALU5_HUMAN ALU
1668	CATTGGCACTC	0,35	1	2,86	0,29	Hs.195614	splicing factor 3b, subunit 3, 130kD
1669	TTAATTAGCAA	0,35	1	2,86	0,29	Hs.183085	Homo sapiens mRNA; cDNA DKFZp434K098 (from clone
1670	CGCGTCAGAGC	0,35	1	2,86	0,29	Hs.182982	golgin-67
1671	AAACTCGCCG	0,35	1	2,86	0,29	Hs.17969	KIAA0663 gene product
1672	TGTACTTTCCT	0,35	1	2,86	0,29	Hs.179661	tubulin, beta polypeptide
1673	CAGACTGGGAG	0,35	1	2,86	0,29	Hs.1790	nuclear receptor subfamily 3, group C, member 2
1674	TTTCTGAAGGG	0,35	1	2,86	0,29	Hs.172910	ESTs, Highly similar to unnamed protein product [H.s
1675	TAAATAAGGAA	0,35	1	2,86	0,29	Hs.17235	ESTs
1676	GATGACAGAGT	0,35	1	2,86	0,29	Hs.171995	kallikrein 3, (prostate specific antigen)
1677	GTTACCGAGTG	0,35	1	2,86	0,29	Hs.171637	ESTs, Weakly similar to KIAA1317 protein [H.sapiens]
1678	GGTCAAATCAT	0,35	1	2,86	0,29	Hs.170162	KIAA1357 protein
1679	GCTTCACTTCC	0,35	1	2,86	0,29	Hs.164303	ESTs
1680	GACAATACACC	0,35	1	2,86	0,29	Hs.161554	hypothetical protein FLJ20159



1681	TTCCAAAAAAA	0,35	1	2,86	0,29	Hs.159971	SWI/SNF related, matrix associated, actin dependent	5
1682	TGTGACCCCTC	0,35	1	2,86	0,29	Hs.159237	hexokinase 3 (white cell)	
1683	TTTGTGCCATT	0,35	1	2,86	0,29	Hs.155507	ESTs	
1684	CCTTGCCCTAT	0,35	1	2,86	0,29	Hs.143746	ESTs	
1685	AGAACAAATAA	0,35	1	2,86	0,29	Hs.135721	ESTs	
1686	AGACTGTACTG	0,35	1	2,86	0,29	Hs.132348	ESTs, Weakly similar to diaphanous 1 [H.sapiens]	10
1687	CCATCCCAGTG	0,35	1	2,86	0,29	Hs.127863	ESTs	
1688	ACAGACTGTTA	0,35	1	2,86	0,29	Hs.125036	tumor endothelial marker 7 precursor	15
1689	GGCGACCCATT	0,35	1	2,86	0,29	Hs.12451	echinoderm microtubule-associated protein-like	
1690	CAGGTCCCATT	0,35	1	2,86	0,29	Hs.11924	ESTs, Weakly similar to ALU1_HUMAN ALU	20
1691	ACAAAGAAAAG	0,35	1	2,86	0,29	Hs.118578	Homo sapiens cDNA FLJ20053 fis, clone COL00809	
1692	ACTGATGCTCA	0,35	1	2,86	0,29	Hs.115467	ESTs	25
1693	TCCTCTTTCAA	0,35	1	2,86	0,29	Hs.113987	lectin, galactoside-binding, soluble, 2 (galectin 2)	
1694	AGGCAGCACTG	0,35	1	2,86	0,29	Hs.11112	ESTs	
1695	CTACTGCACTC	7,71	22	2,85	4,42	Hs.185989	ESTs	30
1696	CCCAGCTAATT	10,23	29	2,83	5,59	Hs.251235	EST	
1697	GTGGCACGCAC	7,79	22	2,82	4,35	Hs.228343	EST	
1698	GCAAATCCCA	3,19	9	2,82	2,04	Hs.268051	ESTs, Weakly similar to ALU2_HUMAN ALU	35
1699	GTGAAACCTTG	12,42	35	2,82	6,56	Hs.161554	hypothetical protein FLJ20159	
1700	ACTGTAATCCC	3,55	10	2,82	2,23	Hs.127809	ESTs	
1701	ATCGCACCCT	6,77	19	2,81	3,81	Hs.142569	ESTs	40
1702	GGGAAACCCCA	3,57	10	2,80	2,2	Hs.278281	ESTs, Weakly similar to alternatively spliced product	
1703	GTGAAACCCCT	9,64	27	2,80	5,16	Hs.229364	ESTs	45
1704	CAGCAGCAAAA	1,79	5	2,79	1,25	Hs.285090	ESTs	
1705	TAGAAGCCAAC	2,52	7	2,78	1,63	Hs.7905	SH3 and PX domain-containing protein SH3PX1	
1706	TTCTTTTTCTT	1,44	4	2,78	1,04	Hs.250722	(Manual assignment) MUG, Myeloid-upregulated protein	50
1707	CCTATAATCCT	1,44	4	2,78	1,04	Hs.158164	ATP-binding cassette, sub-family B (MDR/TAP), member	55
1708	TAAACGTGGCA	1,08	3	2,78	0,82	Hs.284146	hypothetical protein DKFZp762N0610	
1709	CAGAAGTCTTC	1,08	3	2,78	0,82	Hs.23921	ESTs, Weakly similar to ALU7_HUMAN ALU	60
1710	ACCAGCCAAAG	1,08	3	2,78	0,82	Hs.193090	ESTs, Highly similar to	

							AF161437_1 HSPC319 [H.sapien]
5	1711	GAAATGGGGAA	1,08	3	2,78	0,82	Hs.173933 Homo sapiens mRNA for KIAA1439 protein, partial cds
	1712	GTGTGGTATTC	1,08	3	2,78	0,82	Hs.172140 ESTs
	1713	CCGAGTTTTTG	1,08	3	2,78	0,82	Hs.139709 ESTs
10	1714	GGCAAACCTTA	1,08	3	2,78	0,82	Hs.102497 paxillin
	1715	CCACAGGGGAT	5,42	15	2,77	3,05	Hs.119571 collagen, type III, alpha 1 (Ehlers-Danlos syndrome
15	1716	CCTGTGGTCTC	2,17	6	2,76	1,44	Hs.236504 EST, Weakly similar to ALU6_HUMAN ALU SUB-FAMILY
	1717	CACCACCACGC	1,82	5	2,75	1,23	Hs.5862 hypothetical protein
	1718	GTGAAACCCGG	4,37	12	2,75	2,51	Hs.229170 ESTs
20	1719	GTGAAACCCTA	10,58	29	2,74	5,33	Hs.152081 ESTs
	1720	ATATGTATATT	1,46	4	2,74	1,02	Hs.75839 zinc finger protein 6 (CMPX1)
25	1721	GTGAAACCACA	1,46	4	2,74	1,02	Hs.283788 hypothetical protein DKFZp547A023
	1722	GGGATTAAAGC	1,46	4	2,74	1,02	Hs.211579 melanoma adhesion mole- cule
30	1723	TACCTTTGCTA	1,46	4	2,74	1,02	Hs.120980 nuclear receptor co- repressor 2
	1724	AATGAATGAAA	0,73	2	2,74	0,57	Hs.8986 complement component 1, q subcomponent, beta
35	1725	ATATTTTCATTC	0,73	2	2,74	0,57	Hs.79402 polymerase (RNA) II (DNA directed) polypeptide C (33
	1726	TGGAGGGGCGAG	0,73	2	2,74	0,57	Hs.7306 secreted frizzled-related protein 1
40	1727	TCGCGCAATAA	0,73	2	2,74	0,57	Hs.72249 protease-activated recep- tor 3
	1728	CTCAAAATCAA	0,73	2	2,74	0,57	Hs.72165 hypothetical protein FLJ20283
45	1729	TGTACATATGT	0,73	2	2,74	0,57	Hs.268384 homolog of yeast CDH1/HCT1
	1730	TGCAATGTTGT	0,73	2	2,74	0,57	Hs.171957 triple functional domain (PTPRF interacting)
50	1731	TCATTTTGTGA	0,73	2	2,74	0,57	Hs.154567 supervillin
	1732	TAAAACGTGAA	0,73	2	2,74	0,57	Hs.12592 period (Drosophila) ho- molog 3
55	1733	TCATCTGCAAA	0,73	2	2,74	0,57	Hs.105189 ESTs, Weakly similar to AF148856_2 unknown [H.sapien]
	1734	GGCAAATCTA	0,73	2	2,74	0,57	Hs.104627 Homo sapiens cDNA FLJ10158 fis, clone
60	1735	GACCTATCTCT	2,93	8	2,73	1,78	Hs.194431 palladin
	1736	GTGGTGCGTGCG	10,72	29	2,71	5,23	Hs.129727 X-ray repair complement- ing defective repair in China

1737	TCTTGAACAGC	1,11	3	2,70	0,8	Hs.72249	protease-activated recep- tor 3
1738	GGCTTTGGTCT	1,11	3	2,70	0,8	Hs.177592	ribosomal protein, large, P1
1739	CCACCACACCC	1,11	3	2,70	0,8	Hs.117582	CGI-43 protein
1740	ATGAAACCCCG	9,26	25	2,70	4,58	Hs.226396	hypothetical protein FLJ11126
1741	CCACTGCACTG	11,49	31	2,70	5,53	Hs.193220	ESTs
1742	CCACTGCGCTC	4,45	12	2,70	2,45	Hs.260287	ESTs, Weakly similar to ALU7 HUMAN ALU
1743	GAGAAACCCCA	11,13	30	2,70	5,36	Hs.5719	chromosome condensa- tion-related SMC- associated prote
1744	CCTGTAATCCT	23,38	63	2,69	10,5	Hs.165954	ESTs
1745	GACAGTCGGTG	1,49	4	2,68	1	Hs.8203	endomembrane protein emp70 precursor isolog
1746	TTTTCTCTGAA	1,49	4	2,68	1	Hs.75516	tyrosine kinase 2
1747	TTGGCTAGGCC	2,61	7	2,68	1,57	Hs.211539	eukaryotic translation initiation factor 2, subunit
1748	CCCTTGTC CGA	2,61	7	2,68	1,57	Hs.127824	ESTs, Weakly similar to weak similarity to colla- gens
1749	AGCCCAGGAGT	3,37	9	2,67	1,91	Hs.274813	EST
1750	GTGGTGTGCAC	6,45	17	2,64	3,18	Hs.20126	KIAA0317 gene product
1751	CCTGTGATCCT	1,9	5	2,63	1,17	Hs.240395	potassium channel, sub- family K, member 6 (TWIK-2)
1752	CCTGTAAACCC	1,9	5	2,63	1,17	Hs.161554	hypothetical protein FLJ20159
1753	TCAATAAAACC	1,52	4	2,63	0,98	Hs.151411	KIAA0916 protein
1754	ACGAAACCCCA	1,52	4	2,63	0,98	Hs.117582	CGI-43 protein
1755	TGACCACCCTT	1,14	3	2,63	0,78	Hs.42390	nasopharyngeal carcino- ma susceptibility protein
1756	CTCGAATAAAA	1,14	3	2,63	0,78	Hs.34871	KIAA0569 gene product
1757	CGACTGCACTC	1,14	3	2,63	0,78	Hs.182061	Novel human gene map- ping to chromosome 22
1758	CAGAATAATGT	1,14	3	2,63	0,78	Hs.125031	cho- line/ethanolaminephosphot ransferase
1759	CAGAAGGCCAC	0,76	2	2,63	0,55	Hs.8268	ESTs
1760	GAAAGAGCTCT	0,76	2	2,63	0,55	Hs.7337	hypothetical protein FLJ10936
1761	AAAATTATCTT	0,76	2	2,63	0,55	Hs.63657	hypothetical protein FLJ11005
1762	GGTGTCTGTGG	0,76	2	2,63	0,55	Hs.5889	ESTs, Weakly similar to AC004876_5 similar to predic
1763	AACTGAGAAGT	0,76	2	2,63	0,55	Hs.56406	ESTs, Highly similar to unnamed protein product [H.s
1764	TGAGTGGTTTG	0,76	2	2,63	0,55	Hs.29672	ESTs

5	1765	GAAGTTGCCTT	0,76	2	2,63	0,55	Hs.26777	KIAA0843 protein
	1766	TTGTTAAGCCT	0,76	2	2,63	0,55	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PLA- CE1007402
	1767	TATCTCAGAAC	0,76	2	2,63	0,55	Hs.223142	ESTs
	1768	GGTGAATTTTA	0,76	2	2,63	0,55	Hs.210866	EST
10	1769	TGAGCACATAA	0,76	2	2,63	0,55	Hs.194208	suc1-associated neurotro- phic factor target 2 (FGFR s
	1770	GTGCGTGCCTG	0,76	2	2,63	0,55	Hs.182354	ESTs
15	1771	ATTATCCAGCG	0,76	2	2,63	0,55	Hs.182225	RNA binding motif protein 3
	1772	TCTTCTTTCAG	0,76	2	2,63	0,55	Hs.17757	Homo sapiens mRNA; cDNA DKFZp434E1515 (from
20	1773	CTCTCCAAACC	0,76	2	2,63	0,55	Hs.151242	complement component 1 inhibitor (angioedema, heredi
	1774	CCATTGCTCTC	0,76	2	2,63	0,55	Hs.117582	CGI-43 protein
25	1775	AAGATCCTTGT	0,76	2	2,63	0,55	Hs.113503	karyopherin (importin) beta 3
	1776	GGAACCTGGCT	0,76	2	2,63	0,55	Hs.105613	ESTs
	1777	AGTTTGTCAAC	0,76	2	2,63	0,55	Hs.10130	ESTs
30	1778	TCCACAGTGGG	0,38	1	2,63	0,27	Hs.99636	ESTs, Weakly similar to I54197 hypothetical pro- tein
	1779	TACCCCTCTCA	0,38	1	2,63	0,27	Hs.994	phospholipase C, beta 2
35	1780	AAAGATGTACA	0,38	1	2,63	0,27	Hs.95243	transcription elongation factor A (SII)-like 1
	1781	ATTTATAATCC	0,38	1	2,63	0,27	Hs.914	major histocompatibility complex, class II, DP alpha
40	1782	ACTGTTTGTTT	0,38	1	2,63	0,27	Hs.814	major histocompatibility complex, class II, DP beta
	1783	TCGATGTGGCG	0,38	1	2,63	0,27	Hs.81248	CUG triplet repeat, RNA- binding protein 1
45	1784	TTAAGATCTTC	0,38	1	2,63	0,27	Hs.79404	neuron-specific protein
	1785	TTCTTGTGATA	0,38	1	2,63	0,27	Hs.79081	protein phosphatase 1, catalytic subunit, gamma isof
50	1786	AACAATTATCA	0,38	1	2,63	0,27	Hs.7845	Homo sapiens cDNA FLJ20820 fis, clone ADSE00490
	1787	AGAAACACTCA	0,38	1	2,63	0,27	Hs.75782	general transcription factor IIIC, polypeptide 2 (be
55	1788	AGAAATAAAAA	0,38	1	2,63	0,27	Hs.74649	cytochrome c oxidase subunit VIc
	1789	TAAGTGTGGTT	0,38	1	2,63	0,27	Hs.7327	claudin 1
60	1790	AGGAGAGAGCC	0,38	1	2,63	0,27	Hs.6932	Homo sapiens clone 23809 mRNA sequence
	1791	TGGACAAGTCA	0,38	1	2,63	0,27	Hs.64988	ESTs

1792	TTAAACTGCTG	0,38	1	2,63	0,27	Hs.6232	KIAA0764 gene product
1793	AGACCTCACTG	0,38	1	2,63	0,27	Hs.49763	ESTs
1794	TATTTGTATTT	0,38	1	2,63	0,27	Hs.4764	KIAA0763 gene product
1795	TGGATAGATTC	0,38	1	2,63	0,27	Hs.45519	ESTs
1796	TTGATTGATTT	0,38	1	2,63	0,27	Hs.42927	Homo sapiens cDNA FLJ11298 fis, clone PLACE1009794
1797	ACTATATTGTG	0,38	1	2,63	0,27	Hs.42532	ESTs
1798	GAGTCCGGCCT	0,38	1	2,63	0,27	Hs.4069	glucocorticoid modulatory element binding protein 1
1799	TATTTATTTTT	0,38	1	2,63	0,27	Hs.39143	ESTs, Weakly similar to predicted using Gene- finder [
1800	TGACATCCTGA	0,38	1	2,63	0,27	Hs.285056	ESTs
1801	CTGCAAGGACA	0,38	1	2,63	0,27	Hs.284135	Homo sapiens HSPC295 mRNA, partial cds
1802	ATCCCCCAGAA	0,38	1	2,63	0,27	Hs.278386	ESTs
1803	CCACTGCGCTT	0,38	1	2,63	0,27	Hs.252836	EST, Weakly similar to ALU1_HUMAN ALU SUB- FAMILY
1804	TGCCAGACCCT	0,38	1	2,63	0,27	Hs.249721	ESTs
1805	GGTGTGCACCT	0,38	1	2,63	0,27	Hs.24587	signal transduction protein (SH3 containing)
1806	CTTTTATTTTT	0,38	1	2,63	0,27	Hs.245710	heterogeneous nuclear ribonucleoprotein H1 (H)
1807	AGCGCTGGGGA	0,38	1	2,63	0,27	Hs.241471	RNB6
1808	CTAGGACCTGT	0,38	1	2,63	0,27	Hs.240112	KIAA0276 protein
1809	TAGTCCTAGCT	0,38	1	2,63	0,27	Hs.237372	EST
1810	ATTTAATTTTA	0,38	1	2,63	0,27	Hs.235883	ESTs
1811	GGCAACAAAGT	0,38	1	2,63	0,27	Hs.233364	ESTs
1812	CTGTAAGGATC	0,38	1	2,63	0,27	Hs.227730	integrin, alpha 6
1813	AGTCTTCCAGT	0,38	1	2,63	0,27	Hs.226213	cytochrome P450, 51 (lanosterol 14-alpha- demethylase
1814	GCTCCCCCTCC	0,38	1	2,63	0,27	Hs.2157	Wiskott-Aldrich syndrome (eczema- thrombocytopenia)
1815	AGTATTTATGA	0,38	1	2,63	0,27	Hs.203838	ESTs
1816	GCTAAACCCTG	0,38	1	2,63	0,27	Hs.202781	ESTs, Moderately similar to ALU5_HUMAN ALU
1817	CCAGCATTACC	0,38	1	2,63	0,27	Hs.20082	Homo sapiens zinc finger protein NY-REN-21 anti- gen m
1818	CCTGCAATCTC	0,38	1	2,63	0,27	Hs.197793	ESTs
1819	GAAAAATGCGC	0,38	1	2,63	0,27	Hs.193398	ESTs
1820	GCCAGGGCTCA	0,38	1	2,63	0,27	Hs.187913	ESTs, Moderately similar to MRP3 [H.sapiens]
1821	TAAAACTTACA	0,38	1	2,63	0,27	Hs.184075	ESTs
1822	ACCCTTTTTAT	0,38	1	2,63	0,27	Hs.183153	ADP-ribosylation factor 4- like
1823	GTTTCAAACGA	0,38	1	2,63	0,27	Hs.180535	ESTs, Weakly similar to

							S69890 mitogen inducible gen
5	1824	CAGTCTCAGTG	0,38	1	2,63	0,27	Hs.17767 Homo sapiens mRNA; cDNA DKFZp761N07121 (from c
	1825	AAAAATTCATC	0,38	1	2,63	0,27	Hs.170328 moesin
10	1826	TAAATAAACAA	0,38	1	2,63	0,27	Hs.16755 MBIP protein
	1827	CACCTCAAACA	0,38	1	2,63	0,27	Hs.157150 ESTs, Weakly similar to zinc finger protein 106 [M.m
15	1828	AATGTCCTCGG	0,38	1	2,63	0,27	Hs.155987 KIAA0645 gene product
	1829	TGTACCCCGCT	0,38	1	2,63	0,27	Hs.155975 protein tyrosine phosphatase, receptor type, C-assoc
20	1830	CGGGTTTGTGC	0,38	1	2,63	0,27	Hs.155482 hydroxyacyl glutathione hydrolase
	1831	GTCCATCTTAA	0,38	1	2,63	0,27	Hs.153177 ribosomal protein S28
	1832	TTTATTTTITAG	0,38	1	2,63	0,27	Hs.152250 ESTs
25	1833	CCTAAAAAAA	0,38	1	2,63	0,27	Hs.148907 Homo sapiens mRNA; cDNA DKFZp564G223 (from clone
	1834	TGATCGAGCTT	0,38	1	2,63	0,27	Hs.145867 ESTs
30	1835	GAAGATATTCC	0,38	1	2,63	0,27	Hs.14553 sterol O-acyltransferase (acyl-Coenzyme A: cholesterol
	1836	ATGGAGCTGCA	0,38	1	2,63	0,27	Hs.142779 ESTs
	1837	ATAAGACCTTA	0,38	1	2,63	0,27	Hs.142296 jerky (mouse) homolog
35	1838	CAAGCCAAAAA	0,38	1	2,63	0,27	Hs.14229 hypothetical protein FLJ10379
	1839	CAAATGGCAAA	0,38	1	2,63	0,27	Hs.134292 ESTs
40	1840	GAAGTTTAAAT	0,38	1	2,63	0,27	Hs.132463 phosphoinositide-3-kinase, class 2, beta polypeptide
	1841	GAAGGCAAGAT	0,38	1	2,63	0,27	Hs.1321 coagulation factor XII (Hageman factor)
	1842	TTAGTTATGAC	0,38	1	2,63	0,27	Hs.13063 transcription factor CA150
45	1843	CTGTATGTTTA	0,38	1	2,63	0,27	Hs.128777 ESTs
	1844	ACCTGCATTCC	0,38	1	2,63	0,27	Hs.125034 Homo sapiens cDNA FLJ10733 fis, clone
	1845	CCAGCTGCCTG	0,38	1	2,63	0,27	Hs.11782 ESTs
50	1846	AAAAGTGGTGT	0,38	1	2,63	0,27	Hs.117582 CGI-43 protein
	1847	TTTATCTGATA	0,38	1	2,63	0,27	Hs.117582 CGI-43 protein
	1848	TATTTTACCTA	0,38	1	2,63	0,27	Hs.114765 myeloid/lymphoid or mixed-lineage leukemia (trithora
55	1849	ACCTCCACACG	0,38	1	2,63	0,27	Hs.108947 KIAA0050 gene product
	1850	GATTGCTGTGC	0,38	1	2,63	0,27	Hs.100555 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 18 (Myc
60	1851	TGAAGCAGAAA	0,38	1	2,63	0,27	Hs.100407 Homo sapiens mRNA; cDNA DKFZp564H2416 (from

1852	ATTGTGCCACT	10,64	28	2,63	4,88	Hs.272324	Homo sapiens mRNA; cDNA DKFZp566G231 (from clone
1853	TCGGAGCTGTT	4,19	11	2,63	2,2	Hs.4055	chromosome 21 open reading frame 50
1854	GTGGTGTGCGC	3,43	9	2,62	1,87	Hs.278038	ESTs, Highly similar to PMM2_HUMAN
1855	TGCTACGAAAA	2,67	7	2,62	1,53	Hs.146550	myosin, heavy polypeptide 9, non-muscle
1856	CCTGGCCTAAA	2,67	7	2,62	1,53	Hs.111676	protein kinase H11; small stress protein-like protei
1857	TTCAGTGTGAG	21,42	56	2,61	8,99	Hs.621	lectin, galactoside-binding, soluble, 3 (galectin 3)
1858	CCCTACCCTGT	11,51	30	2,61	5,1	Hs.75736	apolipoprotein D
1859	GTGGCGTGCGC	2,31	6	2,60	1,34	Hs.117582	CGI-43 protein
1860	AGCCACCACAC	7,71	20	2,59	3,57	Hs.170310	cat eye syndrome chro- mosome region, candidate 1
1861	TCTACTAAAAA	1,93	5	2,59	1,15	Hs.48802	Homo sapiens clone 23632 mRNA sequence
1862	GCCGGGCACGG	1,93	5	2,59	1,15	Hs.271480	hypothetical protein FLJ20686
1863	GTGCTCAAACC	1,93	5	2,59	1,15	Hs.103915	KIAA0346 protein
1864	CCACTGCACTT	13,54	35	2,58	5,78	Hs.194300	ESTs
1865	GTGGCGGACGC	1,55	4	2,58	0,96	Hs.182577	inositol polyphosphate-5- phosphatase, 75kD
1866	CCACTGCCCTC	4,66	12	2,58	2,31	Hs.1010	regulator of mitotic spindle assembly 1
1867	GTGGCGTGTGC	11,69	30	2,57	4,99	Hs.278627	prenylcysteine lyase
1868	TCTGTAGTCCC	2,34	6	2,56	1,32	Hs.7358	Homo sapiens mRNA; cDNA DKFZp566D1146 (from
1869	CTAATTTAACT	1,17	3	2,56	0,76	Hs.9194	putative glioblastoma cell differentiation-related
1870	GTCTCAGTCAT	1,17	3	2,56	0,76	Hs.78943	bleomycin hydrolase
1871	GACAGTCACTC	1,17	3	2,56	0,76	Hs.6066	Rho guanine nucleotide exchange factor (GEF) 4
1872	CCTGTAGTCCA	1,17	3	2,56	0,76	Hs.277028	EST
1873	CAGAGTTGTAT	1,17	3	2,56	0,76	Hs.109144	ESTs
1874	GGCTGAGCTCA	1,96	5	2,55	1,13	Hs.83004	interleukin 14
1875	GCTTTCTCAAA	1,96	5	2,55	1,13	Hs.177153	EST
1876	CCTGTAGTCCT	7,85	20	2,55	3,48	Hs.179657	plasminogen activator, urokinase receptor
1877	GTGAAACACTG	3,14	8	2,55	1,65	Hs.145357	ESTs, Moderately similar to ALU7_HUMAN ALU
1878	GTGAAGCCCCA	5,13	13	2,53	2,41	Hs.171501	ubiquitin specific protease 11
1879	CCTGTATTCCC	3,16	8	2,53	1,63	Hs.249718	ESTs
1880	TTCAGTGCCTG	2,37	6	2,53	1,3	Hs.180933	CpG binding protein
1881	GGGAAACAGGT	1,58	4	2,53	0,94	Hs.18368	DKFZP564B0769 protein
1882	CCTTTTTTTTT	0,79	2	2,53	0,53	Hs.9956	hypothetical protein

							FLJ20259
	1883	GGGGCTTAGGA	0,79	2	2,53	0,53	Hs.89135 KIAA1528 protein
	1884	CTAGACAGTAA	0,79	2	2,53	0,53	Hs.52526 KIAA0669 gene product
5	1885	GTGTTCTGTGC	0,79	2	2,53	0,53	Hs.241567 RNA binding motif, single stranded interacting prote
	1886	TGCTGTAAAGG	0,79	2	2,53	0,53	Hs.23856 Homo sapiens HSPC091 mRNA, partial cds
10	1887	GAGGAGTGGGT	0,79	2	2,53	0,53	Hs.206770 zinc finger protein 297
	1888	GTAAGACCCTG	0,79	2	2,53	0,53	Hs.164177 ESTs
	1889	GGCCGTTAGAA	0,79	2	2,53	0,53	Hs.135 methylmalonate-semialdehyde dehydrogenase
15							
	1890	AGGCTAAAAGC	0,79	2	2,53	0,53	Hs.113029 ribosomal protein S25
	1891	CTGTGTAATTT	0,79	2	2,53	0,53	Hs.109731 ESTs
	1892	CTGAAGCGTGC	0,79	2	2,53	0,53	Hs.103391 Human insulin-like growth factor binding protein 5 (
20							
	1893	AGAACCTTCAA	3,57	9	2,52	1,78	Hs.181244 major histocompatibility complex, class I, A
	1894	TTCTGTGCTGG	6,36	16	2,52	2,84	Hs.1279 complement component 1, r subcomponent
25							
	1895	TTAGCTGAGTC	1,99	5	2,51	1,12	Hs.153028 cytochrome b-561
	1896	TTGGCCAGACT	3,6	9	2,50	1,76	Hs.91728 polymyositis/scleroderma autoantigen 1 (75kD)
30							
	1897	TTTCATTGCCT	3,6	9	2,50	1,76	Hs.173159 transforming, acidic coiled-coil containing protein
	1898	GTGGCCAGAGG	3,6	9	2,50	1,76	Hs.1420 fibroblast growth factor receptor 3 (achondroplasia,
35							
	1899	ACCGTTCTGTA	2,4	6	2,50	1,28	Hs.117582 CGI-43 protein
	1900	TAACTCCAAAG	1,2	3	2,50	0,74	Hs.24743 hypothetical protein FLJ20171
40							
	1901	TGCCGTAAATG	1,2	3	2,50	0,74	Hs.199067 v-erb-b2 avian erythroblastic leukemia viral oncogen
	1902	TGAACTTTCCT	1,2	3	2,50	0,74	Hs.17567 ESTs
	1903	TAAAGATCCTC	1,2	3	2,50	0,74	Hs.100407 Homo sapiens mRNA; cDNA DKFZp564H2416 (from
45							
	1904	GTGGCTCACAC	22,18	55	2,48	8,11	Hs.138411 Homo sapiens mRNA; cDNA DKFZp586J1922 (from
50							
	1905	GTGGTACACAC	2,02	5	2,48	1,1	Hs.250419 ESTs
	1906	GATCTCTTGGG	2,02	5	2,48	1,1	Hs.115947 keratin 16 (focal non-epidermolytic palmoplantar ker
55							
	1907	GAGGAACTCAA	2,87	7	2,44	1,4	Hs.5008 CGI-87 protein
	1908	AATAAAGCCTT	2,46	6	2,44	1,24	Hs.3314 selenoprotein P, plasma, 1
	1909	TTTACAAGTTA	1,64	4	2,44	0,91	Hs.91246 hypothetical protein DKFZp547O146
60							
	1910	AGGTCAAAAAA	1,64	4	2,44	0,91	Hs.149570 actin related protein 2/3 complex, subunit 4 (20 kD)
	1911	GAGCCCCCGTG	1,64	4	2,44	0,91	Hs.12908 CDC42-binding protein



							kinase beta (DMPK-like)	
1912	GAGTAGCTGAG	1,23	3	2,44	0,72	Hs.260039	sarcospan (Kras oncogene-associated gene)	
1913	GTGCTGCTCCA	0,82	2	2,44	0,52	Hs.7936	BAI1-associated protein 2	5
1914	GAGATTTGTTT	0,82	2	2,44	0,52	Hs.75452	heat shock 70kD protein 2	
1915	GAAGGGGTGCT	0,82	2	2,44	0,52	Hs.61950	DKFZp434A0131 protein	
1916	GCCACAGTACA	0,82	2	2,44	0,52	Hs.55044	DKFZP586H2123 protein	10
1917	TAATTTTTACT	0,82	2	2,44	0,52	Hs.52256	hypothetical protein FLJ20624	
1918	ACTGTTTGGCA	0,82	2	2,44	0,52	Hs.286110	translocase of inner mitochondrial membrane 9 (yeast)	15
1919	TCTGGCTAATT	0,82	2	2,44	0,52	Hs.262198	ESTs	
1920	GTGGAAACCCA	0,82	2	2,44	0,52	Hs.243818	ESTs, Moderately similar to ALU1_HUMAN ALU	
1921	TTGCCCAAGCT	0,82	2	2,44	0,52	Hs.213469	EST	20
1922	AAAACAGTGGC	0,82	2	2,44	0,52	Hs.184109	ribosomal protein L37a	
1923	TGATGTGATAG	0,82	2	2,44	0,52	Hs.181159	Homo sapiens mRNA; cDNA DKFZp434F0217 (from	25
1924	TTTGAACCCTT	0,82	2	2,44	0,52	Hs.16206	uncharacterized hypothalamus protein HT008	
1925	CCTATAATAAA	0,82	2	2,44	0,52	Hs.13885	ESTs, Weakly similar to T09A5.6 [C.elegans]	30
1926	AGAATCACTTA	0,82	2	2,44	0,52	Hs.130815	ESTs	
1927	TATTTTGCAA	0,82	2	2,44	0,52	Hs.11449	DKFZP564O123 protein	
1928	CCTATAACCCC	0,41	1	2,44	0,26	Hs.99410	ESTs	
1929	TCCAACACTAC	0,41	1	2,44	0,26	Hs.94581	sulfotransferase family, cytosolic, 2B, member 1	35
1930	TACCCAAAGAA	0,41	1	2,44	0,26	Hs.9436	ESTs, Weakly similar to NC5R_RAT NADH-5	
1931	TGTTTGTA AAA	0,41	1	2,44	0,26	Hs.9271	KIAA1071 protein	40
1932	TTTTTTTTTTC	0,41	1	2,44	0,26	Hs.90797	Homo sapiens clone 23620 mRNA sequence	
1933	TATCTCTGCAA	0,41	1	2,44	0,26	Hs.82985	collagen, type V, alpha 2	
1934	TTCTTCTGAAA	0,41	1	2,44	0,26	Hs.8087	NAG-5 protein	45
1935	CAGATGTTTAA	0,41	1	2,44	0,26	Hs.77631	glycine cleavage system protein H (aminomethyl carri	
1936	TTTGTAATATT	0,41	1	2,44	0,26	Hs.75546	capping protein (actin filament) muscle Z-line, alph	50
1937	ACCCAGTTGTT	0,41	1	2,44	0,26	Hs.75410	heat shock 70kD protein 5 (glucose-regulated protein	
1938	CTCATTGGTGG	0,41	1	2,44	0,26	Hs.6580	Homo sapiens clone 23718 mRNA sequence	55
1939	TCTTCTCACAA	0,41	1	2,44	0,26	Hs.656	cell division cycle 25C	
1940	CCTTTGTTCAA	0,41	1	2,44	0,26	Hs.6107	ESTs	
1941	TTAGAGATTCC	0,41	1	2,44	0,26	Hs.5947	mel transforming oncogene (derived from cell line NK	60

5	1942	TCCACACCAAA	0,41	1	2,44	0,26	Hs.53656	ESTs, Weakly similar to D29149 proline-rich protein
	1943	TGTAATGGTTT	0,41	1	2,44	0,26	Hs.4930	low density lipoprotein receptor-related protein 4
10	1944	GTACTTACCTT	0,41	1	2,44	0,26	Hs.3454	ESTs, Weakly similar to KIAA0665 protein [H.sapiens]
	1945	CTTAAATGGTT	0,41	1	2,44	0,26	Hs.29679	cofactor required for Sp1 transcriptional activation
15	1946	CTCCAACCTGA	0,41	1	2,44	0,26	Hs.285999	trinucleotide repeat containing 15
	1947	TTAGGCTTTAG	0,41	1	2,44	0,26	Hs.285698	hypothetical protein FLJ20392
	1948	GAAGATGTACG	0,41	1	2,44	0,26	Hs.285077	ESTs
20	1949	TGCCACCATAC	0,41	1	2,44	0,26	Hs.284138	ESTs
	1950	TGTCTGTAGTC	0,41	1	2,44	0,26	Hs.282837	ESTs
	1951	TAAAGTCCATT	0,41	1	2,44	0,26	Hs.278398	KIAA1117 protein
	1952	CCAACTGACTT	0,41	1	2,44	0,26	Hs.277543	KIAA0631 protein
25	1953	ATGGAATGCTA	0,41	1	2,44	0,26	Hs.268551	receptor-interacting serine-threonine kinase 3
	1954	TTGAAACCTCG	0,41	1	2,44	0,26	Hs.267148	ESTs
30	1955	TATATCATATT	0,41	1	2,44	0,26	Hs.266914	hypothetical protein FLJ10355
	1956	TGGCACGCTGC	0,41	1	2,44	0,26	Hs.250890	ESTs, Weakly similar to TOM1 [H.sapiens]
	1957	ACAGAGTCTCA	0,41	1	2,44	0,26	Hs.249031	EST
35	1958	GAAATATTGAT	0,41	1	2,44	0,26	Hs.247043	type 1 tumor necrosis factor receptor shedding amino
	1959	GTGAAACCTGA	0,41	1	2,44	0,26	Hs.242076	EST
40	1960	ATGTCAACCAA	0,41	1	2,44	0,26	Hs.241558	ariadne (Drosophila) homolog 2
	1961	GAAAAGGGCAC	0,41	1	2,44	0,26	Hs.23440	KIAA1105 protein
	1962	TGCAGTCTTTG	0,41	1	2,44	0,26	Hs.232111	ESTs
45	1963	CAGATTTCCAG	0,41	1	2,44	0,26	Hs.21893	ESTs, Weakly similar to AF121081_1 cAMP inducible 2
	1964	AAAAGGAAACC	0,41	1	2,44	0,26	Hs.21415	Homo sapiens mRNA; cDNA DKFZp761K2024 (from
50	1965	ATTGTAAGCTT	0,41	1	2,44	0,26	Hs.210232	ESTs
	1966	GTCTTAAATA	0,41	1	2,44	0,26	Hs.187991	DKFZP564A122 protein
55	1967	TCCGCAGGGAA	0,41	1	2,44	0,26	Hs.184592	Human clone A9A2BRB5 (CAC)n/(GTG)n repeat-
	1968	GCTGGAGCTCA	0,41	1	2,44	0,26	Hs.181315	ESTs, Moderately similar to ALU4_HUMAN ALU
60	1969	TGTTGTAAATA	0,41	1	2,44	0,26	Hs.171501	ubiquitin specific protease 11
	1970	GCTCCTACATT	0,41	1	2,44	0,26	Hs.169488	dentatorubral-pallidolusian atrophy

							(atrophin-1)
1971	CAGGTGCCAAA	0,41	1	2,44	0,26	Hs.168350	KIAA0554 protein
1972	TGCTGCTGCCC	0,41	1	2,44	0,26	Hs.167046	ESTs
1973	GCCTGGGCTGA	0,41	1	2,44	0,26	Hs.164476	hypothetical protein FLJ20626
1974	GTATGAGGTGG	0,41	1	2,44	0,26	Hs.164464	ESTs
1975	GTAAACAGAAA	0,41	1	2,44	0,26	Hs.161554	hypothetical protein FLJ20159
1976	TGAAATAAACT	0,41	1	2,44	0,26	Hs.155212	methylmalonyl Coenzyme A mutase
1977	TTTTGTCAACA	0,41	1	2,44	0,26	Hs.154645	ESTs, Weakly similar to tyrosine kinase [H.sapiens]
1978	GCACGTGTTCT	0,41	1	2,44	0,26	Hs.152096	cytochrome P450, subfam- ily IIJ (arachidonic acid epo
1979	TTAGTCCACAG	0,41	1	2,44	0,26	Hs.150390	zinc finger protein 262
1980	AAATTTCAAGC	0,41	1	2,44	0,26	Hs.146401	small inducible cytokine subfamily E, member 1 (endo
1981	CCCAGCTACTT	0,41	1	2,44	0,26	Hs.143961	ESTs, Moderately similar to ALU1_HUMAN ALU
1982	AAACCAGGAAA	0,41	1	2,44	0,26	Hs.139120	ribonuclease P (30kD)
1983	AATTTCAAGAA	0,41	1	2,44	0,26	Hs.119591	adaptor-related protein complex 2, sigma 1 sub- unit
1984	TACCCTAAAAT	0,41	1	2,44	0,26	Hs.117325	Homo sapiens cDNA FLJ11166 fis, clone PLACE1007242
1985	GGACTGTAGTG	0,41	1	2,44	0,26	Hs.11711	KIAA0329 gene product
1986	CTCCCGCCGGA	0,41	1	2,44	0,26	Hs.109445	KIAA1020 protein
1987	TGAAGTGCCCT	0,41	1	2,44	0,26	Hs.106932	ESTs
1988	GAAGAGGCTGG	0,41	1	2,44	0,26	Hs.105962	ESTs
1989	TTCCCTTCTTC	3,72	9	2,42	1,69	Hs.814	major histocompatibility complex, class II, DP beta
1990	AACCCGGAAGG	3,31	8	2,42	1,54	Hs.87497	butyrophilin, subfamily 3, member A2
1991	GTGGCGCGTGC	6,65	16	2,41	2,66	Hs.24135	hypothetical protein DKFZp761C241
1992	TACCCTAAAC	42,92	103	2,40	13,65	Hs.165662	KIAA0675 gene product
1993	CCTGTGATCCC	16,67	40	2,40	5,77	Hs.249982	cathepsin B
1994	CCGGCCCTACC	1,67	4	2,40	0,89	Hs.271473	epithelial protein up- regulated in carcinoma, membra
1995	GCACGCGTAAC	1,67	4	2,40	0,89	Hs.169552	ESTs, Weakly similar to BRDT [H.sapiens]
1996	AACAAGGTGAG	1,26	3	2,38	0,71	Hs.94952	ESTs, Highly similar to transcription elongation fac
1997	TGCGTCCCTCC	1,26	3	2,38	0,71	Hs.6179	DEAD/H (Asp-Glu-Ala- Asp/His) box polypeptide 17 (72k
1998	GACCCTTTTGG	1,26	3	2,38	0,71	Hs.272848	Homo sapiens mRNA;

							cDNA DKFZp434G1310 (from
5	1999	GATTTTCTGA	1,26	3	2,38	0,71	Hs.241567 RNA binding motif, single stranded interacting prote
	2000	TGATTCTGTTT	1,26	3	2,38	0,71	Hs.146428 collagen, type V, alpha 1
	2001	CCCGGCTAATT	5,89	14	2,38	2,35	Hs.102926 ESTs
10	2002	GTGAAGCCCTG	6,74	16	2,37	2,61	Hs.105407 ectodermal dysplasia 1, anhidrotic
	2003	ACTGAAAGAAG	2,11	5	2,37	1,05	Hs.169756 complement component 1, s subcomponent
	2004	CTGAGAGCTGG	5,95	14	2,35	2,31	Hs.78501 growth arrest-specific 6
15	2005	GTTCCAGCAGC	1,7	4	2,35	0,88	Hs.23918 Homo sapiens clone 25116 mRNA sequence
	2006	CCATTGCGCTC	1,7	4	2,35	0,88	Hs.204299 ESTs, Moderately similar to alternatively spliced pr
20	2007	GGATGCGCAGG	1,7	4	2,35	0,88	Hs.168541 Homo sapiens mRNA full length insert cDNA clone EURO
	2008	TTGGTGGAGGT	0,85	2	2,35	0,5	Hs.76294 CD63 antigen (melanoma 1 antigen)
25	2009	AGAATTATGGG	0,85	2	2,35	0,5	Hs.6975 PRO1073 protein
	2010	TGTGGTGGCAC	0,85	2	2,35	0,5	Hs.46624 HSPC043 protein
	2011	CAGTTCTTGAT	0,85	2	2,35	0,5	Hs.284217 serologically defined colon cancer antigen 33
30	2012	GCAAGACCCCG	0,85	2	2,35	0,5	Hs.262335 ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS
	2013	AAAACAAAACA	0,85	2	2,35	0,5	Hs.24734 oxysterol binding protein
35	2014	AAGACTGACAA	0,85	2	2,35	0,5	Hs.225951 topoisomerase-related function protein 4
	2015	TTCTCCTCTTT	0,85	2	2,35	0,5	Hs.22451 hypothetical protein FLJ10357
40	2016	TCAATCAGTGA	0,85	2	2,35	0,5	Hs.127270 ESTs
	2017	TGGGGTCCCA	0,85	2	2,35	0,5	Hs.123661 ESTs
	2018	CCATTGCACTG	4,69	11	2,35	1,9	Hs.142457 ESTs, Moderately similar to alternatively spliced pr
45	2019	AATAAATTCCT	5,98	14	2,34	2,3	Hs.76307 neuroblastoma, suppres- sion of tumorigenicity 1
	2020	GTGGCAGATGC	2,99	7	2,34	1,34	Hs.273539 ESTs, Weakly similar to ALU2 HUMAN ALU
50	2021	CCTGTTATCCC	2,99	7	2,34	1,34	Hs.228142 EST
	2022	GCGAAACTCCA	2,99	7	2,34	1,34	Hs.112860 KIAA1353 protein
	2023	GTGAAACCTCG	16,26	38	2,34	5,28	Hs.194408 KIAA1244 protein
	2024	GGCAGACACAT	1,29	3	2,33	0,69	Hs.33287 nuclear factor I/B
55	2025	AAAGAGAAGAG	1,29	3	2,33	0,69	Hs.22969 ESTs
	2026	ACAAAGCATTT	17,23	40	2,32	5,46	Hs.103391 Human insulin-like growth factor binding protein 5 (
	2027	TTTAGTGACGT	3,02	7	2,32	1,32	Hs.7104 Kruppel-like factor 13
60	2028	AGCCACCACGC	7,35	17	2,31	2,63	Hs.60772 ESTs
	2029	GCGAAACCTCG	3,46	8	2,31	1,46	Hs.210473 ESTs, Weakly similar to GELS_HUMAN GEL-

							SOLIN	
2030	GCAGTTGGATC	1,73	4	2,31	0,86	Hs.284932	Homo sapiens clone 24650 ubiquitin hydrolase mRNA, p	5
2031	CTTGTGAAGTG	1,73	4	2,31	0,86	Hs.283681	ESTs	
2032	GTGGCTCACGC	24,38	56	2,30	7,21	Hs.228230	EST	
2033	CAGCTATTTCA	4,39	10	2,28	1,69	Hs.153179	fatty acid binding protein 5 (psoriasis-associated)	10
2034	CACACACACAC	1,76	4	2,27	0,84	Hs.63984	cadherin 13, H-cadherin (heart)	
2035	CCACCACACTC	1,76	4	2,27	0,84	Hs.256696	EST, Weakly similar to ALU1_HUMAN ALU SUB-FAMILY	15
2036	CAAGGGTGACA	1,76	4	2,27	0,84	Hs.170222	solute carrier family 9 (sodium/hydrogen exchanger),	20
2037	GCAGCACTTAT	0,88	2	2,27	0,48	Hs.82035	GAP-like protein	
2038	CCTGACCTCAA	0,88	2	2,27	0,48	Hs.7874	muskelin 1, intracellular mediator containing kelch	
2039	GGGGTATGGTT	0,88	2	2,27	0,48	Hs.76144	platelet-derived growth factor receptor, beta polypeptide	25
2040	AGCAGCCGCTC	0,88	2	2,27	0,48	Hs.7104	Kruppel-like factor 13	
2041	CTCCTGGCCCA	0,88	2	2,27	0,48	Hs.5321	ARP3 (actin-related protein 3, yeast) homolog	30
2042	TTATGCCTCCA	0,88	2	2,27	0,48	Hs.43314	ESTs	
2043	TACTTCCTGCG	0,88	2	2,27	0,48	Hs.38039	ESTs	
2044	CCTTGCCAGG	0,88	2	2,27	0,48	Hs.3144	Cas-Br-M (murine) ecotropic retroviral transforming s	35
2045	GTAGGGTTCCT	0,88	2	2,27	0,48	Hs.278597	protein tyrosine phosphatase, non-receptor type 18 (	40
2046	ATAACCAAATG	0,88	2	2,27	0,48	Hs.25726	transposon-derived Buster1 transposase-like protein	
2047	CCTGTGAATAG	0,88	2	2,27	0,48	Hs.200647	EST	45
2048	TGACCAGGGTC	0,88	2	2,27	0,48	Hs.167827	Homo sapiens clone HH419 unknown mRNA	
2049	CAGACCCAAAA	0,88	2	2,27	0,48	Hs.167558	zinc finger protein 161	
2050	TTCTCATAATC	0,88	2	2,27	0,48	Hs.164919	ESTs, Highly similar to KPC2_HUMAN PROTEIN	50
2051	ACTGATGCAAG	0,88	2	2,27	0,48	Hs.161049	ESTs	
2052	AACTCTGATAT	0,88	2	2,27	0,48	Hs.151046	hypothetical protein FLJ11193	55
2053	GGGCATCTCCA	0,88	2	2,27	0,48	Hs.107000	ESTs	
2054	TGGATGTCTGT	0,44	1	2,27	0,24	Hs.96716	ESTs	
2055	TATTAGAAGCA	0,44	1	2,27	0,24	Hs.91065	hypothetical protein DKFZp761B2423	60
2056	CACTGAATATG	0,44	1	2,27	0,24	Hs.86948	small nuclear ribonucleo-	

							protein D1 polypeptide (16kD)
5	2057	AGTTAATAAAG	0,44	1	2,27	0,24	Hs.8065 Homo sapiens mRNA full length insert cDNA clone EURO
	2058	TTATATTTTCT	0,44	1	2,27	0,24	Hs.8021 KIAA1058 protein
10	2059	GTCACCAAACA	0,44	1	2,27	0,24	Hs.79283 selectin P ligand
	2060	TTACACTGTAA	0,44	1	2,27	0,24	Hs.78687 neutral sphingomyelinase (N-SMase) activation associ
15	2061	AAGTTGCATCT	0,44	1	2,27	0,24	Hs.74649 cytochrome c oxidase subunit VIc
	2062	TAGACATTTGA	0,44	1	2,27	0,24	Hs.74649 cytochrome c oxidase subunit VIc
	2063	TTCATAGGTAA	0,44	1	2,27	0,24	Hs.7312 ESTs
20	2064	CATTTTAGGCA	0,44	1	2,27	0,24	Hs.72782 hypothetical protein FLJ11171
	2065	ATACTATAATT	0,44	1	2,27	0,24	Hs.6966 Human DNA sequence from clone RP1-187J11 on
25	2066	CTTCGCTTTGT	0,44	1	2,27	0,24	Hs.69485 ESTs, Weakly similar to similar to other protein pho
	2067	ATGATATATGC	0,44	1	2,27	0,24	Hs.6831 Homo sapiens clone 1400 unknown protein mRNA, partia
30	2068	GCCCCCTTACA	0,44	1	2,27	0,24	Hs.49476 Homo sapiens clone TUA8 Cri-du-chat region mRNA
	2069	TCAGTCCCTGT	0,44	1	2,27	0,24	Hs.3685 hypothetical protein FLJ20209
35	2070	AATTTTCATTA	0,44	1	2,27	0,24	Hs.35092 ESTs
	2071	GCCAGTCCACT	0,44	1	2,27	0,24	Hs.34782 ESTs, Moderately similar to transducin [H.sapiens]
40	2072	TAGAGAGTTTA	0,44	1	2,27	0,24	Hs.29643 ESTs
	2073	GCTGTCCCCTC	0,44	1	2,27	0,24	Hs.278422 DKFZP586G1122 protein
	2074	GTGAAAGCCGT	0,44	1	2,27	0,24	Hs.270662 ESTs, Weakly similar to transformation-related prote
45	2075	TCTTCCAGAAA	0,44	1	2,27	0,24	Hs.256585 ESTs
	2076	TTGGCCGGGAT	0,44	1	2,27	0,24	Hs.254900 ESTs
	2077	GTAAAGAATGT	0,44	1	2,27	0,24	Hs.24790 ESTs
50	2078	AAATTTTGTGA	0,44	1	2,27	0,24	Hs.24650 ESTs, Moderately similar to AF133913_1 ARL-6 interac
	2079	AACGCTGCAAA	0,44	1	2,27	0,24	Hs.24174 KIAA0876 protein
55	2080	GTACCCTAAAA	0,44	1	2,27	0,24	Hs.239970 ESTs, Weakly similar to b3418.1 [H.sapiens]
	2081	TAATCTTTTTT	0,44	1	2,27	0,24	Hs.231463 EST
	2082	AAATTGTATGT	0,44	1	2,27	0,24	Hs.22826 tropomodulin 3 (ubiquitous)
60	2083	CCACTACATTC	0,44	1	2,27	0,24	Hs.22573 ESTs
	2084	GCCGCACTCAG	0,44	1	2,27	0,24	Hs.200577 ESTs
	2085	TCTTGTACATAC	0,44	1	2,27	0,24	Hs.198998 conserved helix-loop-helix

							ubiquitous kinase	
2086	CAGCACCTGAT	0,44	1	2,27	0,24	Hs.198281	pyruvate kinase, muscle	
2087	TTGAATAAAAG	0,44	1	2,27	0,24	Hs.198161	phospholipase A2, group IVB (cytosolic)	5
2088	GGAAGTGTGC	0,44	1	2,27	0,24	Hs.197733	ESTs, Weakly similar to TRP7_HUMAN TRANSIENT	
2089	CCTGGCCTACC	0,44	1	2,27	0,24	Hs.19585	KRAB-zinc finger protein SZF1-1	10
2090	TTTATTTTCAA	0,44	1	2,27	0,24	Hs.194293	ESTs	
2091	TCTCTCTGCCT	0,44	1	2,27	0,24	Hs.184987	ESTs	
2092	AGAGGAAGTAA	0,44	1	2,27	0,24	Hs.177537	ESTs, Weakly similar to ALU1_HUMAN ALU	15
2093	ACCAAAAAAAAA	0,44	1	2,27	0,24	Hs.173724	creatine kinase, brain	
2094	GGGACATTTAT	0,44	1	2,27	0,24	Hs.173108	Homo sapiens clone 24523 mRNA sequence	20
2095	TACCATCCATA	0,44	1	2,27	0,24	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	
2096	TTGATGAAGAA	0,44	1	2,27	0,24	Hs.168075	karyopherin (importin) beta 2	25
2097	GCCCGGTGCCC	0,44	1	2,27	0,24	Hs.1665	zinc finger protein homologous to Zfp-36 in mouse	
2098	AAGAACTGTTT	0,44	1	2,27	0,24	Hs.159456	zinc finger protein 288	30
2099	CCAGCAACTGT	0,44	1	2,27	0,24	Hs.145279	SET translocation (myeloid leukemia-associated)	
2100	ATGGTGCGTGC	0,44	1	2,27	0,24	Hs.140498	ESTs, Weakly similar to ALUE_HUMAN !!!! ALU CLASS	35
2101	CTCTTCAGGGT	0,44	1	2,27	0,24	Hs.13781	Homo sapiens cDNA FLJ11302 fis, clone PLACE1009971	40
2102	TCAATGTGAAA	0,44	1	2,27	0,24	Hs.13467	Homo sapiens BAC clone RP11-121A8 from 7p14-p13	
2103	CTTAATACTAC	0,44	1	2,27	0,24	Hs.13273	KIAA0592 protein	45
2104	GGCTGCAGTAT	0,44	1	2,27	0,24	Hs.129892	KIAA0522 protein	
2105	GGAAGCTGAAG	0,44	1	2,27	0,24	Hs.128629	ESTs	
2106	CCTCGGGCATC	0,44	1	2,27	0,24	Hs.126735	ESTs	
2107	TTTTCTTGCTG	0,44	1	2,27	0,24	Hs.120907	Homo sapiens mRNA; cDNA DKFZp547D135 (from clone	50
2108	GCCTTGCTCT	0,44	1	2,27	0,24	Hs.118837	ESTs	
2109	CTTTAAAAAAA	0,44	1	2,27	0,24	Hs.118162	fibronectin 1	
2110	TGCGGAAAAAA	0,44	1	2,27	0,24	Hs.113207	G protein-coupled receptor 30	55
2111	TGACTTTCTGC	0,44	1	2,27	0,24	Hs.11123	ESTs, Weakly similar to B38919 hypothetical protein	60
2112	CATTTACATAT	0,44	1	2,27	0,24	Hs.109438	Homo sapiens clone 24775 mRNA sequence	

2113	AATGTGTTACT	0,44	1	2,27	0,24	Hs.105751	Ste20-related serine/threonine kinase
2114	ATCTTTATTCC	0,44	1	2,27	0,24	Hs.10351	KIAA0308 protein
2115	TGTTTGAATTC	0,44	1	2,27	0,24	Hs.103422	Homo sapiens mRNA, cDNA DKFZp434F1622 (from
2116	ACAACACCCCA	2,2	5	2,27	1	Hs.21453	Homo sapiens mRNA for inositol 1,4,5-trisphosphate 3
2117	CTGGAAATAAA	1,32	3	2,27	0,67	Hs.69745	ferredoxin reductase
2118	TTATTTATGAA	1,32	3	2,27	0,67	Hs.245188	tissue inhibitor of metalloproteinase 3 (Sorsby fund
2119	TACCAAGGATT	1,32	3	2,27	0,67	Hs.21729	splicing factor 3a, subunit 1, 120kD
2120	GTGCCAAACAC	1,32	3	2,27	0,67	Hs.172216	chromogranin A (parathyroid secretory protein 1)
2121	CCCGGCCCAA	1,32	3	2,27	0,67	Hs.133207	PTPRF interacting protein, binding protein 1 (liprin
2122	AGAATTGCTTG	16,35	37	2,26	4,88	Hs.56542	X-prolyl aminopeptidase (aminopeptidase P) 1, solubl
2123	TCTCTGATGCT	15,06	34	2,26	4,52	Hs.6441	tissue inhibitor of metalloproteinase 2
2124	AACTGCACTC	3,11	7	2,25	1,27	Hs.200454	ESTs, Weakly similar to ALU1_HUMAN ALU
2125	GAAATGAGCAG	2,67	6	2,25	1,13	Hs.77293	KIAA0127 gene product
2126	GCTGGATGCGG	2,67	6	2,25	1,13	Hs.18075	chromosome 9 open reading frame 3
2127	GCAAAACCCTA	2,67	6	2,25	1,13	Hs.108740	DKFZP586A0522 protein
2128	TTTGCTCTCCC	6,68	15	2,25	2,28	Hs.75350	vinculin
2129	GGAGGCTGAGG	21,42	48	2,24	6,01	Hs.185973	membrane fatty acid (lipid) desaturase
2130	GTAAAACCCCA	9,38	21	2,24	2,98	Hs.18955	Homo sapiens cDNA FLJ20667 fis, clone KAIA596
2131	GGAGGGGGCTT	13,42	30	2,24	3,99	Hs.77886	lamin A/C
2132	AGCTAAGTTTG	1,79	4	2,23	0,83	Hs.19447	ESTs, Weakly similar to CL36_HUMAN LIM DOMAIN
2133	CACACAGTTTT	8,06	18	2,23	2,62	Hs.204354	ras homolog gene family, member B
2134	ATGGCGGGTGC	4,04	9	2,23	1,52	Hs.172382	hypothetical protein FLJ20001
2135	GACTTGTATAT	2,7	6	2,22	1,12	Hs.81328	nuclear factor of kappa light polypeptide gene enhan
2136	ATAGTACAGCC	1,35	3	2,22	0,66	Hs.6361	MEK partner 1
2137	AGCCACCGCTC	1,35	3	2,22	0,66	Hs.6195	ESTs
2138	GGCAGGATGAT	1,35	3	2,22	0,66	Hs.274319	hypothetical protein FLJ10509
2139	GCCTGGGACCT	1,35	3	2,22	0,66	Hs.180871	protein kinase C, alpha



							binding protein	
2140	ACAGCCGTGGG	1,35	3	2,22	0,66	Hs.123090	SWI/SNF related, matrix associated, actin dependent	5
2141	AGCCGAGATCA	2,26	5	2,21	0,97	Hs.277663	EST, Weakly similar to ALU1_HUMAN ALU SUB-FAMILY	
2142	AGCCTTTGTTG	11,78	26	2,21	3,47	Hs.9930	collagen-binding protein 2 (colligen 2)	10
2143	GTGTGCCTCCA	2,72	6	2,21	1,1	Hs.75254	interferon regulatory factor 3	
2144	TGGAGAAGAGC	3,63	8	2,20	1,37	Hs.179526	upregulated by 1,25-dihydroxyvitamin D-3	15
2145	GGCCCCATTGC	1,82	4	2,20	0,81	Hs.173421	Human clone CE29 8.1 (CAC)n/(GTG)n repeat-containing	20
2146	AATATTCATAG	0,91	2	2,20	0,47	Hs.8583	similar to APOBEC1	
2147	GCTCCGTAAGG	0,91	2	2,20	0,47	Hs.80712	KIAA0202 protein	
2148	GAGGTGCCCA	0,91	2	2,20	0,47	Hs.77955	ESTs	
2149	AGTGTATTTT	0,91	2	2,20	0,47	Hs.76473	insulin-like growth factor 2 receptor	25
2150	TAAACCTAAAG	0,91	2	2,20	0,47	Hs.60548	hypothetical protein PRO1635	
2151	AGTCAAGCCCC	0,91	2	2,20	0,47	Hs.57687	four and a half LIM domains 3	30
2152	TATCAAAACAT	0,91	2	2,20	0,47	Hs.258939	EST	
2153	ATCCTACTGTT	0,91	2	2,20	0,47	Hs.239218	uncharacterized hypothalamus protein HCDASE	35
2154	GCACCAAATGA	0,91	2	2,20	0,47	Hs.23585	KIAA1078 protein	
2155	CCAATGCTATG	0,91	2	2,20	0,47	Hs.22753	Homo sapiens mRNA; cDNA DKFZp434K0926 (from	40
2156	CATCGTTACAT	0,91	2	2,20	0,47	Hs.173802	KIAA0603 gene product	
2157	TAACCAAAAAC	0,91	2	2,20	0,47	Hs.169241	ELK4, ETS-domain protein (SRF accessory protein 1)	45
2158	CTGAAACCCCA	0,91	2	2,20	0,47	Hs.162132	ESTs	
2159	GGAAGGCAAGC	0,91	2	2,20	0,47	Hs.144998	ESTs, Weakly similar to ALU7_HUMAN ALU	
2160	GAAAGGTGGTT	0,91	2	2,20	0,47	Hs.14394	hypothetical protein FLJ20157	50
2161	TCATAACCTTG	0,91	2	2,20	0,47	Hs.124029	inositol polyphosphate-5-phosphatase, 40kD	
2162	TACCCCATAAA	2,29	5	2,18	0,96	Hs.281083	ESTs	
2163	CGCCCCCTGCG	2,75	6	2,18	1,09	Hs.135805	ESTs, Weakly similar to KIAA1323 protein [H.sapiens]	55
2164	ACAAAGCCCCA	1,38	3	2,17	0,65	Hs.8583	similar to APOBEC1	
2165	CCTATAGTCCT	1,38	3	2,17	0,65	Hs.41694	origin recognition complex, subunit 2 (yeast homolog	60
2166	CCAGTACAGCC	1,38	3	2,17	0,65	Hs.140978	Homo sapiens mRNA; cDNA DKFZp762H106	

							(from clone
	2167	CTGCTGCTGGT	1,38	3	2,17	0,65	Hs.12289 Cdc42 effector protein 2
5	2168	CTTAATCTTGT	1,85	4	2,16	0,8	Hs.75462 BTG family, member 2
	2169	GCCACACCCCC	1,85	4	2,16	0,8	Hs.113916 Burkitt lymphoma receptor 1, GTP-binding protein
	2170	TCCTCCCTACT	6,48	14	2,16	2,04	Hs.70266 yeast Sec31p homolog
10	2171	GTGAGACCCCA	5,57	12	2,15	1,8	Hs.198671 ESTs
	2172	CAGATGCAAAA	5,13	11	2,14	1,68	Hs.89506 paired box gene 6 (aniridia, keratitis)
	2173	CCCCAGGAGAA	2,34	5	2,14	0,93	Hs.169902 solute carrier family 2 (facilitated glucose transpo
15	2174	CTTCTGGGGAC	2,81	6	2,14	1,06	Hs.75082 ras homolog gene family, member G (rho G)
	2175	GTGGCTTACAC	1,88	4	2,13	0,79	Hs.264482 Homo sapiens mRNA; cDNA DKFZp761A0411 (from
20	2176	GCGAGACCCCA	1,88	4	2,13	0,79	Hs.15681 ESTs
	2177	TAAACTATTGG	1,41	3	2,13	0,63	Hs.78851 KIAA0217 protein
25	2178	GACGGCTGCAA	1,41	3	2,13	0,63	Hs.4909 dickkopf (Xenopus laevis) homolog 3
	2179	GTGAAACCGTC	1,41	3	2,13	0,63	Hs.30596 Homo sapiens mRNA full length insert cDNA clone EURO
30	2180	CCACTGGACTC	1,41	3	2,13	0,63	Hs.253913 ESTs, Weakly similar to ALU1_HUMAN ALU
	2181	TGTTAGCAAAT	1,41	3	2,13	0,63	Hs.22666 ESTs
	2182	AAGTACGAGGA	1,41	3	2,13	0,63	Hs.22660 ESTs
35	2183	CTGTTGGAAAA	1,41	3	2,13	0,63	Hs.209863 ESTs
	2184	AACCACTGTGC	1,41	3	2,13	0,63	Hs.188037 ESTs, Moderately similar to ALU7_HUMAN ALU
	2185	CTTCTCCAAAA	0,94	2	2,13	0,46	Hs.99949 prolactin-induced protein
40	2186	GTGGTCAAGTT	0,94	2	2,13	0,46	Hs.92127 ESTs
	2187	CCTTTGCTGAG	0,94	2	2,13	0,46	Hs.7442 Human DNA sequence from clone 742C19 on
45	2188	TTGCTGCCAGC	0,94	2	2,13	0,46	Hs.5566 gap junction protein, beta 2, 26kD (connexin 26)
	2189	TGAATTCCTG	0,94	2	2,13	0,46	Hs.30057 Homo sapiens clone 24749 and 24750 mRNA sequences
50	2190	GTGGTATATGC	0,94	2	2,13	0,46	Hs.279893 hypothetical protein FLJ20342
	2191	GTGGTGCACTC	0,94	2	2,13	0,46	Hs.268573 Homo sapiens mRNA; cDNA DKFZp762N226 (from clone
55	2192	GTGGCACAAGC	0,94	2	2,13	0,46	Hs.258487 EST
	2193	AGCCACCATAC	0,94	2	2,13	0,46	Hs.236051 EST
	2194	TAAACCGTTT	0,94	2	2,13	0,46	Hs.182280 MADS box transcription enhancer factor 2, poly-peptid
60	2195	CCTTGTTTAAC	0,94	2	2,13	0,46	Hs.173965 ribosomal protein S6 kinase, 90kD, polypeptide

						3	
2196	GCTCACTGCAA	0,94	2	2,13	0,46	Hs.163385	EST
2197	TGCCTTGGGCT	0,94	2	2,13	0,46	Hs.1497	retinoic acid receptor, gamma
2198	TTATTGTTCCC	0,94	2	2,13	0,46	Hs.12126	hepatocellular carcinoma- associated antigen 112
2199	GGGACAACCCA	0,94	2	2,13	0,46	Hs.11530	ESTs
2200	TTTTCTTACTG	0,94	2	2,13	0,46	Hs.106204	KIAA1327 protein
2201	TTTTGCTTTTT	0,94	2	2,13	0,46	Hs.102267	lysyl oxidase
2202	ATTTTCATCAA	0,94	2	2,13	0,46	Hs.101282	Homo sapiens mRNA; cDNA DKFZp434B102 (from clone)
2203	TACAGAATGTG	0,47	1	2,13	0,23	Hs.99196	ESTs
2204	TTGTATTGTTG	0,47	1	2,13	0,23	Hs.98445	ESTs
2205	GGGCAGAAGGC	0,47	1	2,13	0,23	Hs.9585	ESTs
2206	TATTGGCCTGG	0,47	1	2,13	0,23	Hs.79572	cathepsin D (lysosomal aspartyl protease)
2207	TGACTGTAAAA	0,47	1	2,13	0,23	Hs.75621	protease inhibitor 1 (anti- elastase), alpha-1-antitr
2208	ACCTGCTTCCC	0,47	1	2,13	0,23	Hs.75458	ribosomal protein L18
2209	TGATACAGAAA	0,47	1	2,13	0,23	Hs.69504	ESTs
2210	AATGAATTCTT	0,47	1	2,13	0,23	Hs.5613	Homo sapiens mRNA; cDNA DKFZp564E2222 (from
2211	ATTTTGTCACT	0,47	1	2,13	0,23	Hs.5459	KIAA1436 protein
2212	CACCCTTACT	0,47	1	2,13	0,23	Hs.5437	Tax1 (human T-cell leu- kemia virus type I) binding pr
2213	CTGGTGCGCCA	0,47	1	2,13	0,23	Hs.5338	carbonic anhydrase XII
2214	CTTTGAAATAG	0,47	1	2,13	0,23	Hs.50476	ESTs
2215	AGTCCTGCTTC	0,47	1	2,13	0,23	Hs.44565	ESTs
2216	TAACATTGAGA	0,47	1	2,13	0,23	Hs.43756	ESTs
2217	CTGAGAAGCGG	0,47	1	2,13	0,23	Hs.41055	ESTs, Highly similar to RL2A_HUMAN 60S RI- BOSOMAL
2218	TATATATAGAG	0,47	1	2,13	0,23	Hs.34853	inhibitor of DNA binding 4, dominant negative helix-
2219	GTCTGCTCCAG	0,47	1	2,13	0,23	Hs.32978	proprotein convertase subtilisin/kexin type 7
2220	CCCCCGAGGCT	0,47	1	2,13	0,23	Hs.31019	ESTs
2221	AATGAAAAATT	0,47	1	2,13	0,23	Hs.30888	cytochrome c oxidase subunit VIIa polypeptide 2 like
2222	TTGTACTAAT	0,47	1	2,13	0,23	Hs.29846	Human DNA sequence from clone 717M23 on
2223	TTCCATTATCA	0,47	1	2,13	0,23	Hs.29356	ESTs
2224	GTTTAAAAAGC	0,47	1	2,13	0,23	Hs.29032	ESTs
2225	CAATTTAAAGT	0,47	1	2,13	0,23	Hs.286249	ESTs
2226	TGTATTTGTAA	0,47	1	2,13	0,23	Hs.286056	ESTs
2227	GTGGCGTGCCT	0,47	1	2,13	0,23	Hs.282652	EST
2228	TAAAATGTGAC	0,47	1	2,13	0,23	Hs.268447	ESTs, Weakly similar to

							ALU8 HUMAN ALU
5	2229	AACAATAAAAA	0,47	1	2,13	0,23	Hs.268135 ESTs, Weakly similar to ALU4 HUMAN ALU
	2230	GAAACACGTAG	0,47	1	2,13	0,23	Hs.26407 ESTs
	2231	ACTTTAACAGG	0,47	1	2,13	0,23	Hs.252387 cadherin EGF LAG seven-pass G-type receptor 1
10	2232	AGCCCCACAAA	0,47	1	2,13	0,23	Hs.250570 ESTs
	2233	TGGTGAGATGA	0,47	1	2,13	0,23	Hs.224829 ESTs
	2234	GGCACCGCGTG	0,47	1	2,13	0,23	Hs.20677 KIAA1303 protein
15	2235	CAAGGATAAGA	0,47	1	2,13	0,23	Hs.2001 thromboxane A synthase 1 (platelet, cytochrome P450,
	2236	CGCCCCGGCGG	0,47	1	2,13	0,23	Hs.196244 ESTs
	2237	GAAGAGAAGGT	0,47	1	2,13	0,23	Hs.180455 RAD23 (S. cerevisiae) homolog A
20	2238	CAGATTTTGTG	0,47	1	2,13	0,23	Hs.177656 calmodulin 1 (phosphorylase kinase, delta)
	2239	ATTAGTTACAA	0,47	1	2,13	0,23	Hs.177635 KIAA1095 protein
	2240	CCCACCACATT	0,47	1	2,13	0,23	Hs.170610 ESTs
25	2241	CTGCTAACCCA	0,47	1	2,13	0,23	Hs.170310 cat eye syndrome chromosome region, candidate 1
	2242	GTTCTCTGCTT	0,47	1	2,13	0,23	Hs.169078 Human clone A9A2BRB6 (CAC)n/(GTG)n repeat-
30	2243	TATGTACAGTT	0,47	1	2,13	0,23	Hs.163001 hypothetical protein PRO0907
	2244	AACCCGGGAGT	0,47	1	2,13	0,23	Hs.161974 EST
35	2245	GTAACCTCAAA	0,47	1	2,13	0,23	Hs.161930 EST
	2246	TTCAATTCTT	0,47	1	2,13	0,23	Hs.159971 SWI/SNF related, matrix associated, actin dependent
40	2247	AGCTAAAAAAA	0,47	1	2,13	0,23	Hs.15953 hypothetical protein FLJ10120
	2248	TTATTTAAAG	0,47	1	2,13	0,23	Hs.158135 KIAA0981 protein
45	2249	GACTCCACATT	0,47	1	2,13	0,23	Hs.156637 Cas-Br-M (murine) ec-tropic retroviral transform-ing s
	2250	AGACAAAATTA	0,47	1	2,13	0,23	Hs.153487 signal transducing adaptor molecule (SH3 domain and
50	2251	ACTGAGAAGAG	0,47	1	2,13	0,23	Hs.130761 ESTs, Moderately similar to AF151803_1 CGI-45 protei
	2252	GGTGCTGAATA	0,47	1	2,13	0,23	Hs.12489 ESTs
55	2253	GATTTCTTTGA	0,47	1	2,13	0,23	Hs.119651 glypican 3
	2254	TGTCAAAGAG	0,47	1	2,13	0,23	Hs.118578 Homo sapiens cDNA FLJ20053 fis, clone COL00809
60	2255	ACGGGGAGAGT	0,47	1	2,13	0,23	Hs.117582 CGI-43 protein
	2256	TGGCTTTATCC	0,47	1	2,13	0,23	Hs.11506 Human clone 23589 mRNA sequenc

2257	GTTGCGTGTC	0,47	1	2,13	0,23	Hs.108300	NOT3 (negative regulator of transcription 3, yeast)	
2258	TAAACGGCCTC	0,47	1	2,13	0,23	Hs.10632	hypothetical protein DKFZp762M136	5
2259	GGCCAGAATGA	0,47	1	2,13	0,23	Hs.102708	DKFZP434A043 protein	
2260	TGAAGCAAAAA	0,47	1	2,13	0,23	Hs.100407	Homo sapiens mRNA; cDNA DKFZp564H2416 (from	10
2261	TCACAGCTGTG	8,94	19	2,13	2,52	Hs.77054	B-cell translocation gene 1, anti-proliferative	
2262	AGAAAAAAAAA	32,99	70	2,12	7,56	Hs.251680	(Manual assignment) not unique, contains loridin	15
2263	GTGGCGCACGC	5,19	11	2,12	1,65	Hs.135723	glycolipid transfer protein	
2264	TCTGTACACCT	8,97	19	2,12	2,51	Hs.182740	ribosomal protein S11	
2265	AGGGAGGGGCC	2,84	6	2,11	1,05	Hs.172153	glutathione peroxidase 3 (plasma)	20
2266	AGGACACCGCC	2,37	5	2,11	0,91	Hs.77793	c-src tyrosine kinase	
2267	CGAGGGCACTC	2,37	5	2,11	0,91	Hs.26915	spectrin, beta, non-erythrocytic 2	
2268	TGCTGCCAGAC	1,9	4	2,11	0,77	Hs.79219	RalGDS-like gene; KIAA0959 protein	25
2269	TACTGGTTTAT	1,9	4	2,11	0,77	Hs.30299	IGF-II mRNA-binding protein 2	
2270	CCCCCACCTAA	7,18	15	2,09	2,04	Hs.77422	proteolipid protein 2 (colonic epithelium-enriched)	30
2271	TGAATGATACG	1,93	4	2,07	0,76	Hs.278614	protease, serine, 15	
2272	TGAAACTGCAA	1,93	4	2,07	0,76	Hs.147189	HYA22 protein	
2273	TGAGTCTGGCT	4,83	10	2,07	1,48	Hs.4055	chromosome 21 open reading frame 50	35
2274	GGAGTGTGCTC	14,06	29	2,06	3,36	Hs.9615	myosin regulatory light chain 2, smooth muscle isofo	
2275	TCATCGGGCTG	0,97	2	2,06	0,44	Hs.78335	microtubule-associated protein, RP/EB family, member	40
2276	GAGACCTTGGA	0,97	2	2,06	0,44	Hs.72249	protease-activated receptor 3	45
2277	CACTGGACGAG	0,97	2	2,06	0,44	Hs.71574	ESTs	
2278	TGTACTTATTA	0,97	2	2,06	0,44	Hs.6906	v-ral simian leukemia viral oncogene homolog A (ras	
2279	ACCACCCTGTT	0,97	2	2,06	0,44	Hs.4864	KIAA0892 protein	50
2280	ATTCTCATTC	0,97	2	2,06	0,44	Hs.36794	D-type cyclin-interacting protein 1	
2281	GGACATTTTTC	0,97	2	2,06	0,44	Hs.16986	hypothetical protein FLJ11046	55
2282	CATCTTAAATG	0,97	2	2,06	0,44	Hs.15467	hypothetical protein FLJ20725	
2283	GAATCATTTAT	0,97	2	2,06	0,44	Hs.154668	KIAA0391 gene product	
2284	ATCAAATGCAA	4,37	9	2,06	1,36	Hs.79070	v-myc avian myelocytomatosis viral oncogene homolog	60

2285	AGCACCAGAAC	1,46	3	2,05	0,61	Hs.60103	KIAA0690 protein
2286	TCCTGACCACC	1,46	3	2,05	0,61	Hs.26002	LIM domain binding 1
2287	CTTATAATCCC	1,46	3	2,05	0,61	Hs.259541	ESTs
2288	ACCCATCGCCT	1,46	3	2,05	0,61	Hs.165428	ESTs
2289	CCATTGCACTA	1,46	3	2,05	0,61	Hs.115140	ESTs, Weakly similar to ALU1 HUMAN ALU
2290	TACCCCAGAAC	4,39	9	2,05	1,35	Hs.145320	ESTs
2291	CTCTCACCCTG	8,79	18	2,05	2,27	Hs.75108	ribonuclease/angiogenin inhibitor
2292	CAAGGGCTTGC	7,35	15	2,04	1,96	Hs.156764	RAP1B, member of RAS oncogene family
2293	TTTGCACCTTG	3,43	7	2,04	1,12	Hs.75188	wee1+ (S. pombe) homolog
2294	GCCAGGAGCTA	3,43	7	2,04	1,12	Hs.18141	ladinin 1
2295	TAAATACTCC	1,96	4	2,04	0,75	Hs.8125	Homo sapiens mRNA; cDNA DKFZp586E1521 (from
2296	TGATTGATTTG	1,96	4	2,04	0,75	Hs.5912	F-box only protein 7
2297	TAAAACTTTC	1,96	4	2,04	0,75	Hs.204096	lipophilin B (uteroglobin family member), prostatein
2298	TCACTGCACTC	7,85	16	2,04	2,06	Hs.261038	ESTs
2299	ACCAAAGCCCC	4,95	10	2,02	1,43	Hs.284281	Human putative ribosomal protein S1 mRNA
2300	AATAGGGTCAA	3,96	8	2,02	1,22	Hs.64797	amyloid beta (A4) precursor-like protein 2
2301	CCTATAGTCCC	5,45	11	2,02	1,53	Hs.140697	ESTs, Weakly similar to unnamed protein product [H.s
2302	CCTCCCTGCTC	1,49	3	2,01	0,59	Hs.90790	ESTs
2303	ACCTAGCCACT	1,49	3	2,01	0,59	Hs.89463	potassium large conductance calcium-activated channel
2304	CAGCTCAGCTG	1,49	3	2,01	0,59	Hs.58414	filamin C, gamma (actin-binding protein-280)
2305	TCAATAAATGT	1,49	3	2,01	0,59	Hs.106747	ESTs, Weakly similar to AF217508_1 uncharacterized b
2306	CACTCACACCC	1,99	4	2,01	0,73	Hs.24447	sigma receptor (SR31747 binding protein 1)
2307	GTGAAACCTGT	3,49	7	2,01	1,1	Hs.272795	hypothetical protein FLJ20359
2308	ATCATACCACG	0	2	2,00	2,8	Hs.97259	ESTs
2309	AACGGGGCCCT	0	2	2,00	2,8	Hs.97203	small inducible cytokine subfamily A (Cys-Cys), memb
2310	TCCCCGGTCAG	0	2	2,00	2,8	Hs.80562	gelsolin (amyloidosis, Finnish type)
2311	GCGCATCAAAA	0	2	2,00	2,8	Hs.59761	ESTs
2312	AATTTCAAGCA	0	2	2,00	2,8	Hs.5476	serine protease inhibitor, Kazal type, 5
2313	ATCCCACTACT	0	2	2,00	2,8	Hs.3991	ESTs

2314	ATCCGCTGGGG	0	2	2,00	2,8	Hs.30954	phosphomevalonate kinas	
2315	ACTGTGGACTG	0	2	2,00	2,8	Hs.285122	ESTs, Weakly similar to S53869 laminin beta-2 chain	5
2316	AGAGAAGAATG	0	2	2,00	2,8	Hs.2841	neuromedin U	
2317	AGGATTGTTTG	0	2	2,00	2,8	Hs.283545	ESTs	
2318	GTAAAGATTTG	0	2	2,00	2,8	Hs.278629	ESTs	10
2319	ACTATGGATAG	0	2	2,00	2,8	Hs.275511	EST	
2320	GTTAGGCACGA	0	2	2,00	2,8	Hs.272800	hypothetical protein FLJ20456	
2321	TGCCACCAACA	0	2	2,00	2,8	Hs.271411	beta-site APP-cleaving enzyme 2	15
2322	AAATGGGAACA	0	2	2,00	2,8	Hs.271226	ESTs	
2323	GGGGTTTGTTT	0	2	2,00	2,8	Hs.258455	EST	
2324	ACATAGTCTGA	0	2	2,00	2,8	Hs.25766	ESTs	20
2325	TATGCTGAAAT	0	2	2,00	2,8	Hs.255277	ESTs	
2326	TCACTCCATT	0	2	2,00	2,8	Hs.254914	EST, Weakly similar to NICE-1 protein [H.sapiens]	
2327	TCTTGGAACA	0	2	2,00	2,8	Hs.25431	KIAA1219 protein	25
2328	CAATAAAATTC	0	2	2,00	2,8	Hs.250236	EST	
2329	GGCTTTTGTTT	0	2	2,00	2,8	Hs.230730	EST, Moderately similar to RLA1_HUMAN 60S ACIDIC	30
2330	AGTTTGTTTTA	0	2	2,00	2,8	Hs.212570	EST	
2331	TTCCAAGTGA	0	2	2,00	2,8	Hs.198862	fibulin 2	
2332	CAAGTGGGTGT	0	2	2,00	2,8	Hs.187685	ESTs	
2333	TGCAGGGACCT	0	2	2,00	2,8	Hs.173043	metastasis-associated 1- like 1	35
2334	TACTTCACCCA	0	2	2,00	2,8	Hs.169517	aldehyde dehydrogenase 5	
2335	CTTTGATTTAT	0	2	2,00	2,8	Hs.165590	ribosomal protein S13	40
2336	TGTTGTTTTT	0	2	2,00	2,8	Hs.145211	Homo sapiens mRNA; cDNA DKFZp434K1111 (from	
2337	GTAGCGCCTCC	0	2	2,00	2,8	Hs.143212	cystatin F (leukocystatin)	45
2338	CTAGTGGCGGC	0	2	2,00	2,8	Hs.142043	ESTs, Weakly similar to ALU8_HUMAN ALU	
2339	ACCTCACCTGG	0	2	2,00	2,8	Hs.137585	UDP glycosyltransferase 2 family, polypeptide B11	50
2340	CTTGTTCAAAA	0	2	2,00	2,8	Hs.137560	ESTs, Moderately similar to AMSH [H.sapiens]	
2341	CCTCTTTCCAG	0	2	2,00	2,8	Hs.134615	ESTs	
2342	TCTTAGTTCTA	0	2	2,00	2,8	Hs.130729	ESTs	
2343	CACCTTATAGT	0	2	2,00	2,8	Hs.117582	CGI-43 protein	55
2344	AGCTTCTACCA	0	2	2,00	2,8	Hs.11261	small proline-rich protein 2A	
2345	GTCAAGCCCAA	0	2	2,00	2,8	Hs.105033	ESTs, Weakly similar to SPR2J protein [M.musculus]	60
2346	AACCTTATCATT	0	2	2,00	2,8	Hs.103368	ESTs	

2347	ATGTGCTTCCG	1	2	2,00	0,43	Hs.76494	proline arginine-rich end leucine-rich repeat protei
2348	CCTTTTGTCC	1	2	2,00	0,43	Hs.62601	Homo sapiens mRNA; cDNA DKFZp586K1318 (from
2349	CTCTGTTTACA	1	2	2,00	0,43	Hs.5947	mel transforming onco- gene (derived from cell line NK
2350	GAAGTGCTGCT	1	2	2,00	0,43	Hs.21812	ESTs
2351	CCATTGCAGTC	1	2	2,00	0,43	Hs.207659	EST
2352	CCACTGCACGC	1	2	2,00	0,43	Hs.202669	thiopurine S- methyltransferase
2353	GTGGTGTACAC	1	2	2,00	0,43	Hs.168102	Human proteinase acti- vated receptor-2 mRNA, 3'UTR
2354	ATAAATAAATT	1	2	2,00	0,43	Hs.16677	hypothetical protein FLJ10506
2355	TTGATAAATAA	1	2	2,00	0,43	Hs.139226	replication factor C (activa- tor 1) 2 (40kD)
2356	GCAAAAGCCCG	1	2	2,00	0,43	Hs.109798	G8 protein
2357	TAAATATGGG	0,5	1	2,00	0,22	Hs.98401	Homo sapiens mRNA full length insert cDNA clone EURO
2358	CTTTGGTTTGC	0,5	1	2,00	0,22	Hs.8895	ESTs
2359	CCAAAGGAGAA	0,5	1	2,00	0,22	Hs.8889	serine hydroxymethyltransferase
2360	TGTACCTTTTC	0,5	1	2,00	0,22	Hs.8172	EST (soluble)
2361	TGTTAAGTGTT	0,5	1	2,00	0,22	Hs.78825	matrin 3
2362	TACAAGCTGAG	0,5	1	2,00	0,22	Hs.77508	glutamate dehydrogenase 1
2363	TCTGCGGGTGG	0,5	1	2,00	0,22	Hs.76159	ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton
2364	TATCAATATTC	0,5	1	2,00	0,22	Hs.7306	secreted frizzled-related protein 1
2365	ATGTTTTGTAA	0,5	1	2,00	0,22	Hs.6853	carbohydrate (N- acetylglucosamine 6-O) sulfotransfer
2366	GCTTTTGTG	0,5	1	2,00	0,22	Hs.6048	FEM-1-like death receptor binding protein
2367	CTGGAGACCCA	0,5	1	2,00	0,22	Hs.56729	lymphocyte-specific pro- tein 1
2368	TTCAGAATAAA	0,5	1	2,00	0,22	Hs.50848	hypothetical protein FLJ20331
2369	ACAATGAAGCA	0,5	1	2,00	0,22	Hs.285665	Homo sapiens mRNA; cDNA DKFZp564P013 (from clone
2370	GCCTGTGGGGT	0,5	1	2,00	0,22	Hs.285565	ESTs
2371	CAGCAAGGCTT	0,5	1	2,00	0,22	Hs.283714	30 kDa protein
2372	CAAGGCACCAA	0,5	1	2,00	0,22	Hs.28107	ESTs
2373	TACCAGAGTCC	0,5	1	2,00	0,22	Hs.279927	hypothetical protein
2374	ATTTTTGTAA	0,5	1	2,00	0,22	Hs.27413	adaptor protein containing



							pH domain, PTB domain and
2375	TCTGTTACACC	0,5	1	2,00	0,22	Hs.272759	KIAA1457 protein
2376	ACGTTTGATTT	0,5	1	2,00	0,22	Hs.27263	KIAA1458 protein
2377	AAGAGATGTTT	0,5	1	2,00	0,22	Hs.26799	DKFZP564D0764 protein
2378	TTGGTCAGGGT	0,5	1	2,00	0,22	Hs.264381	EST
2379	TGGAGCTATGA	0,5	1	2,00	0,22	Hs.261655	EST
2380	AGACTCAGGCC	0,5	1	2,00	0,22	Hs.24305	ESTs
2381	GTTTCATCCTTG	0,5	1	2,00	0,22	Hs.236894	ESTs, Highly similar to LRP1_HUMAN LOW-DENSITY
2382	TATCTTGTTGC	0,5	1	2,00	0,22	Hs.23296	ESTs
2383	GTTTGTTTCCT	0,5	1	2,00	0,22	Hs.21143	ESTs, Weakly similar to KIAA1532 protein [H.sapiens]
2384	AAGACACTGTT	0,5	1	2,00	0,22	Hs.20707	hypothetical protein R31240_1
2385	CCTAGAATCTG	0,5	1	2,00	0,22	Hs.20196	adenylate cyclase 9
2386	GTCGGGGGAGA	0,5	1	2,00	0,22	Hs.18844	ESTs
2387	ATGTTGTCAAT	0,5	1	2,00	0,22	Hs.1845	MHC class I region ORF
2388	TTTTCCTCAG	0,5	1	2,00	0,22	Hs.184242	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase)
2389	ACATTTCATTA	0,5	1	2,00	0,22	Hs.18192	Ser/Arg-related nuclear-matrix protein (plenty of pr
2390	TTAGCCAGGGT	0,5	1	2,00	0,22	Hs.180610	splicing factor proline/glutamine rich (polypyrimidi
2391	GGTGGAAAAAA	0,5	1	2,00	0,22	Hs.178728	methyl-CpG binding domain protein 3
2392	GGGCAGAATAA	0,5	1	2,00	0,22	Hs.164690	ESTs
2393	GGTGCCCGGCA	0,5	1	2,00	0,22	Hs.163593	ribosomal protein L18a
2394	TAGCTGAGGCA	0,5	1	2,00	0,22	Hs.159557	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
2395	CGGATTCAATT	0,5	1	2,00	0,22	Hs.14763	ESTs
2396	AAGAAAGGGAA	0,5	1	2,00	0,22	Hs.140908	ESTs
2397	TCAAAGGGCA	0,5	1	2,00	0,22	Hs.125158	ESTs
2398	CTCTCCTTGCC	0,5	1	2,00	0,22	Hs.118738	KIAA0800 gene product
2399	TTGCAGAGGGG	0,5	1	2,00	0,22	Hs.110373	ESTs
2400	TGTCTGCAGAA	0,5	1	2,00	0,22	Hs.107418	ESTs
2401	AGCTTCCGCTT	0,5	1	2,00	0,22	Hs.106529	CGI-65 protein
2402	CTCACACACAC	0,5	1	2,00	0,22	Hs.104311	novel protein with MAM domain

## Patentansprüche

1. Verfahren zur Identifizierung der in Haut exprimierten Gene bei Menschen in vitro, **dadurch gekennzeichnet**, daß man

- ein Gemisch von in menschlicher Haut exprimierten genetisch codierten Faktoren aus menschlicher Haut gewinnt und
- das in a) gewonnenen Gemisch einer Seriellen Analyse der Genexpression (SAGE) unterwirft, und dadurch die in menschlicher Haut exprimierten Gene identifiziert und ihre Expression quantifiziert.

2. Verfahren zur Identifizierung der für die Homeostase der Haut bedeutsamen Gene bei Menschen in vitro, **dadurch gekennzeichnet**, daß man

- ein Gemisch von in menschlicher Haut exprimierten genetisch codierten Faktoren aus menschlicher Haut gewinnt,
- das in a) gewonnenen Gemisch einer Seriellen Analyse der Genexpression (SAGE) unterwirft, und dadurch

die in menschlicher Haut exprimierten Gene identifiziert und ihre Expression quantifiziert und  
c) die Analyseergebnisse aus b) mit Expressionsmustern anderer Gewebe vergleicht und so die Gene identifiziert, die in Haut und anderen Geweben unterschiedlich stark (differenziell) exprimiert werden.

3. Verfahren zur Bestimmung der Homeostase der Haut bei Menschen in vitro, dadurch gekennzeichnet, daß man  
a) ein Gemisch von Proteinen, mRNA-Molekülen oder Fragmenten von Proteinen oder mRNA-Molekülen aus menschlicher Haut gewinnt,  
b) das gewonnene Gemisch auf das Vorhandensein und gegebenenfalls die Menge von mindestens einem der Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen untersucht, die mittels Serieller Analyse der Genexpression (SAGE) als in Haut und anderen Geweben unterschiedlich stark (differenziell) exprimiert identifiziert werden,  
c) die Untersuchungsergebnisse aus b) mit den mittels Serieller Analyse der Genexpression (SAGE) identifizierten Expressionsmustern vergleicht und  
d) das in b) untersuchte Gemisch gesunder bzw. in Homeostase befindlicher Haut zuordnet, wenn es überwiegend Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen enthält, die in Haut stärker exprimiert werden als in anderen Geweben, oder das in b) untersuchte Gemisch kranker bzw. in gestörter Homeostase befindlicher Haut zuordnet, wenn es überwiegend Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen enthält, die in anderen Geweben stärker exprimiert werden als in Haut.

4. Verfahren nach Anspruch 3, dadurch gekennzeichnet, daß man  
in Schritt b) das gewonnene Gemisch auf das Vorhandensein und gegebenenfalls die Menge von mindestens einem der Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen untersucht, die in den Tabellen 1 bis 5 in Spalte 7 durch ihre UniGene-Accession-Number definiert werden,  
in Schritt c) die Untersuchungsergebnisse aus b) mit den in den Tabellen 1 bis 5 in den Spalten 3 und 4 angegebenen relativen Expressionsfrequenzen sowie den in Spalte 5 angegebenen Expressionsquotienten vergleicht und  
in Schritt d) das in b) untersuchte Gemisch gesunder bzw. in Homeostase befindlicher Haut zuordnet, wenn es überwiegend Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen enthält, die in Haut mindestens doppelt so stark exprimiert werden wie in anderen Geweben, oder das in b) untersuchte Gemisch kranker bzw. in gestörter Homeostase befindlicher Haut zuordnet, wenn es überwiegend Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen enthält, die in anderen Geweben mindestens doppelt so stark exprimiert werden wie in Haut.

5. Verfahren nach Anspruch 3 oder 4, dadurch gekennzeichnet, daß man  
in Schritt b) das gewonnene Gemisch auf das Vorhandensein und gegebenenfalls die Menge von mindestens einem der Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen untersucht, die in den Tabellen 2 bis 5 in Spalte 7 durch ihre UniGene-Accession-Number definiert werden,  
in Schritt c) die Untersuchungsergebnisse aus b) mit den in den Tabellen 2 bis 5 in den Spalten 3 und 4 angegebenen relativen Expressionsfrequenzen sowie den in Spalte 5 angegebenen Expressionsquotienten vergleicht und  
in Schritt d) das in b) untersuchte Gemisch gesunder bzw. in Homeostase befindlicher Haut zuordnet, wenn es überwiegend Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen enthält, die in Haut mindestens 5-fach so stark exprimiert werden wie in anderen Geweben, oder das in b) untersuchte Gemisch kranker bzw. in gestörter Homeostase befindlicher Haut zuordnet, wenn es überwiegend Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen enthält, die in anderen Geweben mindestens 5-fach so stark exprimiert werden wie in Haut.

6. Verfahren nach einem der Ansprüche 3 bis 5, dadurch gekennzeichnet, daß man  
in Schritt b) das gewonnene Gemisch auf das Vorhandensein und gegebenenfalls die Menge von mindestens einem der Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen untersucht, die in den Tabellen 3 bis 5 in Spalte 7 durch ihre UniGene-Accession-Number definiert werden,  
in Schritt c) die Untersuchungsergebnisse aus b) mit den in den Tabellen 3 bis 5 in den Spalten 3 und 4 angegebenen relativen Expressionsfrequenzen sowie den in Spalte 5 angegebenen Expressionsquotienten vergleicht und  
in Schritt d) das in b) untersuchte Gemisch gesunder bzw. in Homeostase befindlicher Haut zuordnet, wenn es überwiegend Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen enthält, die in Haut mindestens 10-fach so stark exprimiert werden wie in anderen Geweben, oder das in b) untersuchte Gemisch kranker bzw. in gestörter Homeostase befindlicher Haut zuordnet, wenn es überwiegend Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen enthält, die in anderen Geweben mindestens 10-fach so stark exprimiert werden wie in Haut.

7. Verfahren nach einem der Ansprüche 3 bis 6, dadurch gekennzeichnet, daß man  
in Schritt b) das gewonnene Gemisch auf das Vorhandensein und gegebenenfalls die Menge von mindestens einem der Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen untersucht, die in den Tabellen 4 und 5 in Spalte 7 durch ihre UniGene-Accession-Number definiert werden,  
in Schritt c) die Untersuchungsergebnisse aus b) mit den in den Tabellen 4 und 5 in den Spalten 3 und 4 angegebenen relativen Expressionsfrequenzen sowie den in Spalte 5 angegebenen Expressionsquotienten vergleicht und  
in Schritt d) das in b) untersuchte Gemisch gesunder bzw. in Homeostase befindlicher Haut zuordnet, wenn es überwiegend Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen enthält, die in Haut mindestens 20-fach so stark exprimiert werden wie in anderen Geweben, oder das in b) untersuchte Gemisch kranker bzw. in gestörter Homeostase befindlicher Haut zuordnet, wenn es überwiegend Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen enthält, die in anderen Geweben mindestens 20-fach so stark exprimiert werden wie in Haut.

8. Verfahren nach einem der Ansprüche 3 bis 7, dadurch gekennzeichnet, daß man  
in Schritt b) das gewonnene Gemisch auf das Vorhandensein und gegebenenfalls die Menge von mindestens einem der Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen untersucht, die in Tabelle 5

in Spalte 7 durch ihre UniGene-Accession-Number definiert werden.

in Schritt c) die Untersuchungsergebnisse aus b) mit den in Tabelle 5 in den Spalten 3 und 4 angegebenen relativen Expressionsfrequenzen sowie den in Spalte 5 angegebenen Expressionsquotienten vergleicht und in Schritt d) das in b) untersuchte Gemisch gesunder bzw. in Homeostase befindlicher Haut zuordnet, wenn es überwiegend Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen enthält, die in Haut mindestens 100-fach so stark exprimiert werden wie in anderen Geweben, oder das in b) untersuchte Gemisch kranker bzw. in gestörter Homeostase befindlicher Haut zuordnet, wenn es überwiegend Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen enthält, die in anderen Geweben mindestens 100-fach so stark exprimiert werden wie in Haut.

9. Verfahren zur Bestimmung der Homeostase der Haut bei Menschen in vitro, dadurch gekennzeichnet, daß man a) ein Gemisch von Proteinen, mRNA-Molekülen oder Fragmenten von Proteinen oder mRNA-Molekülen aus menschlicher Haut gewinnt,

b) in dem gewonnenen Gemisch mindestens zwei der Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen quantifiziert, die mittels eines Verfahrens nach Anspruch 2 als für die Homeostase der Haut bedeutsam identifiziert werden,

c) die Expressionsverhältnisse der mindestens zwei Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen zueinander bestimmt,

d) die Expressionsverhältnisse aus c) mit den Expressionsverhältnissen vergleicht, die für die in b) quantifizierten Moleküle typischerweise in homeostatischer Haut vorliegen, insbesondere mit den Expressionsverhältnissen, die sich aus Tabelle 6, Spalte 3 bzw. aus den Tabellen 1 bis 5, Spalte 4 ergeben, und

e) das in a) gewonnene Gemisch gesunder bzw. in Homeostase befindlicher Haut zuordnet, wenn die Expressionsverhältnisse der untersuchten Haut den Expressionsverhältnissen in Homeostase befindlicher Haut entsprechen, oder das in a) gewonnene Gemisch kranker bzw. in gestörter Homeostase befindlicher Haut zuordnet, wenn die Expressionsverhältnisse der untersuchten Haut von den Expressionsverhältnissen in Homeostase befindlicher Haut abweichen.

10. Verfahren nach einem der Ansprüche 1 bis 9, dadurch gekennzeichnet, daß man in Schritt a) das Gemisch aus einer Hautprobe, insbesondere aus einer Vollhautprobe oder aus einer Epidermisprobe gewinnt.

11. Verfahren nach einem der Ansprüche 3 bis 9, dadurch gekennzeichnet, daß man in Schritt a) das Gemisch mittels Mikrodialyse gewinnt.

12. Verfahren nach einem der Ansprüche 3 bis 8, 10 und 11, dadurch gekennzeichnet, daß man die Untersuchung in Schritt b) auf das Vorhandensein und gegebenenfalls die Menge von mindestens einem der Proteine oder Proteinfragmente mittels einer Methode durchführt, die ausgewählt ist unter

- Ein- oder zweidimensionaler Gelelektrophorese

- Affinitätschromatographie

- Protein-Protein-Komplexierung in Lösung

- Massenspektrometrie, insbesondere Matrix Assistierter Laser Desorptions Ionisation (MALDI) und insbesondere

- Einsatz von Proteinchips,

oder mittels geeigneter Kombinationen dieser Methoden.

13. Verfahren nach einem der Ansprüche 9 bis 11, dadurch gekennzeichnet, daß man in Schritt b) die Quantifizierung mindestens zweier Proteine oder Proteinfragmente mittels einer Methode durchführt, die ausgewählt ist unter

- Ein- oder zweidimensionaler Gelelektrophorese

- Affinitätschromatographie

- Protein-Protein-Komplexierung in Lösung

- Massenspektrometrie, insbesondere Matrix Assistierter Laser Desorptions Ionisation (MALDI) und insbesondere

- Einsatz von Proteinchips,

oder mittels geeigneter Kombinationen dieser Methoden.

14. Verfahren nach einem der Ansprüche 3 bis 8, 10 und 11, dadurch gekennzeichnet, daß man die Untersuchung in Schritt b) auf das Vorhandensein und gegebenenfalls die Menge von mindestens einem der mRNA-Moleküle oder mRNA-Molekülfragmente mittels einer Methode durchführt, die ausgewählt ist unter

- Northern Blots,

- Reverse Transkriptase Polymerasekettenreaktion (RT-PCR),

- RNase-Schutzexperimente,

- Dot-Blots,

- cDNA-Sequenzierung,

- Klon-Hybridisierung,

- Differential Display,

- Subtraktive Hybridisierung,

- cDNA-Fragment-Fingerprinting,

- Total Gene Expression Analysis (TOGA)

- Serielle Analyse der Genexpression (SAGE) und insbesondere

- Einsatz von Nukleinsäurechips,

oder mittels geeigneter Kombinationen dieser Methoden.

15. Verfahren nach einem der Ansprüche 9 bis 11, dadurch gekennzeichnet, daß man in Schritt b) die Quantifizierung mindestens zweier mRNA-Moleküle oder mRNA-Molekülfragmente mittels einer Methode durchführt, die ausgewählt ist unter

- Northern Blots,

- Reverse Transkriptase Polymerasekettenreaktion (RT-PCR),
- RNase-Schutzexperimente,
- Dot-Blots,
- cDNA-Sequenzierung,
- Klon-Hybridisierung,
- Differential Display,
- Subtraktive Hybridisierung,
- cDNA-Fragment-Fingerprinting,
- Total Gene Expression Analysis (TGEA)
- Serielle Analyse der Genexpression (SAGE) und insbesondere
- Einsatz von Nukleinsäurechips,

oder mittels geeigneter Kombinationen dieser Methoden.

16. Verfahren nach einem der Ansprüche 3 bis 8, 10, 11, 12 und 14, dadurch gekennzeichnet, daß man in Schritt b) auf das Vorhandensein und gegebenenfalls die Menge von 1 bis etwa 5000, bevorzugt 1 bis etwa 1000, insbesondere etwa 10 bis etwa 500, vorzugsweise etwa 10 bis etwa 250, besonders bevorzugt etwa 10 bis etwa 100 und ganz besonders bevorzugt etwa 10 bis etwa 50 der Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen untersucht, die in den Tabellen 1 bis 5 in Spalte 7 durch ihre UniGene-Accession-Number definiert werden.

17. Verfahren nach einem der Ansprüche 9 bis 11, 13 und 15, dadurch gekennzeichnet, daß man in Schritt b) 1 bis etwa 5000, bevorzugt 1 bis etwa 1000, insbesondere etwa 10 bis etwa 500, vorzugsweise etwa 10 bis etwa 250, besonders bevorzugt etwa 10 bis etwa 100 und ganz besonders bevorzugt etwa 10 bis etwa 50 der Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen quantifiziert, die in den Tabellen 1 bis 5 in Spalte 7 durch ihre UniGene-Accession-Number definiert werden.

18. Test-Kit zur Bestimmung der Homeostase der Haut bei Menschen in vitro, umfassend Mittel zur Durchführung der Verfahren nach einem der Ansprüche 3 bis 17.

19. Biochip zur Bestimmung der Homeostase der Haut bei Menschen in vitro, umfassend einen Träger und

auf diesem immobilisierte Sonden, die zur spezifischen Bindung an mindestens eines der Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen befähigt sind, die in den Tabellen 1 bis 5 in Spalte 7 durch ihre UniGene-Accession-Number definiert werden.

20. Biochip nach Anspruch 19, umfassend 1 bis etwa 5000, bevorzugt 1 bis etwa 1000, insbesondere etwa 10 bis etwa 500, vorzugsweise etwa 10 bis etwa 250, besonders bevorzugt etwa 10 bis etwa 100 und ganz besonders bevorzugt etwa 10 bis etwa 50 voneinander verschiedene Sonden.

21. Biochip nach Anspruch 19 oder 20, umfassend Nukleinsäuresonden, insbesondere RNA- oder PNA-Sonden, besonders bevorzugt DNA-Sonden.

22. Biochip nach Anspruch 21, umfassend Sonden mit einer Länge von etwa 10 bis etwa 1000, insbesondere etwa 10 bis etwa 800, vorzugsweise etwa 100 bis etwa 600, besonders bevorzugt etwa 200 bis etwa 400 Nukleotiden.

23. Biochip nach Anspruch 19 oder 20, umfassend Peptid- oder Proteinsonden, insbesondere Antikörper.

24. Verwendung der Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen, die in den Tabellen 1 bis 5 in Spalte 7 durch ihre UniGene-Accession-Number definiert werden, als Marker für die Homeostase der Haut bei Menschen.

25. Testverfahren zum Nachweis der Wirksamkeit von kosmetischen oder pharmazeutischen Wirkstoffen zur Aufrechterhaltung oder Förderung der Homeostase der Haut bzw. zur Behandlung pathologischer Zustände der Haut, wie Neurodermitis, Sonnenbrand, Psoriasis, Sklerodermie, Ichtyosis, atopische Dermatitis, Akne, Seborrhoe, Lupus erythematoses, Rosacea, Melanoma, Basalioma, Hautkarzinom, Hautsarkom, in vitro, dadurch gekennzeichnet, daß man

a) den Hautstatus durch ein Verfahren nach einem der Ansprüche 3 bis 17, oder mittels eines Test-Kits nach Anspruch 18, oder mittels eines Biochips nach einem der Ansprüche 19 bis 23 bestimmt,

b) einen Wirkstoff zur Aufrechterhaltung oder Förderung der Homeostase der Haut bzw. zur Behandlung pathologischer Zustände der Haut einmal oder mehrmals auf die Haut aufbringt,

c) erneut den Hautstatus durch ein Verfahren nach einem der Ansprüche 3 bis 17, oder mittels eines Test-Kits nach Anspruch 18, oder mittels eines Biochips nach einem der Ansprüche 19 bis 23 bestimmt, und

d) die Wirksamkeit des Wirkstoffs durch den Vergleich der Ergebnisse aus a) und c) bestimmt.

26. Test-Kit zum Nachweis der Wirksamkeit von kosmetischen oder pharmazeutischen Wirkstoffen zur Aufrechterhaltung oder Förderung der Homeostase der Haut bzw. zur Behandlung pathologischer Zustände der Haut in vitro, umfassend Mittel zur Durchführung des Verfahrens nach Anspruch 25.

27. Verwendung der Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen, die in den Tabellen 1 bis 5 in Spalte 7 durch ihre UniGene-Accession-Number definiert werden, zum Nachweis der Wirksamkeit von kosmetischen oder pharmazeutischen Wirkstoffen zur Aufrechterhaltung oder Förderung der Homeostase der Haut bzw. zur Behandlung pathologischer Zustände der Haut, wie Neurodermitis, Sonnenbrand, Psoriasis, Sklerodermie, Ichtyosis, atopische Dermatitis, Akne, Seborrhoe, Lupus erythematoses, Rosacea, Melanoma, Basalioma, Hautkarzinom, Hautsarkom.

28. Screening-Verfahren zur Identifikation von kosmetischen oder pharmazeutischen Wirkstoffen zur Aufrechterhaltung oder Förderung der Homeostase der Haut bzw. zur Behandlung pathologischer Zustände der Haut, wie Neurodermitis, Sonnenbrand, Psoriasis, Sklerodermie, Ichtyosis, atopische Dermatitis, Akne, Seborrhoe, Lupus erythematoses, Rosacea, Melanoma, Basalioma, Hautkarzinom, Hautsarkom in vitro, dadurch gekennzeichnet, daß man

a) den Hautstatus durch ein Verfahren nach einem der Ansprüche 3 bis 17, oder mittels eines Test-Kits nach Anspruch 18, oder mittels eines Biochips nach einem der Ansprüche 19 bis 23 bestimmt.

- b) einen potentiellen Wirkstoff zur Aufrechterhaltung oder Förderung der Homeostase der Haut bzw. zur Behandlung pathologischer Zustände der Haut einmal oder mehrmals auf die Haut aufbringt.
  - c) erneut den Hautstatus durch ein Verfahren nach einem der Ansprüche 3 bis 17, oder mittels eines Test-Kits nach Anspruch 18, oder mittels eines Biochips nach einem der Ansprüche 19 bis 23 bestimmt, und
  - d) wirksame Wirkstoffe durch den Vergleich der Ergebnisse aus a) und c) identifiziert.
29. Verwendung der Proteine, mRNA-Moleküle oder Fragmente von Proteinen oder mRNA-Molekülen, die in den Tabellen 1 bis 5 in Spalte 7 durch ihre UniGene-Accession-Number definiert werden, zur Identifikation von kosmetischen oder pharmazeutischen Wirkstoffen zur Aufrechterhaltung oder Förderung der Homeostase der Haut bzw. zur Behandlung pathologischer Zustände der Haut, wie Neurodermitis, Sonnenbrand, Psoriasis, Sklerodermie, Ichthyosis, atopische Dermatitis, Akne, Seborrhoe, Lupus erythematodes, Rosacea, Melanoma, Basalioma, Hautkarzinom, Hautsarkom.
30. Verfahren zur Herstellung einer kosmetischen oder pharmazeutischen Zubereitung zur Aufrechterhaltung oder Förderung der Homeostase der Haut bzw. zur Behandlung pathologischer Zustände der Haut, wie Neurodermitis, Sonnenbrand, Psoriasis, Sklerodermie, Ichthyosis, atopische Dermatitis, Akne, Seborrhoe, Lupus erythematodes, Rosacea, Melanoma, Basalioma, Hautkarzinom, Hautsarkom, dadurch gekennzeichnet, daß man
- a) wirksame Wirkstoffe mit Hilfe des Verfahrens nach Anspruch 28, oder der Verwendung nach Anspruch 29 bestimmt und
  - b) als wirksam befundene Wirkstoffe mit kosmetisch und pharmakologisch geeigneten und verträglichen Trägern vermischt.

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